

COMPARATIVE MULTI-OMICS ANALYSIS OF BACTERIAL AND FUNGAL  
ENDOPHYTES FOR ALLEVIATING COMBINED SALINITY AND  
CADMIUM STRESSFazal Rahman<sup>\*1</sup>, Inam Ul Haq<sup>2</sup>, Babar Ali Khan<sup>3</sup>, Maryam Bibi<sup>4</sup>, Muhammad Yaseen<sup>5</sup>,  
Hanif Ullah<sup>6</sup>, Shoaib Ahmad<sup>7</sup>, Razia<sup>8</sup><sup>\*1</sup>PhD Scholar, Department of Chemistry, Shaheed Benazir Butto University Sheringal, KPK,  
Pakistan<sup>2,3</sup>M.Phil Scholer, Department of Botany, Abdul Wali Khan University Mardan (Garden Campus)<sup>4,5,6</sup>M.Phil Scholer, Department of Botany, University of Malakand<sup>7</sup>PhD Scholer, Department of Botany, National Research Tomsk State University, Tomsk Russia<sup>8</sup>M.Phil Scholer, Department of Botany, University of Malakand<sup>\*1</sup>fazalrahmanuom5@gmail.com, <sup>2</sup>uinam406@gmail.com, <sup>3</sup>babarazam2917@gmail.com,<sup>4</sup>maryamimran.7229@gmail.com, <sup>5</sup>yaseenbotanistuom@gmail.com, <sup>6</sup>hanif.bot@uom.edu.pk,<sup>7</sup>shoaibahmad.edu@gmail.com, <sup>8</sup>raziabjr23@gmail.comDOI: <https://doi.org/10.5281/zenodo.22805273>**Keywords**

Bacterial endophytes; Fungal endophytes; Salinity stress; Cadmium stress; multi-omics integration; Plant-microbe interactions; Synthetic microbial consortia; Stress tolerance mechanisms

**Article History**

Received: 30 January 2026

Accepted: 15 March 2026

Published: 31 March 2026

Copyright @Author

Corresponding Author: \*

Fazal Rahman

**Abstract**

The concurrent occurrence of soil salinization and cadmium contamination poses a severe threat to global agricultural productivity, creating synergistic phytotoxic effects that overwhelm plant intrinsic defense mechanisms. Endophytic microorganisms have emerged as critical biological regulators that enhance host tolerance through diverse molecular strategies; however, the comparative functional roles of bacterial versus fungal endophytes under combined stress remain inadequately characterized. This review presents a comprehensive comparative multi-omics analysis of bacterial and fungal endophytes in mitigating simultaneous salinity and cadmium stress. Bacterial endophytes, predominantly *Bacillus*, *Pseudomonas*, and *Enterobacter* species, demonstrate superior capabilities in biomass preservation, active sodium extrusion via  $\text{Na}^+/\text{H}^+$  antiporters, ACC deaminase-mediated ethylene suppression, and nitrogen fixation. Conversely, fungal endophytes including *Epichloë*, *Trichoderma*, and Dark Septate Endophytes excel in osmotic adjustment through compatible solute accumulation, profound antioxidant system induction, and mycelial cadmium biosorption. Through integrated multi-omics approaches encompassing genomics, transcriptomics, proteomics, metabolomics, and ionomics we elucidate the systems-level molecular dialogue governing plant-endophyte symbiosis. Transcriptomic profiling reveals global reprogramming of stress-responsive transcription factors (MYB, WRKY, bHLH) and metabolic pathways (TCA cycle, phenylpropanoid biosynthesis), while metabolomics identifies protective osmolytes (proline, trehalose) and secondary metabolites as key stress-alleviating compounds. Ionomics analysis confirms endophyte-mediated maintenance of  $\text{K}^+/\text{Na}^+$  homeostasis and restricted cadmium translocation to shoots. We propose that synthetic microbial consortia combining complementary

*bacterial and fungal endophytes, guided by multi-omics signatures and precision gene editing, represent a viable strategy for climate-resilient agriculture in salt-affected and metal-contaminated soils.*

## 1. INTRODUCTION

Global agricultural productivity is increasingly severely threatened by the concurrent occurrence of multiple abiotic stresses, among which soil salinization and heavy metal contamination represent two of the most recalcitrant environmental challenges. Globally, salinization affects an estimated 833 million hectares of soil, severely impairing crop development through osmotic stress, ionic toxicity, and metabolic imbalances (Rahim et al., 2025). Simultaneously, anthropogenic activities such as industrial discharge, mining, wastewater irrigation, and the excessive application of chemical fertilizers have led to widespread cadmium ( $\text{Cd}^{2+}$ ) accumulation in arable land. Cadmium is a non-essential, highly toxic heavy metal with high chemical mobility and persistence, exerting severe phytotoxic effects at concentrations as low as  $5\text{--}10\text{ }\mu\text{g/g}$  plant dry weight (Kumar, 2020). When salinity ( $\text{NaCl}$  or  $\text{Na}_2\text{CO}_3$ ) and cadmium co-occur, a scenario frequently observed in coastal, arid, and industrial-adjacent agroecosystems their combined impact is often synergistic rather than merely additive, compounding cellular degradation, photosynthesis collapse, and severe yield loss (Oyebamiji et al., 2024).

To survive such multifaceted stress environments, plants rely on complex molecular defense networks and mutualistic associations with endophytic microorganisms. Endophytes, comprising diverse bacterial and fungal taxa that asymptotically colonize internal host tissues, act as biological regulators of host growth, ion homeostasis, stress signaling, and contaminant detoxification. While both bacterial and fungal endophytes confer enhanced tolerance to individual stresses, their functional strategies, metabolic contributions, and physiological trade-offs differ significantly under combined salinity and cadmium stress (Salam et al., 2026).

