

Rhizosphere Microbiome–Biofertilizer Nexus: Integrating Biological Inputs and Abiotic Stress Tolerance Mechanisms in Horticultural Crops

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ABSTRACT

Climate change is intensifying abiotic stresses such as drought and salinity, threatening horticultural productivity worldwide and creating an urgent need for sustainable, ecologically resilient production strategies. Using a structured narrative review approach, this study synthesizes peer-reviewed literature published between 2020 and 2026, retrieved from Scopus, Web of Science, PubMed, and Google Scholar; to evaluate how beneficial soil microorganisms and biological inputs enhance horticultural crop performance under stress. The objective is to examine the efficacy of Plant Growth-Promoting Rhizobacteria (PGPR), Arbuscular Mycorrhizal Fungi (AMF), and other microbial inoculants in improving growth and yield in tomato (*Solanum lycopersicum*), mediating drought tolerance in grapevine (*Vitis vinifera*) through osmotic adjustment and antioxidant defense, and mitigating salinity-induced ionic toxicity in date palm (*Phoenix dactylifera*) via halotolerant microbial mechanisms. Unlike previous reviews that typically examine a single crop, a single stress type, or a single microbial group in isolation, this review integrates rhizosphere microbial diversity, biofertilizer function, and multi-stress tolerance mechanisms within a single conceptual framework, the Rhizosphere Microbiome–Biofertilizer Nexus. Findings show that rhizosphere microbial diversity functions as a central mediator of nutrient cycling and stress signaling. Comparative evidence across studies further indicates that microbiome engineering and synthetic microbial consortia represent an emerging frontier in horticultural science, although consistent field performance remains constrained by formulation and site-specific limitations. The review concludes that the accumulated evidence positions microbial-based biological inputs as an increasingly indispensable, rather than merely supplementary, component of sustainable horticulture, with direct implications for climate-adaptive agricultural policy and food security.

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1. INTRODUCTION

Global agriculture currently faces an unprecedented convergence of challenges, including a burgeoning human population, declining soil fertility, and the intensifying impacts of climate change (Chaudhary et al., 2022; Yar, 2024). Horticultural crops, which are vital for nutritional security, dietary diversity, and rural economic stability, are particularly sensitive to environmental fluctuations. The scale of the threat is increasingly quantifiable: extreme weather disasters, primarily drought and extreme heat, have historically reduced national cereal production by 9-10 percent and inflicted production losses in the order of hundreds of billions of US dollars worldwide (Lesk et al., 2016).

Salinity presents a parallel and growing constraint, with the most comprehensive global assessment to date estimating that approximately 1,381 million hectares, or 10.7 percent of the world's total land area, are already salt-affected, a figure projected to expand substantially under continued climate warming and unsustainable irrigation practices; in the most severely affected regions, salinity alone can reduce yields of salt-sensitive crops by up to 70 percent (FAO, 2024). Because fruit and vegetable crops contribute disproportionately to human micronutrient intake relative to their cultivated area, losses of this magnitude carry consequences for food security that extend well beyond caloric output.

Traditional intensive farming practices, heavily reliant on synthetic chemical fertilizers and pesticides, have further compounded these pressures, driving soil acidification, water contamination, and the loss of microbial biodiversity (Fasusi et al., 2021). Consequently, there is an urgent need to transition toward sustainable agricultural systems that leverage biological processes to maintain productivity while minimizing environmental footprints (Ammar et al., 2023; Gul & Karimi, 2024). Drought and salinity impose distinct but interacting physiological burdens on horticultural crops. Drought stress disrupts water relations, closes stomata, and suppresses photosynthesis, leading to severe growth inhibition (Ren et al., 2026). Salinity stress simultaneously imposes an osmotic constraint on water uptake and an ionic toxicity from the accumulation of Na⁺ and Cl⁻ in plant tissues, disrupting membrane integrity and metabolic function (Yang et al., 2026). Both stresses converge on shared downstream consequences, including oxidative damage and hormonal imbalance, which is why microbial interventions capable of addressing several of these pathways simultaneously are of particular scientific and practical interest.

The rhizosphere, the narrow zone of soil surrounding plant roots, serves as a biological "hotspot" where intricate interactions between plants and microorganisms occur (Daurova et al., 2026). This microbial community, often referred to as the plant's second genome, plays a fundamental role in nutrient acquisition, pathogen suppression, and stress alleviation. Biofertilizers, defined as substances containing living microorganisms that colonize the rhizosphere or the interior of the plant, have emerged as a cornerstone of sustainable horticulture (Samantaray et al., 2024). These biological inputs do not merely supply nutrients; they actively modulate the host plant's physiological and molecular pathways to enhance resilience (Yang et al., 2026), and, at the community level, can be deliberately assembled into synthetic consortia designed for specific stress-mitigation functions (Wang et al., 2024).

