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MICROBIAL INOCULANTS FOR MULTI-STRESS TOLERANCE IN CROPS: MICROBIOLOGICAL MECHANISMS AND COMMUNITY INTERACTIONS

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Abstract-Climate change is aggravating occurrence, extent and co-occurrence of abiotic stresses like drought, salinity and heat hence posing an immense challenge to crop productivity and soil health across the world. These stresses nearly always interact in native agroecosystems, but most mitigation approaches have focused on individual responses to stress and the microbiology of stress. This review provides a critical synthesis of the current developments in the field of agricultural microbiology as as far as multi-stress tolerance microbial inoculants are concerned on the crop plants. It specifically focuses on microbiological processes, inter-microbial community behavior and cross-tolerance effects when subjected to combined abiotic stress conditions. The role of stress-tolerant plant-growth-promoting rhizobacteria, endophytic bacteria, arbuscular mycorrhizal fungi, and useful fungi in strengthening the ability of plants to withstand drought, salinity and heat was evaluated. Single-taxon, and consortium-based approaches are discussed, with their merits and shortcomings being discussed. The principal microbial pathways that support multi-stress tolerance such as ACC deaminase activity, phytotranscriptional modulation, exopolysaccharide and osmolyte production, antioxidant enzyme induction, volatile organic compound signaling, and transcriptional reorganization of host stress-responsive genes are discussed. It also explores the role of microbial network features like functional redundancy, keystone taxa and community stability in propelling phytomicrobiome stability under complicated stress conditions. The findings of metagenomics, metatranscriptomics and systems-biology studies are combined to provide an insight into how the microbiome assemble, how they modify functions in response to multifaceted stresses, and how plants and microbes coordinate themselves. Lastly, key problems in translation such as rhizosphere competence, interactions of native microbiome, formulation stability, and unequal performance in the field are crucially assessed. Future research directions that would establish next -generation ecologically sound multi-stress-tolerant microbial inoculants are suggested. Taken together, this review highlights the dominant role of microbiome-based strategies in ensuring the ability of agriculture to be sustainable and climate-resilient.

Keywords: *Multi-stress tolerance, Plant–microbe interactions, Microbial consortia, Abiotic stress, Rhizosphere microbiome.*

Introduction-

The increasing rate and severity of abiotic stressors, such as drought, salinity, and heat, are a serious menace to the future of food security in the world by disrupting crop production and soil well-being (Singh et al., 2023). All of these limitations are likely to a certain degree to happen simultaneously or sequentially due to the impact of climatic changes, which leads to the losses of production up to 51 to 82 percent, which is why resilient and sustainable strategies are necessary to enhance crop resilience (Ali et al., 2023). Although the agronomic interventions are often implemented to address individual stressors, integration of beneficial plant microbiomes presents a strong mechanism of instilling cross-tolerance of combined abiotic stresses (Ali et al., 2023; Singh et al., 2023). Positive microbes such as stress-tolerant plant-growth-promoting rhizobacteria, endophytes and symbiotic fungi have dynamic relationships with host plants and can be used to endure multifaceted environmental perturbations both directly and indirectly (Singh et al., 2023). These microbial consortia, which are taxonomically diverse endophytes, arbuscular mycorrhizal fungi, and plant-growth-promoting rhizobacteria, are synergistic in order to alleviate the physiological and molecular effects of drought, heat, and salinity (Ali et al., 2023; Michael, 2021). Based on this, the proposed review provides a critical assessment of the microbiological processes and interaction in the community that support the engineering of the next-generation microbial inoculants to confer multi-stress tolerance to crop plants (Ali et al., 2023; Khan, 2023).

Multi-Stress Microbial Inoculants of Crop Plants.

The use of positive microorganisms as bioinoculants is an ecologically friendly and advanced solution to promote plant development in various abiotic stresses, especially because scientific communities have moved away from the single stressor to the multistressor interactions of stress factors on plants in natural ecosystems (Singh et al., 2023; Staiano et al., 2025). Plant-growth-stimulating microorganisms, which include a wide range of bacteria, fungi, and mycorrhizae, are increasingly acknowledged to have the ability to increase resilience in plants through the ability to modify physiological activities, enhance nutrient uptake, and cause systemic resistance (Ali et al., 2023; Naseem et al., 2025). Recent sequencing technologies have further clarified the complex phyto-microbiome and found out the synergistic functioning of taxonomically diverse microbial communities to mitigate the physiological and molecular effects of drought, heat, and salinity (Meng et al., 2023; Singh et al., 2023). Here, the modern literature on stress-tolerant plant-growth-promoting bacteria, endophytes and beneficial fungi has been synthesised systematically and how individual taxa or consortia might allow cross-tolerance to a range of abiotic stressors listed (Ali et al., 2023; Muhammad et al., 2025).