Elucidating the intricate symbiotic mechanisms under dual-stress conditions requires a systems-

level perspective. Recent breakthroughs in high-throughput multi-omics technologies encompassing genomics, metagenomics, transcriptomics, proteomics, metabolomics, ionomics, and phenomics have revolutionized our understanding of plant-endophyte interactions. By integrating multi-omics layers, researchers can trace functional pathways from gene expression down to protein synthesis, metabolic flux, and physiological phenotype. This review delivers a comprehensive comparative analysis of bacterial and fungal endophytes in mitigating combined salinity and cadmium stress, evaluating their multi-omics signatures, cross-talk networks, and potential for sustainable climate-resilient agriculture (Etesami & Beattie, 2017).

## 2. Physiological and Biochemical Toxicity of Combined Salinity and Cadmium Stress

The co-occurrence of salinity and cadmium creates a severe multi-layered toxic environment within plant tissues. Salinity impairs root water uptake through osmotic stress and causes intracellular sodium ( $\text{Na}^+$ ) and chloride ( $\text{Cl}^-$ ) accumulation, which competes with potassium ( $\text{K}^+$ ) uptake and disrupts essential enzymatic machinery (Gul et al., 2023). Concurrently,  $\text{Cd}^{2+}$  enters root cells by hijacking non-specific divalent cation transporters dedicated to essential nutrients such as iron ( $\text{Fe}^{2+}$ ), zinc ( $\text{Zn}^{2+}$ ), manganese ( $\text{Mn}^{2+}$ ), and calcium ( $\text{Ca}^{2+}$ ). Once inside,  $\text{Cd}^{2+}$  damages chloroplast ultrastructure, distorts thylakoid membranes, inhibits electron transport, and induces severe carbon starvation (Kaushal et al., 2025).

The physiological cascade triggered by this dual toxicity converges on the hyper-induction of reactive oxygen species (ROS), including hydrogen peroxide ( $\text{H}_2\text{O}_2$ ), superoxide radicals ( $\text{O}_2^-$ ), and hydroxyl radicals ( $\text{OH}^\cdot$ ). High ROS accumulation triggers membrane lipid peroxidation quantified by elevated malondialdehyde (MDA) content and causes protein denaturation, nucleic acid

degradation, and accelerated cellular apoptosis (Ben-Laouane et al., 2025). Furthermore, combined stress destabilizes primary carbon and nitrogen metabolic networks. Enzymes critical to sucrose synthesis and starch turnover, such as sucrose synthase (SS), sucrose phosphate synthase (SPS), hexokinase (HXK), and glucosidases ( $\alpha$ -GC,  $\beta$ -GC), exhibit suppressed or erratic activity, starving the plant of energy necessary for stress adaptation (Abed et al., 2025).

Under axenic conditions, plants attempt to counteract these cascading damages by activating endogenous antioxidant enzymes and synthesizing osmolytes. However, under combined salinity and cadmium stress, the plant's intrinsic physiological defenses are rapidly overwhelmed (Sontakke et al., 2025). The excessive metabolic cost of simultaneous ion extrusion, vacuolar cadmium sequestration, and ROS neutralization leads to stunted root and shoot development, leaf chlorosis, and eventual photosynthetic collapse. This physiological threshold highlights the absolute necessity of microbial endosymbionts, which supply exogenous metabolic capabilities that fortify host resistance (Boutafda et al., 2026).

### 3. Comparative Mechanisms of Bacterial vs. Fungal Endophytes in Stress Mitigation

Bacterial and fungal endophytes have evolved distinct evolutionary strategies to ameliorate combined salinity and heavy metal stress in host plants. A meta-analysis of endophyte-plant interactions demonstrates that bacterial endophytes are generally more effective at preserving host plant biomass and maintaining growth rates under stress. In contrast, fungal endophytes excel at regulating host osmotic potential, phytohormonal balances, and antioxidant defense networks, frequently slowing plant vegetative growth as an adaptive trade-off to endure severe environmental stress (Yan et al., 2019).

#### 3.1 Bacterial Endophytic Strategies

Bacterial endophytes belonging to genera such as *Bacillus*, *Pseudomonas*, *Enterobacter*, *Pantoea*, *Burkholderia*, and *Sphingomonas* deploy direct

metabolic mechanisms to alter host physiology and root-zone biochemistry. Under high salinity, bacterial endophytes express active  $\text{Na}^+/\text{H}^+$  antiporters and cation efflux pumps that actively transport  $\text{Na}^+$  out of the cytoplasm, preserving host intracellular  $\text{K}^+/\text{Na}^+$  ratios (Fadiji et al., 2025). Concurrently, they synthesize 1-aminocyclopropane-1-carboxylate (ACC) deaminase, an enzyme that cleaves the immediate precursor of ethylene, thereby suppressing stress-induced ethylene spikes and preventing premature senescence and growth arrest (Orozco-Mosqueda et al., 2026).

To mitigate  $\text{Cd}^{2+}$  toxicity, bacterial endophytes secrete low-molecular-weight organic acids (e.g., citric, oxalic, and malic acids) and biosurfactants that alter root surface charge and soil pH. They produce siderophores that chelate  $\text{Cd}^{2+}$ , restricting its bioavailability and root uptake, or facilitating safe intracellular accumulation within bacterial cell walls and extracellular polymeric substances (EPS). Furthermore, bacterial endophytes boost host nitrogen and phosphorus availability via biological nitrogen fixation and phosphate solubilization via acid phosphatase secretion, supplying essential nutrients needed to rebuild stress-damaged cellular components (Das et al., 2025).