Existing literature on this topic, while extensive, remains fragmented rather than critically integrated. Ammar et al., (2023); Chaudhary et al., (2022) provide broad overviews of biofertilizer classes and mechanisms but do not examine crop-specific stress interactions in depth. Fasusi et al., (2021) focus on rhizosphere management for general agricultural sustainability rather than on horticultural crops under multi-stress conditions specifically. Samantaray et al., (2024) advance the field by linking bio-inoculants to abiotic stress amelioration, yet, in common with most PGPR-effectiveness studies, evidence is drawn largely from single-stress, single-crop trial designs rather than from a comparative synthesis across stress types.

Similarly, studies on AMF-mediated drought mitigation (e.g., in grapevine and citrus systems) and on microbial consortia for salinity amelioration have tended to develop in parallel literatures with limited cross-referencing, so that mechanistic parallels between drought and salinity tolerance pathways are rarely made explicit. This pattern of largely siloed, single-variable investigation is itself a limitation: most previous studies have examined the effectiveness of one type of microbe against one type of stress in one crop system, while the integration of rhizosphere microbial community structure, applied biofertilizers, and multi-stress tolerance mechanisms across several horticultural crops has not been systematically synthesized. This constitutes the central research gap this review addresses.

The novelty of the present review lies precisely in this integration. Rather than treating biofertilizer efficacy, rhizosphere microbial diversity, drought tolerance, and salinity mitigation as separate literatures, this review deliberately places all four within a single conceptual framework, the Rhizosphere Microbiome–Biofertilizer Nexus, and examines them jointly across three model horticultural systems (tomato, grapevine,

and date palm) that together span vegetable and perennial fruit crops. This integrative, cross-crop, cross-stress framing distinguishes the present synthesis from prior single-stress or single-crop reviews and allows convergent mechanisms, such as cross-tolerance and microbiome engineering, to be identified across contexts in which they have so far been discussed separately.

Accordingly, this review aims to: (i) evaluate the impact of biofertilizers on the growth and physiology of model horticultural crops such as tomato; (ii) elucidate the physiological and biochemical indicators of drought and salinity tolerance in fruit crops; and (iii) explore the structural diversity of the rhizosphere microbiome as a driver of horticultural performance. Beyond its scientific contribution, this synthesis carries practical implications for sustainable agricultural policy: by clarifying which microbial mechanisms are most consistently associated with stress tolerance across crop systems, the review provides an evidence base that can inform the prioritization of biofertilizer research investment, the design of extension programs for growers transitioning away from synthetic inputs, and the formulation of climate-adaptive horticultural policy in regions, such as Afghanistan and other arid or semi-arid countries, where both drought and secondary soil salinization are pressing constraints on food security. By synthesizing data from recent studies (2020-2026), this review addresses the identified gap and provides a critical, integrative perspective on the future of microbial-based stress management in horticulture.

2. METHOD

This review adopts a narrative synthesis methodology rather than a systematic review or meta-analysis. This choice was deliberate: the body of evidence on the rhizosphere microbiome-biofertilizer nexus spans heterogeneous crop systems (annual vegetables and perennial fruit trees), stress types (drought and salinity), and outcome measures (physiological, biochemical, and yield-related indicators) that are not readily reducible to a common effect size for meta-analytic pooling. A systematic review with a fixed, narrowly defined research question would also have been poorly suited to the conceptually integrative aim of this study, which is to identify convergent mechanisms and cross-cutting themes across otherwise separate literatures. A narrative synthesis, by contrast, permits this kind of thematic integration while remaining transparent and reproducible in its search and selection procedures, which are detailed below.

Because this review is literature-based, no physical research site was involved; the "location" of the research is constituted by the international scientific databases searched. Peer-reviewed articles published between 2020 and 2026 were identified through structured searches of Scopus, Web of Science, PubMed, and Google Scholar, using combinations of the keywords "biofertilizer," "rhizosphere microbiome," "plant growth-promoting rhizobacteria," "arbuscular mycorrhizal fungi," "drought tolerance," "salinity stress," and "horticultural crops." Boolean operators (AND/OR) were used to combine these terms across titles, abstracts, and keywords.

Studies were included if they reported empirical or review-level evidence on microbial-mediated abiotic stress tolerance mechanisms in tomato, grapevine, date palm, or other horticultural species, and were published in English in a peer-reviewed source. Non-peer-reviewed sources (e.g., preprints, theses, conference abstracts without full text), duplicate records, and articles unrelated to horticultural systems or to microbial-mediated stress tolerance were excluded. The literature identification and screening process is summarized in Figure 1.