Bacteria that grow and promote growth in plants in the presence of stress.

Plant-growth-promoting rhizobacteria, especially those that belong to genera of *Bacillus* and *Pseudomonas* have shown extraordinary abilities to counteract physiological effects of drought, salinity and heat stress in a variety of biochemical pathways. As an example, genome mining has discovered particular drought-adaptive clusters of genes in the bacteria, as well as, in *Bacillus velezensis*, and in the bacteria, *Pseudomonas fluorescens*, which are directly attributed to improved plant growth on water-limited environments (Shahzad et al., 2025). These adaptive responses include the synthesis of exopolysaccharides and osmolytes to maintain cellular hydration and cell integrity under osmotic stress, and synthesis of phytohormones and heat shock proteins to stabilize the plant metabolism during extremes in temperature (Hnini et al., 2025; Shahzad et al., 2025). Besides, certain isolates, like, but not limited to, *Bacillus altitudinis* FD48, have significantly enhanced relative water content and membrane stability in rice during drought, showing the direct physiological value of such bacteria (Singh et al., 2023). Similarly, isolates of *Pseudomonas lini* and *Serratia plymuthica* have also increased the drought resistance of jujube seedlings, and isolates of *Enterobacter ludwigii* have greatly relieved water shortage in alfalfa (Hnini et al., 2025).

Endophytic Bacteria and Secretinolyses and their Stress Acclimation.

Living microorganisms that are endophytic, and do not cause disease, are key to better host stress acclimation, having intimate physical associations that enable them to take up direct metabolic interaction and regulate plant defence pathways. To serve as an illustration, thermotolerance in wheat is induced by bacterial endophytes like *Enterobacter sp.*, and these actions are not accompanied by substantial changes in the native endophytic microbiome, whereas *Enterobacter, Pseudomonas, Streptomyces,* and *Variovorax spp.* that inhabit desert environments are capable of enhancing drought and salinity tolerance of host plants (Dagher et al., 2025; Kozaeva et al., 2024).

Positive Fungi in Multi-Stress Resistance.

There exist beneficial fungi, such as arbuscular mycorrhizal fungi and *Trichoderma* spp. which have a significant role in multi-stress resilience by enhancing the effectiveness of water uptake, ion homeostasis regulation, and systemic defence activation. An example is that, under water-stress conditions, inoculation with a fungi (e.g. *Trichoderma spp.*) promotes the activity of antioxidant enzymes, uptake, chlorophyll production, proline concentration, and production of phytohormones, which in turn stimulate growth and tolerance to drought

(Hnini et al., 2025), and co-inoculation techniques of fungi with a bacterium (e.g. *pseudomonas fluorescens*) and a rhizophage.

Single Taxa Versus Microbial Consortia Strategies.

Single-strain inoculants are more easily attributed in mechanistic terms and formulated, but microbial consortia are showing increasingly greater and more consistent stress resistance by functional complementarity and niche partitioning. Cosmopolitan microbes can be used to create resistant self-sustaining communities by football players (consortia) that can resist environmental change and outcompete native soil microorganisms, which is crucial in single-strain settings but minimal in consortia (Ray et al., 2020). An example is the heat tolerance enhanced by the inoculation of wheat with the symbioses, *Azospirillum*, and *Bacillus velezensis* which reduce oxidative stress, and the rapid growth of the heat-stressed tomato by the inoculation with *paraburkholderia phytofirmans* through ACC deaminase activity (Shahzad et al., 2025). Likewise, concomitant presence of an arbuscular mycorrhizal fungus and *Bacillus thuringiensis, *Azospirillum brasilense* and *Bradyrhizobacter japonicum*, mitigates the deleterious effects of drought in soybean, whereas a combination of *Azospirillum brasilense* and *Bacillus thuringiensis* alleviates drought effects in *Lavandula dentata*, allowing it to survive in semiarid environments (Hnini et al., 2023)

Microbiological Mechanisms that confer Multi-Stress Tolerance.