#### 3.2 Fungal Endophytic Strategies

Fungal endophytes, including *Epichloë*, *Trichoderma*, Dark Septate Endophytes (DSEs), *Serendipita*, *Tetraploa*, and various *Sordariomycetes*, establish extensive internal hyphal networks that alter host systemic biology. Dark Septate Endophytes and Arbuscular Mycorrhizal Fungi (AMF) exhibit exceptional resistance to cadmium and salinity, utilizing their chitin- and glucan-rich cell walls to passively biosorb and immobilize  $\text{Cd}^{2+}$  ions, thereby preventing their translocation into photosynthetic shoot tissues (Zhang et al., 2025).

Fungal endophytes induce profound osmotic adjustment in host plants by driving the synthesis and accumulation of compatible solutes, including proline, trehalose, glycine betaine, and polyols. Rather than pushing biomass expansion, fungal

endophytes reprogram host transcription to prioritize ROS clearance (Mathur & Ulanova, 2023). They upregulate host enzymatic antioxidants superoxide dismutase (SOD), catalase (CAT), ascorbate peroxidase (APX), glutathione reductase (GR), and glutathione S-transferase (GST) and non-enzymatic antioxidants

like reduced glutathione (GSH) and phenolic secondary metabolites. Additionally, fungal endophytes actively sequester  $\text{Cd}^{2+}$  into host root vacuoles via enhanced metal tolerance protein (MTP) and heavy metal ATPase (HMA) transporter activity (Durand et al., 2021).

**Table 1: Comparative Mechanisms and Functional Outcomes of Bacterial vs. Fungal Endophytes Under Dual Stress.**

| Feature / Mechanism                | Bacterial Endophytes                                            | Fungal Endophytes                                                  | Functional Outcome under Combined Stress                                              |
|------------------------------------|-----------------------------------------------------------------|--------------------------------------------------------------------|---------------------------------------------------------------------------------------|
| Growth & Biomass Strategy          | Direct growth promotion; biomass preservation.                  | Growth adjustment trade-off; adaptive growth retardation.          | Sustained structural integrity and prevented complete crop failure.                   |
| Osmotic & $\text{Na}^+$ Regulation | Active $\text{Na}^+$ extrusion via efflux pumps; EPS secretion. | High compatible solute accumulation (trehalose, proline).          | Preserved cell turgor and cellular $\text{K}^+/\text{Na}^+$ homeostasis.              |
| $\text{Cd}^{2+}$ Handling          | Extracellular chelation via siderophores; organic acid binding. | Mycelial biosorption; cell wall binding; vacuolar sequestration.   | Restricted $\text{Cd}^{2+}$ translocation to shoots and grains.                       |
| Phyt hormone Modulation            | High ACC deaminase activity; IAA synthesis.                     | Modulation of ABA, SA, and JA signaling networks.                  | Reduced stress ethylene; enhanced root architecture and stomatal regulation.          |
| Antioxidant System                 | Moderate ROS scavenging; bacterial enzymatic production.        | Profound induction of host SOD, CAT, APX, GST, GSH, and phenolics. | Minimized lipid peroxidation (MDA) and membrane damage.                               |
| Nutrient Mobilization              | Nitrogen fixation (19-47% plant N); phosphate solubilization.   | Extended hyphal networks for phosphorus and micronutrient uptake.  | Countered nutrient deficits caused by $\text{Na}^+$ and $\text{Cd}^{2+}$ competition. |

#### 4. Multi-Omics Integration: Decoding Endophyte-Mediated Stress Tolerance

The integration of multi-omics disciplines provides a systems-level framework for mapping the cascade of molecular events triggered by bacterial and fungal endophytes during combined salinity and cadmium stress. Genomic and metagenomic profiling establishes the baseline potential of microbial symbionts, identifying stress-tolerance operons, metal resistance genes, and biosynthetic gene clusters (BGCs) (Flores et al., 2026). This genomic blueprint is functionally transcribed into RNA, where transcriptomics and metatranscriptomics capture systemic gene expression changes in both host and symbiont,

revealing global reprogramming of defense, transport, and metabolic pathways (Kumar et al., 2026).

These RNA transcripts are subsequently translated into dynamic protein networks. Proteomics and metaproteomics quantify protein accumulation, enzymatic activation, and post-translational modifications, providing direct evidence of functional biochemical machinery, such as active antioxidant enzymes, heat shock proteins, and photosystem repair complexes. Finally, metabolomics and ionomics measure the phenotypic end-products of these protein actions. Metabolomics traces the accumulation of protective osmolytes, secondary metabolites, and

energy intermediates, while ionomics tracks elemental fluxes, confirming the spatial exclusion

of  $\text{Na}^+$ , restoration of  $\text{K}^+$  balance, and vacuolar immobilization of  $\text{Cd}^{2+}$  (Karaliya et al., 2025).