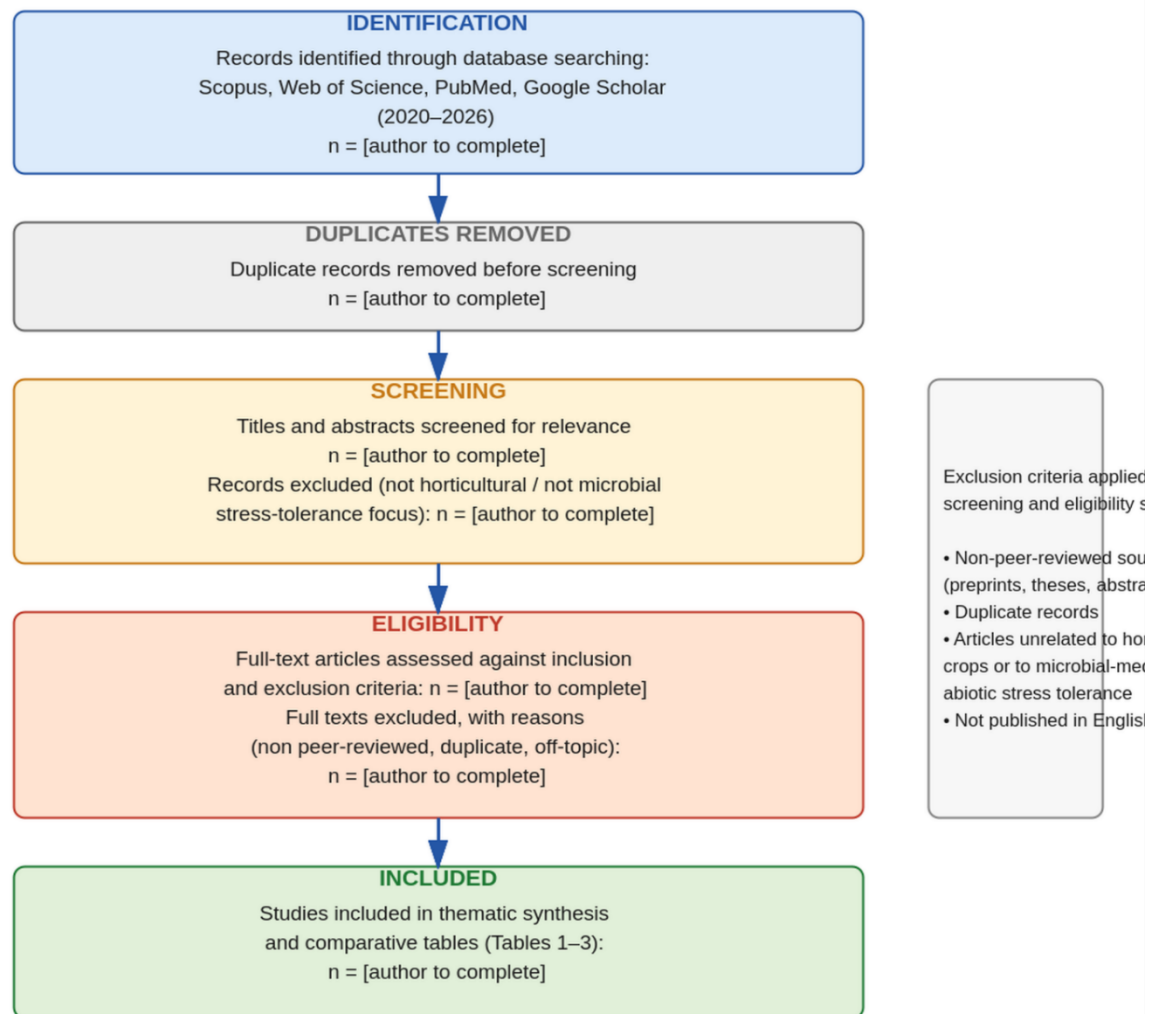


Figure 1. Literature identification and screening flow

Figure 1 Literature identification and screening flow for this narrative review, showing the number of records identified through database searching, the number of duplicates removed, the number of titles and abstracts screened, the number of full texts assessed for eligibility, and the final number of studies included in the thematic synthesis (see table in the Method section; record counts to be completed by the corresponding author from the original search log).

Quality appraisal of candidate studies was based on four criteria: (i) publication in a peer-reviewed, indexed journal; (ii) methodological transparency regarding experimental design, microbial taxa, and measured indicators; (iii) direct relevance to horticultural (as opposed to purely agronomic staple-crop) systems; and (iv) recency, with preference given to studies published within the review window (2020–2026) unless earlier foundational work was required for context.