The ability of microbial inoculants to provide cross-tolerance to drought, salinity and heat depends on complex network of biochemical and molecular pathways that adjust the physiology of the plant on several levels. These are synergistic processes that decrease ethylene concentrations through the ACC deaminase, produce exopolysaccharides to protect root cells and maintain cell turgor during osmotic pressure (Coleman-Derr and Tringe, 2014; Muhammad et al., 2025). In addition, the oxidative damage induced by environmental extremes is alleviated by the induction of antioxidant enzyme systems as well as scavenging reactive oxygen species. Stress-responsive genes and volatile organic compounds by microbes also coordinate plant adaptation (Ait‑El‑Mokhtar et al., 2023; Idbella et al., 2025). According to emerging data, the quality of the proposed product is frequently augmented with the help of additional strains that are combined into consortia and which exploit the functional diversity to further increase the growth of plants, their tolerance to stress, and the stability of rhizosphere (Benmrid et al., 2025).

ACC Deaminase Action and Phytohormone Alteration.

This enzyme is 1-aminocyclopropane 1-carboxylase deaminase which is crucial in reducing the effects of stress on the inhibitory effect of ethylene by breaking the precursor ACC down into a-keto butyrate and ammonia, which would otherwise lead to senescence and growth arrest (Gahlot, 2026). CCC Using this phytohormonal regulation, the ACC deaminase-producing bacteria including *Burkholderia phytofirmans* and *Pseudomonas putida* maintain root elongation and biomass accretion under heat and salinity stress respectively, whilst *Azospirillum brasilense* alters abscisic acid levels to enhance drought tolerance (Khan, 2023; Kumar et al., 2020). On top of controlling ethylene, microbial inoculants produce auxins such as indole -acetic acid to trigger the growth of roots systems, thus enhancing water and nutrient uptake in cases of their limited supply (Bhardwaj et al., 2014; Ibanez et al., 2023).

Exopolysaccharide Synthesis and Osmolyte Synthesis.

Plant-growth-promoting bacteria generate exopolysaccharides that are essential intermediates of soil structure and root-microbe interface to boost water retention and create protective biofilms to counter desiccation and ion toxicity (Ferreira et al., 2025; Han, 2024). These big-molecular-weight polymers enhance adhesion of bacteria to the root surfaces and combine soil particles to stabilize the rhizosphere environment and increase the hydraulic conductivity of the soil during drought and saline environments (Alturki et al., 2023; Morcillo and Manzanera, 2021). Simultaneously, the presence of beneficial microbes facilitates the osmoprotective compounds that include proline, glycine betaine, and soluble sugars to accumulate and keep the cell intact and functional under osmotic stress due to the balance in internal water potential (Pradhan et al., 2025). This osmotic adaptation often goes together with microbial induction of host antioxidant enzymes systems such as superoxide dismutase, catalase, and peroxidase that, collectively, counteract the reactive oxygen species produced on drought, salinity, and heat stress (Saleem et al., 2021; Sani and Yong, 2021; Verma et al., 2024).

Enzyme Induction of antioxidant enzymes and reactive oxygen species scavenging.

Abiotic stresses (a drought, salinity, heat, etc.) usually cause the overproduction of reactive oxygen species in plant tissues, which causes oxidative damage of lipids, proteins, and nucleic acids. To alleviate this toxicity, beneficial microbes enhance the enzymatic antioxidant defence systems of the plant such as superoxide dismutase, catalase, and peroxidase which when combined together have the ability to scavenge harmful radicals and maintain cellular homeostasis (Fadiji et al., 2022; Vaghela et al., 2025). This enzyme activation is typically accompanied by the osmolytes synthesis of small-molecule by microorganisms, which structure stability cellular components and counteracts the deleterious effects of oxidative stress, e.g. trehalose and proline (Gamalero & Glick, 2022; Paravar et al., 2023).

The use of Volatile Organic Compounds in Stress Signalling in the Plant.