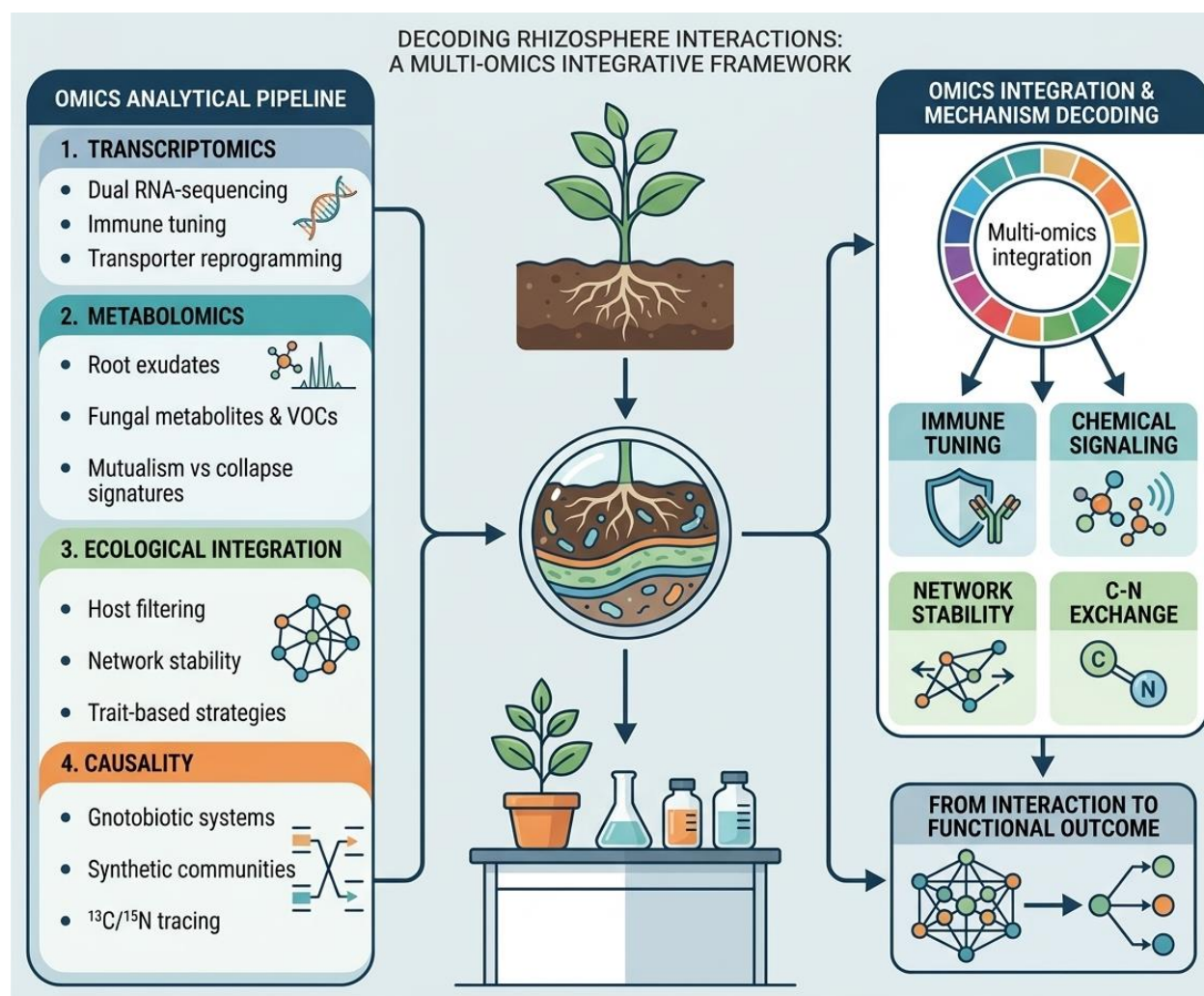


Figure 1: Multi-Omics Integrative Framework and Analytical Pipeline for Decoding Rhizosphere and Endophyte-Host Interactions Under Abiotic Stress

#### 4.1 Genomics and Metagenomics

Genomic sequencing of endophytes has unraveled the genetic architecture underlying their stress-mitigating capabilities. For example, the complete genome assembly of halotolerant endophytes such as *Tetraploa* sp. E00680 and *Pantoea* sp. EEL5 revealed key genes encoding  $\text{Na}^+/\text{H}^+$  antiporters (*SOS1*, *NHX* family), betaine transporters, heavy metal efflux pumps, and tryptophan biosynthesis clusters (Ahmad et al., 2026). In fungal endophytes, AMF display significant genomic diversity, with genome sizes ranging from 39.6 Mb

in *Paraglomus occultum* to 784 Mb in *Gigaspora margarita*, where large genomes contain high proportions of active transposable elements that facilitate rapid genomic adaptation under environmental stress. Metagenomics further reveals that stress exposure alters host endosphere microbiome diversity, enriching functional bacterial and fungal taxa equipped with heavy-metal resistance operons and osmotic defense gene clusters (Meena et al., 2017).

#### 4.2 Transcriptomics and Metatranscriptomics

Transcriptomic profiling demonstrates that endophyte infection induces global transcriptional reprogramming in host tissues under stress. Infection by *Epichloë gansuensis* in *Achnatherum inebrians* alters the expression of over 21% of host transcripts under salt stress, shifting host resources toward secondary metabolism and stress defense. Under combined salinity and cadmium stress, transcriptomic data reveal strong upregulation of genes involved in phenylpropanoid biosynthesis, purine metabolism, the tricarboxylic acid (TCA) cycle, and starch/sucrose metabolism (Khan et al., 2026).

Endophyte inoculation triggers differential expression of major transcription factor (TF) families, including MYB, WRKY, bHLH, and CPP TFs. Genome-wide association studies (GWAS) and transcriptomic linkage under stress have identified candidate genes such as *PLA1* (phospholipase A1), *SPS2* (sucrose phosphate synthase 2), *DTX50* (detoxification efflux carrier), and *NRT1* (nitrate transporter 1), which directly govern secondary metabolite sulfation, sucrose accumulation, heavy metal transport, and root nitrogen assimilation (Simarmata et al., 2026).