Selected studies were thematically organized into four domains: (i) biofertilizer efficacy in vegetable crops, (ii) rhizosphere microbial diversity and function, (iii) drought stress physiology and microbial mitigation, and (iv) salinity stress physiology and microbial mitigation. A structured data-extraction matrix was used to code each included article according to crop species, microbial taxon or consortium, growth-promoting or stress-mitigation mechanism, physiological and biochemical indicators measured, and reported outcome.

The results of this coding exercise are presented comparatively in Tables 1-3. Data synthesis proceeded in three stages: (i) familiarization, in which each article was read in full and summarized against the coding matrix; (ii) thematic comparison within each of the four domains to identify convergent findings, contradictions, and methodological limitations; and (iii) integrative narrative synthesis across domains, in which cross-cutting mechanisms (such as cross-tolerance and microbiome engineering) and priority directions for future research were identified, forming the basis of the integrative discussion presented in the following section.

3. RESULTS AND DISCUSSION

Biofertilizers: Mechanisms, Types, and Agricultural Applications

Biofertilizers represent a diverse group of biological agents that enhance plant growth through various direct and indirect mechanisms. They are generally classified based on their microbial composition, including Plant Growth-Promoting Rhizobacteria (PGPR), Arbuscular Mycorrhizal Fungi (AMF), cyanobacteria, and nitrogen-fixing bacteria such as Rhizobium and Azospirillum (Chaudhary et al., 2022). The primary mechanisms of action include biological nitrogen fixation, phosphate and potassium solubilization, and the production of siderophores for iron sequestration (Ammar et al., 2023). Furthermore, many bio-inoculants produce phytohormones such as auxins, gibberellins, and cytokinins, which directly stimulate root architecture and vegetative growth (Ren et al., 2026).

In vegetable production, tomato (*Solanum lycopersicum*) has served as a primary model for assessing biofertilizer efficacy. Recent evidence suggests that the application of multi-strain microbial consortia is often more effective than single-strain inoculants due to functional complementarity (Zhang et al., 2025). This advantage is not merely additive: rationally designed consortia can achieve stable co-colonization and division of metabolic labor among strains, so that nitrogen provision, phosphate solubilization, and phytohormone signaling are distributed across community members rather than concentrated in a single organism, which reduces the metabolic burden on any one strain and improves the odds that at least part of the consortium persists under variable field conditions (Wang et al., 2024). For instance, combining *Bacillus* species with *Trichoderma* fungi has been shown to significantly enhance nutrient uptake and chlorophyll content, leading to substantial yield increases. However, the performance of biofertilizers is frequently influenced by soil type, climatic conditions, and the existing microbial landscape, which represents a significant challenge in achieving consistent field results.

Table 1. Effects of Biofertilizers on Growth and Yield Parameters of Tomato (*Solanum lycopersicum*) Selected Studies (2020-2026)

Study (Author, Year)	Biofertilizer Type	Key Parameters Measured	Main Findings	Source
Zhang et al., (2025)	<i>Bacillus subtilis</i> + <i>Pseudomonas</i> spp.	Plant height, biomass, fruit number	25% increase in yield; improved P-uptake	Agronomy
Ren et al., (2026)	<i>Azotobacter</i> + AMF	Chlorophyll content, lycopene	Enhanced photosynthetic rate and fruit quality	Vegetable Research
Chaudhary et al., (2022)	<i>Rhizobium</i> sp.	Root length, nitrogen content	Significant increase in vegetative vigor	Frontiers in Plant Science

Critical analysis of current literature reveals that while the growth-promoting effects of biofertilizers are well documented, the molecular cross-talk between the inoculant and the host plant is still being unraveled. There is a notable inconsistency in how different tomato cultivars respond to the same microbial strain, suggesting a strong genotype-by-microbe interaction. Moreover, the long-term survival of introduced strains in competitive soil environments remains a major bottleneck for the commercial adoption of biofertilizers (Fasusi et al., 2021), and formulation instability during storage and transport further limits the reliability of translating laboratory-demonstrated effects into field-ready products (Fadiji et al., 2024).

Rhizosphere Microbial Diversity: Structure, Function, and Interaction with Plant Roots

The rhizosphere is an ecological niche characterized by high microbial density and activity, driven by the secretion of plant root exudates (Daurova et al., 2026). These exudates, which include sugars, organic acids, and secondary metabolites, act as signaling molecules that recruit specific microbial taxa. The structure of this microbial community is highly dynamic, influenced by host species, developmental stage, and environmental stressors (Samantaray et al., 2024).