Microbial volatile organic compounds are airborne signalling molecules that have the ability to regulate plant physiology and cause systemic tolerance to abiotic stresses even without making physical contact. The specific compounds 2,3-butanediol and 3-hydroxy-2-butanone were shown to boost photosynthesis, uptake of iron, and stomatal closure, which gave resistance to drought and salinity at a systemic level

(Poudel et al., 2021; Shaffique et al., 2022). These emissions cause stress tolerance in related plants by causing the biosynthesis of reactive oxygen species scavengers and changes in gene expression (Khan & Zulfiqar, 2023).

In addition to volatile signalling, microbial inoculants directly alter transcriptional state of host plants by up- or down-regulating stress-responsive genes in pathways, including abscisic acid biosynthesis, ion transport and cellular detoxification, which are known as induced systemic tolerance (Zandi &Schnug, 2022; Zhao et al., 2025).

Control of Stress-Reactive Genes in Plants.

The beneficial microorganisms regulate host gene expression to promote abiotic stress tolerance through up-regulation of the relevant pathways in stress perception, signal transduction, and stress protective metabolism. The stress-tolerant bacteria inoculation often induces genes that encode antioxidant enzymes (superoxide dismutase and catalase) and at the same time suppresses ethylene-biosynthetic pathways to avoid stress-induced senescence (Dhiman et al.,2026; Singh etal., 2023). Besides, they induce defence signatures and secondary metabolic features, which trigger systemic resistance responses and regulate hormonal crosstalk to support plant development under unfavourable environments (Ali et al., 2023; Khanna et al., 2022). This transcriptional reprogramming is often accompanied by better production of secondary metabolites - flavonoids, phytoalexins and carotenoids - strong antioxidants against reactive oxygen species and an amplified protective defence of the cell (Koza et al., 2022; Lopes et al., 2021). These secondary metabolites are often mediated by microbial release of effector molecules which priming the immune system of the plant to generate a defence priming state that ensures more swift and strong activation of defence responses once more when exposed to stress (Liu &, Zhang, 2015). It is epigenetic and metabolic preparedness leading to this primed state, which allows the plant to efficiently utilize its defenses resources, and reduces the fitness costs associated with constitutive defence activation and maximizes the resilience of the plant in changing environmental environments.

Under Combined Abiotic Stresses, Microbial Community Interactions.

The dynamic interaction between plants, microbes and environmental stressors leads to an intricate ecological network where the abiotic factors play an important role in influencing the structure, assembly and functions of the microbiomes (Ali et al., 2023). Although there is a surging development in the understanding of plant-microbe interactions during isolated stressors, there is a paucity of mechanistic understanding of microbiome reorganization in response to minor or joint abiotic interferences (Ali et al., 2023). The available literature suggests that individual stressors such as salinity, temperature, etc. induce specific changes in microbial communities composition, typically increasing or decreasing specific genera e.g. Enterobacter or changing the recruitment pattern of hormone-responsive microbes, but the collective response to co-occurring stressors is more complex and remains unresolved (Ali et al., 2023).

Microbial Network Redundancy: Functional Redundancy.

Functional redundancy in the phytomicrobiome serves as a important ecological buffer and in this way, this ensures that essential services of the ecosystem do not suffer as a result of environmental disruption by the loss of individual microbial taxa (Singh et al., 2023). This insurance system enables various, taxonomically different yet functionally alike taxa to play similar roles, e.g. fixing nitrogen or solubilising phosphates, and consequently stabilises interactions between plants and microbes during drought, salinity or heat stress (Khanna et al., 2022). In turn, this redundancy is an important aspect that contributes to the preservation of community functionality under multi-stress conditions and ensures that the plant is not affected by the failure of single inoculants or the repression of native beneficial populations by the extreme abiotic factors (Ali et al., 2023). Although it provides a buffer, the identification of the key-stone taxa is critical towards the comprehension of how certain microbial hubs integrate community-wide responses to stress and provide stability of the network under high stress conditions.

Keystone Taxa in Multi-Stress environment Identified.

The keystone taxa are microbial species that have highly connectedness and disproportionally impact the structure and activity of the phytomicrobiome and are commonly critical hubs that activate interactions between plants and microbes and influence community assembly in adverse environments (Jones et al., 2019). They have a disproportionate impact on the overall community topology compared to their abundance, and often support the acquisition of useful symbionts, and repress pathogenic taxa due to competitive exclusion or the generation of antimicrobial metabolites (Jones et al., 2019).

Stability and Resilience of microbial Networks.