#### 4.3 Proteomics and Metaproteomics

Proteomic workflows using liquid chromatography-mass spectrometry (LC-MS) confirm that transcriptomic shifts lead to functional protein accumulation. Under dual stress, endophyte-inoculated plants display

upregulation of proteins critical for redox homeostasis, protein folding and repair (heat shock proteins, HSPs), cell wall catabolism, and intercellular signaling. Proteomic profiling shows increased abundance of key antioxidant enzymes (SOD, CAT, APX, GR, GST) and proteins involved in photosynthesis, mitigating  $\text{Cd}^{2+}$ -induced degradation of photosystem II reaction centers and electron transport proteins (Kumar & Nautiyal, 2026).

#### 4.4 Metabolomics and Ionomics

Metabolomics provides direct insight into cellular physiological states by profiling differentially accumulated metabolites (DAMs). Under combined salinity and cadmium stress, endophyte-colonized plants show massive accumulation of low-molecular-weight metabolites, including sugars (sucrose, trehalose, fructose), amino acids (proline,  $\gamma$ -aminobutyric acid [GABA], glutamate), and organic acids (caffeic acid, fumaric acid, citric acid). Fungal endophytes additionally trigger the accumulation of phenolic secondary metabolites and flavonoids, which serve as non-enzymatic ROS scavengers and internal metal chelators (Katam et al., 2022).

Ionomic profiling quantifies element fluxes across plant tissues. Integrated ionomics reveals that endophytes maintain cellular ion balance by decreasing tissue  $\text{Na}^+$  content, elevating  $\text{K}^+$  and  $\text{Ca}^{2+}$  retention, and restricting  $\text{Cd}^{2+}$  translocation from roots to shoots (Lin et al., 2026).

**Table 2: Integrated Multi-Omics Layers, Molecular Markers, and Symbiotic Functions in Mitigating Salinity and Cadmium Toxicity.**

| Omics Discipline | Key Molecular Targets / Pathways                                                      | Endophytic Microbial Agents                                                        | Integrated Stress Alleviation Mechanism                                                           |
|------------------|---------------------------------------------------------------------------------------|------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------|
| Genomics         | BGCs; <i>SOS1</i> ; <i>NHX</i> ; <i>HMA</i> ; <i>MTP</i> ; betaine transport operons. | <i>Pantoea</i> sp. EEL5, <i>Tetraploa</i> sp. E00680, <i>Gigaspora margarita</i> . | Mapped genetic loci driving $\text{Na}^+$ efflux, metal transport, and osmolyte synthesis.        |
| Transcriptomics  | <i>PLA1</i> , <i>SPS2</i> , <i>DTX50</i> , <i>NRT1</i> ; CPP, MYB, WRKY TFs.          | <i>Epichloë gansuensis</i> , <i>Sordariomycetes</i> sp. EF0801.                    | Systemic transcriptional reprogramming (>20% genome); activated TCA cycle and sucrose metabolism. |

|                     |                                                                                                      |                                                                   |                                                                                                                 |
|---------------------|------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------|
| <b>Proteomics</b>   | SOD, CAT, APX, GR, GST; HSPs; Photosystem II repair proteins.                                        | <i>Pseudomonas qingdaonensis</i> ZCR6, <i>Bacillus subtilis</i> . | Maintained photosynthetic electron transport; restored redox homeostasis and cell wall repair.                  |
| <b>Metabolomics</b> | Caffeic acid, fumaric acid, trehalose, GABA, proline, flavonoids.                                    | <i>Enterobacter bugandensis</i> , <i>Trichoderma</i> spp., DSEs.  | Enhanced osmotic adjustment, non-enzymatic ROS quenching, and carbon allocation.                                |
| <b>Ionomics</b>     | K <sup>+</sup> /Na <sup>+</sup> ratio preservation; root-to-shoot Cd <sup>2+</sup> transfer control. | <i>Bacillus amyloliquefaciens</i> , AMF species.                  | Reduced root Na <sup>+</sup> accumulation; locked Cd <sup>2+</sup> in root vacuoles, preventing shoot transfer. |

### 5. Systemic Cross-Talk and Metabolic Reprogramming in Plant-Endophyte Symbiosis

Multi-omics data reveal that the alleviation of combined salinity and cadmium stress relies on intricate metabolic cross-talk between the host plant and endophyte. A core pathway in this symbiotic exchange is tryptophan metabolism. Host root exudates supply precursor amino acids, including tryptophan, which endophytes utilize to synthesize indole-3-acetic acid (IAA). Secreted IAA acts directly on host root tissue, altering root architecture by stimulating lateral root development and root hair elongation. Expanded root surfaces enhance water and nutrient absorption under saline osmotic shock while simultaneously increasing root apoplastic binding sites for Cd<sup>2+</sup>, effectively immobilizing the metal in underground tissues and limiting shoot translocation (Sontakke et al., 2025).

Simultaneously, endophyte colonization reprograms central carbon allocation. Under dual stress, endophytes upregulate host sucrose phosphate synthase (SPS) and sucrose synthase (SS) activity while regulating hexokinase (HXK)

and glucosidases ( $\alpha$ -GC,  $\beta$ -GC), driving the synthesis and storage of sucrose and trehalose. Accumulating soluble sugars serves a dual role: providing osmotic protection against salinization and supplying carbon skeletons to feed the accelerated TCA cycle. Elevated TCA cycle activity increases ATP generation, fueling energy-demanding defense mechanisms such as active Na<sup>+</sup> extrusion via *SOS1* transporters and Cd<sup>2+</sup> ATPases (*HMA2/HMA3*) vacuolar pumping (Kumar et al., 2026).