Advances in high-throughput sequencing, such as 16S rRNA and ITS metagenomics, have allowed researchers to map the rhizosphere "core microbiome" of various fruit trees. In perennial horticultural systems, such as citrus and apple orchards, microbial diversity is often positively correlated with tree longevity and productivity (Fasusi et al., 2021). For example, the presence of beneficial Proteobacteria and Bacteroidetes has been linked to enhanced phosphorus mobilization in the rhizosphere of fruit trees (Chaudhary et al., 2022).

Table 2. Dominant Microbial Taxa in the Rhizosphere of Fruit Trees and Their Growth-Promoting Functions (2020-2026)

Microbial Taxon	Associated Crop	Growth-Promoting Mechanism	Effect Observed	Source
Pseudomonas fluorescens	Citrus	Siderophore production	Reduced iron-deficiency chlorosis	Adeleke et al., (2024)
Bacillus amyloliquefaciens	Apple	VOC production	Enhanced branching and biomass	Zhang et al., (2025)
Glomus intraradices (AMF)	Grapevine	Mycelial network formation	Increased water and P absorption	Samantaray et al., (2024)
Streptomyces spp.	Mango	Antibiotic synthesis	Suppression of soil-borne pathogens	Fasusi et al., (2021)
Azospirillum brasilense	Banana	Nitrogen fixation	Improved leaf nitrogen status	Ammar et al., (2023)

The interaction networks within the rhizosphere are governed by complex feedback loops. Plants can actively alter their exudate profile under stress, thereby attracting beneficial microbes that confer systemic resistance (Daurova et al., 2026). However, competition between introduced bio-inoculants and the native microbiome can sometimes lead to microbial interference, whereby the biofertilizer fails to establish itself. This is precisely why the field has begun shifting from single-strain augmentation toward microbiome engineering, in which the entire resident community is deliberately reshaped, rather than a single foreign strain being added in isolation (Han & Yoshikuni, 2022; Samantaray et al., 2024). Engineering the broader plant holobiont in this way is increasingly framed as a route to climate-resilient horticulture, since it targets the ecological compatibility between introduced and resident microbes rather than the performance of an isolated strain alone (Portal-Gonzalez et al., 2025).

Drought Stress Tolerance in Horticultural Crops: Physiological and Biochemical Perspectives

Drought is perhaps the most significant abiotic threat to horticultural productivity in the twenty-first century. In fruit crops such as grapevine (*Vitis vinifera*), drought stress triggers a cascade of physiological responses, beginning with stomatal closure to minimize transpirational water loss (Chattaraj et al., 2025). While this preserves water, it simultaneously limits CO₂ intake, thereby reducing photosynthetic efficiency (Yang et

al., 2026). Biochemical responses involve the accumulation of compatible solutes, such as proline and soluble sugars, which facilitate osmotic adjustment (Ren et al., 2026).