Network stability is the key to the survival and recovery of microbial networks to abiotic perturbations, which are paramount in ensuring that phytomicrobiome is capable of supporting normal functions during and after stressors like drought or salinity (Gao et al., 2022). The existence of a so-called core microbiome these networks is often supported by a critically abundant microbial taxon, which undergoes multifactorial activity, including the promotion of plant growth, and abiotic stress regulation, in a resilient manner (Khan, 2023). The large amount of sequencing data available provides a worthwhile chance to construct synthetic communities with several desirable characteristics, including strong colonisation capacity and functional specialization, as opposed to the single characteristics or taxonomic identity (Dubey et al., 2025). Network analysis has become an effective method to explain such interactions and has shown that as the size and the connectivity of the rhizosphere increase, niche partitioning and stress-resilience increase (Song et al., 2020). Studies have shown that climatic extremes are able to reshape these associations of associations, and the negative association patterns have been found to increase extra strength and stability when faced with turbulence (Bazany et al., 2022).

Clues provided by Metagenomics and Metatranscriptomics.

Omics technologies High-throughput today has transformed the study of plant-microbe interactions by allowing the full characterisation of microbial community structure, functional possibilities, and gene expression profiles in complex abiotic stress conditions (Khan, 2023). Metagenomic studies have shown that Stress responses to drought and salinity disproportionately change the taxonomic composition of the rhizosphere and frequently enrich towards specific core-and-hub microbiota that play important role in host functions despite fluctuations in the environment (Ait-El-Mokhtar et al., 2023; Liu et al., 2025). In addition to these structural observations, metatranscriptomic profiling offers a time-dependent picture of microbial behavior by showing how the regulation of the interaction between plants and microbes is linked to the direct correlation of environmental response and plant immune and symbiosis responses in fine-tuning the associated microbiota in response to nutritional needs and defence responses (Russ et al., 2023).

Systems Biology Techniques of plant-microbe interactions.

It is expected that systems-biology seeks to combine multi-omics to elucidate the intricate network of molecular interactions that dictate the holobiont functionality of plants and microbes under environmental disturbances, taking the reductionist perceptions to a holistic perspective of understanding of resilience properties (Ait-El-Mokhtar et al., 2023). Combined with advances in high-throughput culturing, synthetic biology and computational tools, integrated omics methodologies are also providing a clearer understanding of the organization and functions of diverse natural microbiomes and providing a window to develop artificially engineered microbial assemblies to enhance crop growth, fitness, and resistance to pathogens and many abiotic stresses (Souza et al., 2020; Zenda et al., 2021).

Translational Problems and Field Practices.

Although this has been widely characterised as multi-stress-tolerant microbial characteristics in controlled conditions, the effective transfer of the characteristics to field-scale operation is still a major bottleneck in agricultural microbiology.

The rhizosphere competence and colonisation dynamics are the following:

The effective settlement of the plant-microbe symbioses in the field is essentially limited by the capacity of introduced inoculants to effectively compete with the native populations of microbes over the niche space and root exudates, which is often aggravated by the resource-limited conditions provided by abiotic stress (Sharma, 2020).

The phenomenon of interaction with the Native Microbiome.

The presence of exogenous microbial strains is bound to result in intricate interactions with the host microbiome of the soil whereby competition, antagonism, or synergism can drastically affect the effectiveness and longevity of the inoculant (Gonzalez-Guzman et al., 2021). The heterogeneity of soil and high microbial competition frequently restricts the survival and functionality of inoculated strains, and thus, to create microbial consortia with specific properties, precision microbiome engineering based on multi-omics data is highly recommended to establish sound interactions with native community members (Gahlot, 2026).

Stability Formulations and Delivery Systems.

Formulation technologies to maintain cell viability and metabolic activity throughout storage and delivery systems to provide effective root colonisation under changing field conditions are important in the commercial viability of microbial inoculants (Alturki et al., 2023). Nevertheless, favorable characteristics exhibited by pure cultures in the laboratory often do not occur in the microbial community situation of complexity in the field, which presents a major translational divide between controlled laboratory experiments and practical agricultural application (Russ et al., 2023).

Efficacy in the Field under Various Conditions.