Furthermore, environmental co-stress acts as a biological elicitor that triggers epigenetic modifications within endophytic genomes. Combined salinity and cadmium stress alters DNA methylation and histone acetylation patterns, activating silent Biosynthetic Gene Clusters (BGCs) in fungal and bacterial endophytes. Activation of these silent clusters yields novel secondary metabolites, including specialized phenolics, lipopeptides, and biosurfactants, which further strengthen host cellular defense networks (Ahmad et al., 2026).

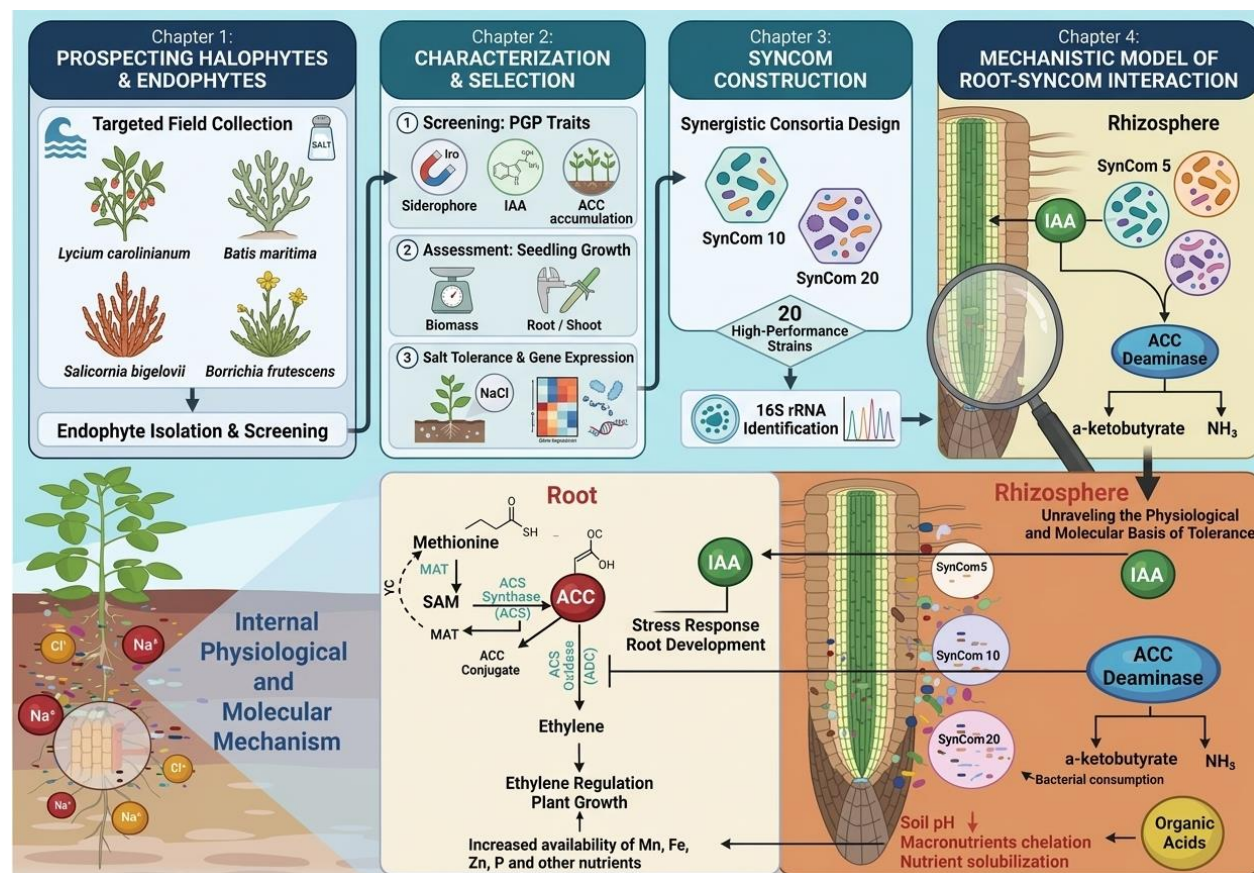


Figure 2: Workflow for Endophyte Isolation, SynCom Construction, and Physiological/Molecular Mechanisms of Plant Growth Promotion and Stress Tolerance

## 6. Emerging Biotechnological Interventions and Field Translation

Despite significant progress in laboratory multi-omics studies, translating endophyte-mediated stress alleviation to field-scale agriculture presents several technical challenges. A major constraint is the "culturable bottleneck": the majority of endophytes detected via metagenomic sequencing remain unculturable using standard media (Ramatsitsi & Manyevere, 2025). To overcome this, genome-guided targeted isolation and metatranscriptomics-assisted culture formulation are being developed to isolate recalcitrant endophytes with specialized stress-mitigating capabilities. Another challenge is performance inconsistency under field conditions, where environmental fluctuations, soil microbiota competition, and variable stress intensities can reduce the efficacy of single-strain bio-inoculants

(Ahmad et al., 2026). To resolve this, researchers are employing synthetic biology and microbial ecology to design Synthetic Microbial Consortia (SynComs). By combining bacterial endophytes (which excel at biomass maintenance, Na<sup>+</sup> extrusion, and nitrogen fixation) with fungal endophytes (which provide superior osmotic adjustment, secondary metabolite synthesis, and mycelial heavy metal biosorption), SynComs establish stable, functionally complementary symbioses (Qiu et al., 2026). Additionally, combining multi-omics with precision gene editing tools like CRISPR/Cas9 enables targeted modification of host regulatory nodes. Editing promoter regions of candidate genes identified through multi-omics such as *SOS1*, *HMA3*, or stress-responsive transcription factors can enhance host responsiveness to endophyte signaling. Integrating multi-omics workflows, SynCom bio-

formulations, and molecular breeding provides a viable pathway for restoring agricultural productivity in salt-affected and heavy metal-polluted soils (Etesami & Beattie, 2017).