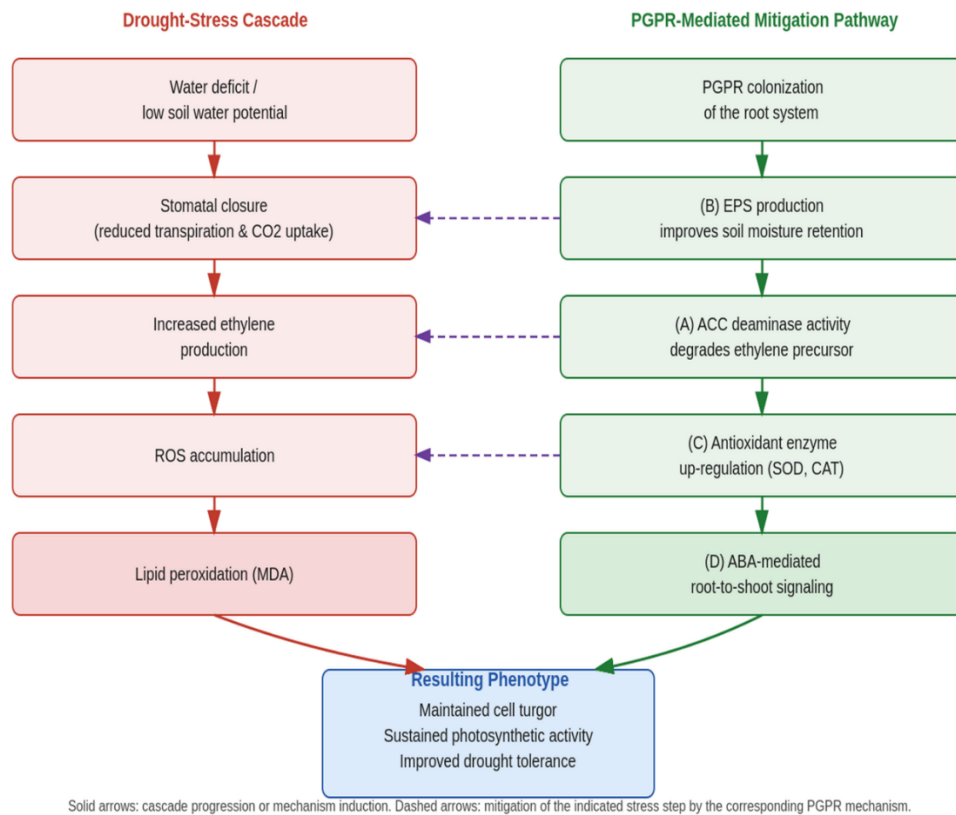


Figure 2. Drought-Stress Respons and PGR-Mediate Mitigation in Grapevine (*Vitis Vinifera*)

Figure 2 Schematic diagram of drought stress response and PGPR mitigation in grapevine. The stress pathway (left) shows increased ethylene production, stomatal closure, and ROS accumulation leading to lipid peroxidation (measured as MDA). The PGPR mitigation pathway (right) shows microbial colonization of the roots, highlighting: (A) ACC deaminase activity reducing ethylene; (B) production of exopolysaccharides (EPS) improving soil moisture retention; (C) up-regulation of antioxidant enzymes (SOD, CAT); and (D) enhanced root-to-shoot signaling via ABA modulation. The center of the diagram shows the resulting drought-tolerance phenotype, characterized by maintained turgor and photosynthetic activity.

Microbial bio-inoculants, particularly PGPR and AMF, have been shown to mitigate drought stress through several pathways. One critical mechanism is the production of the enzyme 1-aminocyclopropane-1-carboxylate (ACC) deaminase, which degrades the precursor of ethylene, a stress hormone that inhibits root growth (Samantaray et al., 2024). By lowering ethylene levels, PGPR allow for continued root elongation even under low water potential, enabling the plant to access deeper soil moisture (Chattaraj et al., 2025). As summarized conceptually in Figure 2, the drought-stress pathway (increased ethylene production, stomatal closure, and ROS-driven lipid peroxidation) is counterbalanced by a PGPR-mediated mitigation pathway involving ACC deaminase activity, exopolysaccharide (EPS) production, antioxidant enzyme up-regulation, and ABA-mediated root-to-shoot signaling, together producing a drought-tolerant phenotype characterized by maintained turgor and photosynthetic activity.

Table 3. Physiological and Biochemical Drought Tolerance Indicators in Grapevine and Selected Fruit Crops (2020-2026)

Crop	Stress Type	Key Indicator	Response Under Stress	Mitigation Strategy	Source
Grapevine	Severe drought	Proline content	3-fold increase	AMF inoculation	Samantaray et al., (2024)
Grapevine	Moderate drought	Stomatal conductance	60% reduction	PGPR (Bacillus)	Chattaraj et al., (2025)
Citrus	Water deficit	MDA levels	Significant increase	Pseudomonas spp.	Adeleke et al., (2024)
Apple	Drought	SOD/CAT activity	Initial rise, then decline	Biochar + PGPR	Zhang et al., (2025)
Peach	Drought	Water use efficiency	Decreased	Azospirillum	Ammar et al., (2023)

Critical observations suggest that the efficacy of microbial-mediated drought tolerance is highly dependent on the timing of inoculation. Pre-conditioning plants with beneficial microbes before the onset of stress appears to be more effective than curative applications (Yang et al., 2026). Furthermore, the role of microbial volatile organic compounds in systemic drought signaling is an emerging area that warrants deeper investigation (Ren et al., 2026).

Salinity Stress: Impacts on Photosynthetic Pigments, Antioxidant Defense, and Growth

Salinity affects a substantial share of irrigated land globally and poses a severe threat to salt-sensitive horticultural crops (FAO, 2024; Yang et al., 2026). The primary impacts of salinity are osmotic stress, which limits water uptake, and ionic toxicity, primarily due to the accumulation of Na⁺ and Cl⁻ ions in plant tissues (Samantaray et al., 2024). These ions interfere with metabolic processes and disrupt the integrity of cellular membranes.

In species such as the date palm (*Phoenix dactylifera*), which is relatively halotolerant, salinity stress still leads to a significant reduction in photosynthetic pigments, including chlorophyll a, chlorophyll b, and carotenoids (Ammar et al., 2023). This degradation is often the result of oxidative stress caused by the overproduction of reactive oxygen species (ROS). To counter this, plants activate an antioxidant defense system comprising enzymes such as superoxide dismutase (SOD), catalase (CAT), and ascorbate peroxidase (APX) (Yang et al., 2026). Halotolerant PGPR play a pivotal role in salinity mitigation. These microbes can maintain high internal osmotic pressure and produce exopolysaccharides that bind Na⁺ ions in the rhizosphere, preventing their uptake by the plant (Chattaraj et al., 2025). Moreover, halotolerant PGPR can modulate the expression of high-affinity potassium transporters, helping the plant maintain a favorable K⁺/Na⁺ ratio (Ren et al., 2026).