There is a high level of variability in the performance of microbial inoculants in shifting between the controlled and open-field conditions, with the introduced strains often not improving plant growth because of the intricate interaction of soil properties, weather changes, and crop management strategies (Malusa et al., 2021). The variation of the soil structure and conditions further complicates predictions of microbial behaviour in a wide range of field environments, and much advantageous bacterial strains are ecosystem-specific, which reduces their usefulness beyond exceptionally well-defined conditions (Sabater et al., 2025). To a large extent, this inconsistency can be explained by the fact that microbial traits tend to be suppressed or not activated by the unpredictable biotic and abiotic interactions of the plant-soil system, which results in the context-dependent expression of microbial traits (Malusa et al., 2021).

The gaps in knowledge and research directions in the future.

Although plant growth-associated assessments and traits have advanced substantially in depiction, there are certain gaps in comprehension of the precise molecular discussions that allow cross-defense against various abiotic stressors, specifically how combined stressors dissimilarly regulate the expression of microbial genes as contrasted with circumstances where a single-stress condition is in place (Kaul et al., 2021).

Unresolved Mechanistic Questions Unresolved Mechanistic Questions.

One of the troubling gaps that have not yet been resolved is the common mismatch between in-vitro efficacy and in-planta performance through which the most effective strains in the laboratory setting do not form or bring a benefit in the soil setting because of extremely complex and context-dependent plant-microbe and microbe-microbe interactions (Benbrik et al., 2025). Moreover, how exactly multi-stress conditions drive microbiome assembly is poorly understood, especially whether these dynamics are host-mediated or environmental factors are the driving forces (Khanghahi et al., 2024). By clarifying the comparative roles of host genetic regulation and environmental selection pressures, it is crucial to forecast microbiome reaction to climate change, as well as selectively breed crops that are able to actively enlist effective stress-relieving microbes (Ali et al., 2023; Coleman-Derr and Tringe, 2014).

Development of Next Generation Multi Stress Tolerant Inoculants.

The development of inoculants in the future should focus on the choice of microbial strains with ecologically useful characteristics that allow survival and competitiveness in the rhizosphere, instead of being confined to the laboratory screening of plant growth-promoting potential (Benmrid et al., 2023). The application of microbes in consortia formulations is a potentially efficient approach to not only reducing the salinity stress in plants but also biotic stress (Jovanovic & Radovic, 2021).

The introduction of hi-tech technologies known as omics.

The high-throughput metagenomics, metatranscriptomics, and metaproteomics studies are critical to understand the multifaceted functional dynamics in the interaction of plants and microbes under integrated abiotic stress, which helps to identify stress-responsive genes and proteins, which can be used as biomarkers of resilience (Alturki et al., 2023). The identification of the multifaceted core of beneficial microbiota when subjected to a combination of stress factors in the plant microbiome will require a comprehensive insight into the functional and mechanistic aspects of the interaction between plants and microorganisms in the different environment (Ali et al., 2023).

Agricultural Ecological Trends towards Sustainability.

The sustainability and environmental friendliness of the non-native microbial consortia implementation in agricultural systems can be assessed through stringent evaluation of the capacity to ensure that useful functions are not unintentionally disrupted by native soil food webs or that the introduction of antibiotic resistance genes is promoted (Ali et al., 2023). Hence, identifying bona fide plant receptors and transcriptional regulators that control microbiome assembling under combined stress conditions has to be a primary focus of further research to be used in plant breeding or genetic engineering to produce robust, stress-resilient microbiomes (Ali et al., 2023).

Conclusion

The tapping of the multi-stress-tolerant microbial inoculants will be a key approach to improve crop resilience during the unpredictable climatic conditions and the rising soil erosion (Alturki et al., 2023). Though the mechanistic interpretation of plant-microbe interactions has grown substantially, the effectiveness of transferring laboratory-proven strains into the stable field-based practice is an overwhelming challenge because of the complexity of natural soil ecosystems and the variability of the environment (Gonzalez-Guzman et al., 2021). To overcome these translational barriers, there will be a need to shift the paradigm to integrative strategies that will incorporate advanced technologies in the omics field, synthetic community design, and extensive field validation to create robust inoculants that can work under actual agricultural conditions (Alturki et al., 2023; Naseem et al., 2025). Finally, the reasoned development of the next-generation microbial inoculants, based on an in-depth comprehension of microbiome assemblies and functionality, will be mandatory in the attainment of sustainable agricultural output under the increasing conditions of abiotic strains (Ali et al., 2022, 2023).

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