### Conclusion

The escalating prevalence of combined salinity and cadmium stress in agricultural ecosystems demands innovative, sustainable solutions beyond conventional breeding and chemical amendments. This comprehensive multi-omics analysis establishes that bacterial and fungal endophytes employ fundamentally distinct yet complementary strategies to alleviate dual stress in host plants. Bacterial endophytes prioritize rapid biomass preservation through active ion extrusion, ACC deaminase activity, and nutrient mobilization, while fungal endophytes emphasize osmotic adjustment, profound antioxidant activation, and mycelial metal sequestration. The integration of genomics, transcriptomics, proteomics, metabolomics, and ionomics has unveiled the intricate molecular networks governing these symbiotic interactions, revealing stress-responsive transcription factors, metabolic pathway reprogramming, and systemic cross-talk mechanisms that collectively fortify host resistance. Key molecular markers including *SOS1*, *NHX*, *HMA* transporters, antioxidant enzymes (SOD, CAT, APX, GR), and protective metabolites (proline, trehalose, flavonoids) have been identified as critical determinants of endophyte-mediated stress tolerance. The synergistic potential of combining bacterial and fungal endophytes into synthetic microbial consortia offers a promising avenue for field translation, addressing the performance inconsistencies of single-strain inoculants. However, successful implementation requires overcoming the culturable bottleneck, understanding field-scale microbial competition, and integrating multi-omics-guided approaches with precision breeding technologies such as CRISPR/Cas9. Future research should prioritize longitudinal field studies, mechanistic dissection of epigenetic regulation in endophytes, and development of robust bio-formulations that

maintain efficacy under fluctuating environmental conditions. Ultimately, harnessing the complementary capabilities of bacterial and fungal endophytes through multi-omics-informed synthetic biology represents a transformative pathway toward restoring agricultural productivity in salt-affected and heavy metal-contaminated soils, contributing to global food security in an era of climate change.

### REFERENCES

- Abed, M. M., Aydin, M., Yiğider, E., Ekin, M., & Yildirim, E. (2025). Systematic Literature Review for Mechanisms and Costs of Plant Adaptation to Biotic and Abiotic Stresses. *Phyton* (0031-9457), 94(12).
- Ahmad, A., Ahmed, M. M., Akhtar, A., Liu, W., Yang, R., Sun, X., ... & Chen, S. (2026). Unlocking Grass Stress Resistance: Fungal Endophyte-Mediated Pathogen Recognition and RNA Regulation. *International Journal of Molecular Sciences*, 27(9), 3899.
- Ahmad, A., Ahmed, M. M., Akhtar, A., Shuihong, C., Zafar, Z., Ullah, R., ... & Khan, M. B. (2026). New insight into endophytic Fungi-Plant symbioses under climate change: molecular crosstalk, nutrient exchange, and ecosystem resilience. *Applied Microbiology*, 6(3), 47.
- Ahmad, A., Ahmed, M. M., Akhtar, A., Shuihong, C., Zafar, Z., Ullah, R., ... & Khan, M. B. (2026). New insight into endophytic Fungi-Plant symbioses under climate change: molecular crosstalk, nutrient exchange, and ecosystem resilience. *Applied Microbiology*, 6(3), 47.
- Ben-Laouane, R., Boutasknit, A., Ait-El-Mokhtar, M., & Baslam, M. (2025). Engineering resilience in woody plants: multi-omics, genome editing, and microbiome strategies to boost abiotic stress tolerance. *Frontiers in Sustainable Food Systems*, 9, 1670566.