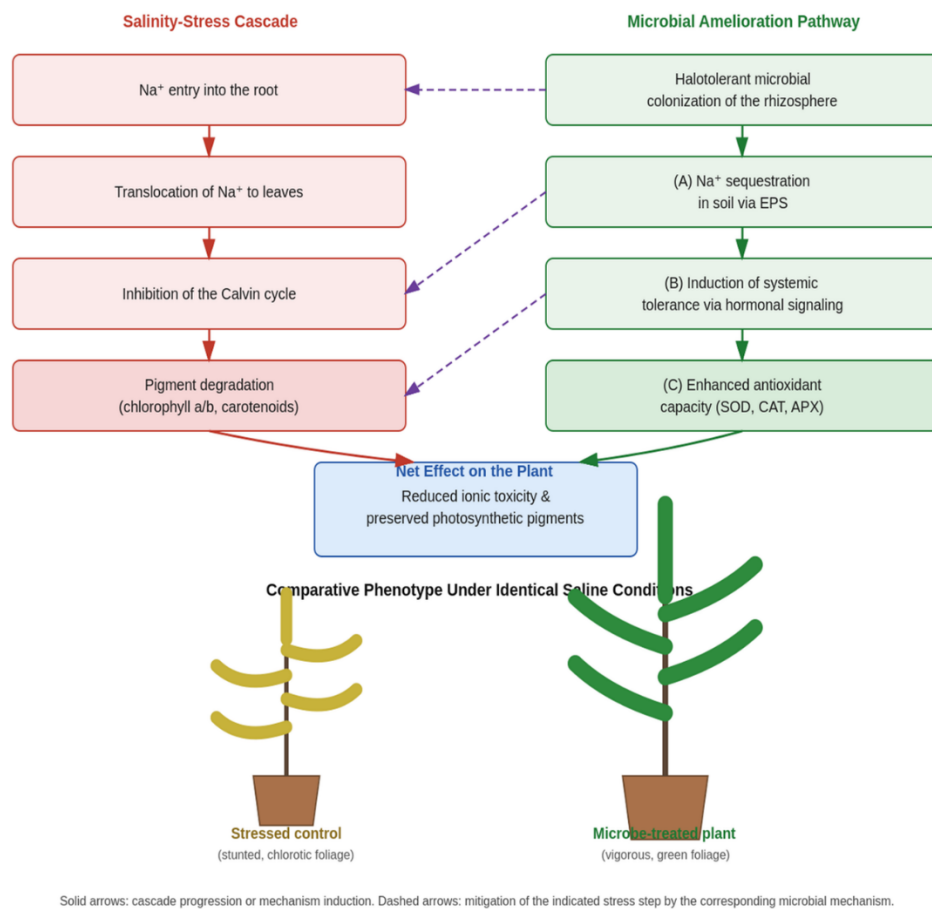


Figure 3. Salinity-Stress Cascade and Microbial Amelioration in Date Palm (*Phoenix dactylifera*)

As illustrated conceptually in Figure 3, the salinity-stress cascade, Na⁺ entry into the root, translocation to leaves, and subsequent inhibition of the Calvin cycle and pigment degradation, is countered by microbial amelioration mechanisms, including rhizospheric Na⁺ sequestration, induction of systemic tolerance, and enhancement of antioxidant capacity.



Dashed conceptual linkage — see Figures 1 and 2 for the full stress-specific mitigation pathways summarized here.

Figure 4. Molecular Cross-Talk Linking Microbial Drought and Salinity mitigation Pathways

Figure 4 presents a complementary molecular schematic of the signaling crosstalk linking the drought and salinity mitigation pathways shown in Figures 2 and 3. Evidence suggests that the use of AMF in conjunction with halotolerant PGPR provides a synergistic effect in saline environments (Samantaray et al., 2024). AMF hyphae can bypass the salt-exclusion zone around the roots to access water and nutrients, while PGPR handle the biochemical detoxification of ions. However, the long-term stability of these microbial effects in naturally saline soils, where salt concentrations fluctuate, remains a critical knowledge gap (Fasusi et al., 2021).