- Boutafda, A., Kounbach, S., Zourif, A., Benhida, R., & Danouche, M. (2026). Silicon at the Soil-Plant-Microbiome Interface: Rhizospheric Reconfiguration and Crop Resilience to Environmental Stresses. *Plants*, 15(9), 1320.
- Das, D., Sharma, P. L., Paul, P., Baruah, N. R., Choudhury, J., Begum, T., ... & Kalita, J. (2025). Harnessing endophytes: innovative strategies for sustainable agricultural practices. *Discover Bacteria*, 2(1), 1.
- Durand, A., Leglize, P., & Benizri, E. (2021). Are endophytes essential partners for plants and what are the prospects for metal phytoremediation?. *Plant and soil*, 460(1), 1-30.
- Etesami, H., & Beattie, G. A. (2017). Plant-microbe interactions in adaptation of agricultural crops to abiotic stress conditions. In *Probiotics and plant health* (pp. 163-200). Singapore: Springer Singapore.
- Fadiji, A. E., Lanrewaju, A. A., Omomowo, I. O., Parra-Cota, F. I., & de Los Santos-Villalobos, S. (2025). Harnessing seed endophytic microbiomes: a hidden treasure for enhancing sustainable agriculture. *Plants*, 14(15), 2421.
- Flores, G. A., Cusumano, G., Venanzoni, R., & Angelini, P. (2025). Biodiversity-driven natural products and bioactive metabolites. *Plants*, 15(1), 104.
- Gul, N., Wani, I. A., Mir, R. A., Nowshahri, J. A., Aslam, S., Gupta, R., ... & Aslam, S. (2023). Plant growth promoting microorganisms mediated abiotic stress tolerance in crop plants: a critical appraisal. *Plant Growth Regulation*, 100(1), 7-24.
- Karalija, E., Macanović, A., & Ibragić, S. (2025). Revisiting traditional medicinal plants: integrating multiomics, in vitro culture, and elicitation to unlock bioactive potential. *Plants*, 14(13), 2029.
- Katam, R., Lin, C., Grant, K., Katam, C. S., & Chen, S. (2022). Advances in plant metabolomics and its applications in stress and single-cell biology. *International journal of molecular sciences*, 23(13), 6985.
- Kaushal, S. S., Mayer, P. M., Shatkey, R. R., Maas, C. M., Cañedo-Argüelles, M., Hintz, W. D., ... & Grant, S. B. (2025). Salinization of inland waters.
- Khan, I., Ullah, N., Maqbool, H., Hashmi, A., Khan, B., Khalid, A., ... & Chaudhary, H. J. (2026). Holistic review on *Paenibacillus*: The multifunctional genus in heavy metal detoxification, pesticide degradation, and abiotic stress mitigation for Sustainable Agriculture. *Plant and Soil*, 518(2), 1245-1280.
- Kumar, D., Sattiraju, K. S., & Reddy, M. S. (2026). A systems approach to endophyte-mediated plant holobiont and microbiome dynamics. *Plants*, 15(5), 802.
- Kumar, P., Patel, M., & Dwivedi, P. (2026). Systems-Level Decoding of Root-to-Shoot Microbiome Dynamics via Integrated Multi-Omics and Network Analysis. *Journal of Plant Growth Regulation*, 1-25.
- Kumar, S. (2020). Abiotic stresses and their effects on plant growth, yield and nutritional quality of agricultural produce. *International Journal of Food Science and Agriculture*, 4(4).
- Kumar, V., & Nautiyal, C. S. (2026). From hidden allies to precision symbionts: unleashing endophytes for sustainable agroecosystems. *World Journal of Microbiology and Biotechnology*, 42(4), 172.
- Lin, D., Li, Q., Suleiman, M., An, M., & Zhu, Y. (2026). Microbiome and metabolomics analysis of different bryophytes under cadmium stress. *BMC Plant Biology*, 26(1), 808.
- Mathur, V., & Ulanova, D. (2023). Microbial metabolites beneficial to plant hosts across ecosystems. *Microbial Ecology*, 86(1), 25-48.
- Meena, K. K., Sorty, A. M., Bitla, U. M., Choudhary, K., Gupta, P., Pareek, A., ... & Minhas, P. S. (2017). Abiotic stress responses and microbe-mediated mitigation in plants: the omics strategies. *Frontiers in plant science*, 8, 172.

- Orozco-Mosqueda, M. D. C., Glick, B. R., & Santoyo, G. (2026). Cross-talk within plant niches: endophytic and arbuscular mycorrhizal fungi for sustainable crop production. *FEMS Microbiology Reviews*, 50, fuaf063.
- Oyebamiji, Y. O., Adigun, B. A., Shamsudin, N. A. A., Ikmal, A. M., Salisu, M. A., Malike, F. A., & Lateef, A. A. (2024). Recent advancements in mitigating abiotic stresses in crops. *Horticulturae*, 10(2), 156.
- Qiu, C. W., Zhang, S., Gao, Z. F., Chen, Z. H., Zhang, C., Ali, M. A., & Wu, F. (2026). First Tetraploa Genome and Multi-Omics Analysis Reveal Key Plant-Microbe-Soil Interactions for Salt Tolerance and Yield Improvement of Wheat. *Plant Biotechnology Journal*.
- Rahim, H. U., Ali, W., Uddin, M., Ahmad, S., Khan, K., Bibi, H., & Alatalo, J. M. (2025). Abiotic stresses in soils, their effects on plants, and mitigation strategies: a literature review. *Chemistry and Ecology*, 41(4), 552-585.
- Ramatsitsi, N., & Manyevere, A. (2025). Roles of endophytic fungi in plant resilience under abiotic stress: A mechanistic review with implications for climate-smart agriculture. *Plant Signaling & Behavior*, 20(1), 2578712.
- Salam, A., Khan, A. R., Zeeshan, M., Afridi, M. S., Yang, L., Zheng, Q., ... & Zhao, C. (2026). Nano-Enabled Solutions for Plant Abiotic Stress Tolerance and Soil Contaminant Remediation: A Review. *Plants*, 15(4), 535.
- Simarmata, T., Irwandhi, Khumairah, F. H., Hibatullah, F. H., Ambarita, D. D., Kamaluddin, N. N., ... & Barasarathi, J. (2025). Integrating metabolomics and transcriptomics for SynCom-driven rhizomicrobiome engineering in salinity-stressed rice. *Journal of Plant Interactions*, 20(1), 2567358.
- Sontakke, O. P., Salunke, T. R., Bhosale, K. S., Kenjale, P. A., Ahire, M. L., & Mankar, G. D. (2025). Decoding the Plant-Microbiome Dialogue under Heavy Metal Stress. *Symbiosis*, 97(1), 1-33.
- Sontakke, O. P., Salunke, T. R., Bhosale, K. S., Kenjale, P. A., Ahire, M. L., & Mankar, G. D. (2025). Decoding the Plant-Microbiome Dialogue under Heavy Metal Stress. *Symbiosis*, 97(1), 1-33.
- Yan, L., Zhu, J., Zhao, X., Shi, J., Jiang, C., & Shao, D. (2019). Beneficial effects of endophytic fungi colonization on plants. *Applied microbiology and biotechnology*, 103(8), 3327-3340.
- Zhang, Y. Y., Wen, L., Wang, T. T., & Li, Y. Z. (2025). Role of Endophyte in Salinity Stress Amelioration by Growth, Physiology, and Biochemistry Mechanisms of Defense: A Meta-Analysis. *Physiologia Plantarum*, 177(4), e70337.