Integrative Perspective: The Rhizosphere Microbiome–Biofertilizer–Abiotic Stress Triangle

The synthesis of the four domains discussed, biofertilizer efficacy, rhizosphere diversity, drought tolerance, and salinity mitigation, reveals a complex abiotic stress triangle in which the rhizosphere microbiome acts as the central mediator (Chaudhary et al., 2022). Comparing across studies, the success of biological inputs appears to depend less on the intrinsic traits of any single inoculant than on its capacity to integrate into and enhance the existing microbial network (Daurova et al., 2026); studies that report inoculant failure tend to attribute it to poor establishment within, rather than direct antagonism from, the resident community, whereas studies reporting success more often describe functional complementarity among co-inoculated strains (Wang et al., 2024).

A critical emerging theme is the concept of cross-tolerance, whereby exposure to one stress (e.g., moderate salinity) mediated by microbes can prime the plant for another stress (e.g., drought) (Yang et al., 2026). This is likely due to overlap in signaling pathways, such as activation of the ABA-dependent pathway and induction of similar antioxidant genes (Ren et al., 2026). Furthermore, the advent of synthetic microbial consortia allows for the design of microbial communities with

specific functional traits tailored to regional stress profiles ([Samantaray et al., 2024](#); [Shayanthan et al., 2022](#)).

Despite these advances, several challenges persist, and a genuinely critical reading of the literature must address why they persist rather than simply cataloguing them. The lab-to-field gap remains significant because controlled-environment trials typically standardize soil moisture, temperature, and native microbial background, whereas open fields expose introduced strains to competition, predation, and abiotic fluctuation simultaneously; consortia and formulations that lack redundancy across these stressors are the ones most likely to fail once translated to field conditions ([Shayanthan et al., 2022](#)).

Commercial-scale application is further constrained by formulation instability, inconsistent shelf-life, and sensitivity to storage temperature and pH, all of which reduce the viable microbial load actually delivered to the rhizosphere at the time of application ([Fadiji et al., 2024](#)). There is also a need for more rigorous, long-term studies that track the ecological impact of repeated biofertilizer applications on native soil health ([Fasusi et al., 2021](#)). Future research should leverage multi-omics approaches, integrating metagenomics, proteomics, and metabolomics, to gain a holistic understanding of the rhizosphere-biofertilizer nexus ([Daurova et al., 2026](#); [Portal-Gonzalez et al., 2025](#)).

Practical Implications, Economic Feasibility, and Field-Scale Application

Translating the mechanistic findings above into practice requires attention to agricultural management, biofertilizer formulation, and climate-adaptation strategy. For agricultural management, the timing-dependence of microbial efficacy noted above (pre-conditioning versus curative application) implies that biofertilizer programs are likely to be most cost-effective when integrated into the planting schedule rather than deployed reactively once stress symptoms appear. For formulation, the persistence problems documented by [Fadiji et al., \(2024\)](#) suggest that investment in carrier technologies and multi-strain formulations with functional redundancy, rather than in single-strain products alone, is likely to yield more consistent returns under variable field conditions.

Digital and precision-agriculture tools, including remote sensing and variable-rate application systems, offer a complementary pathway for matching biofertilizer inputs to site-specific soil and moisture conditions, and their integration with biological inputs represents a promising but still underexplored area of sustainable horticultural management ([Getahun et al., 2024](#)). Economic feasibility remains a genuine constraint on adoption. Multi-strain consortia and engineered synthetic communities are typically more expensive to produce and formulate than single-strain inoculants, and the inconsistency of field performance documented throughout this review directly affects the return on investment that growers can expect, particularly smallholders in resource-constrained settings such as much of rural Afghanistan.

Realizing the productivity gains summarized in Tables 1-3 at scale will therefore likely require parallel investment in extension services, subsidized access to quality-assured biofertilizer products, and further field-scale (as opposed to greenhouse-scale) validation trials before broad policy recommendations can be made with confidence.

4. CONCLUSION

The integration of biological inputs through the rhizosphere microbiome–biofertilizer nexus represents a promising strategy for advancing sustainable horticulture by enhancing crop growth, improving yield, and strengthening tolerance to drought and salinity through coordinated physiological and biochemical mechanisms. The evidence synthesized in this review also highlights the central role of rhizosphere microbial diversity and the growing importance of functionally designed microbial consortia for achieving more reliable performance across diverse agricultural environments.

Nevertheless, because this review is based on a narrative synthesis, focuses primarily on tomato, grapevine, and date palm, and relies substantially on controlled-environment studies, the conclusions remain qualitative and require broader validation under field conditions. Future research should therefore prioritize long-term multi-site field trials and multi-omics approaches to better understand microbiome engineering and cross-tolerance mechanisms. In practice, integrating microbial-based management with locally adapted consortium design, appropriate application timing, quality assurance, and agricultural extension will strengthen climate-resilient horticultural production and support long-term food security.

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