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Original Article

A SYSTEMATIC REVIEW OF SALINITY STRESS RESPONSES IN THE COMMON BEAN (PHASEOLUS VULGARIS L.)

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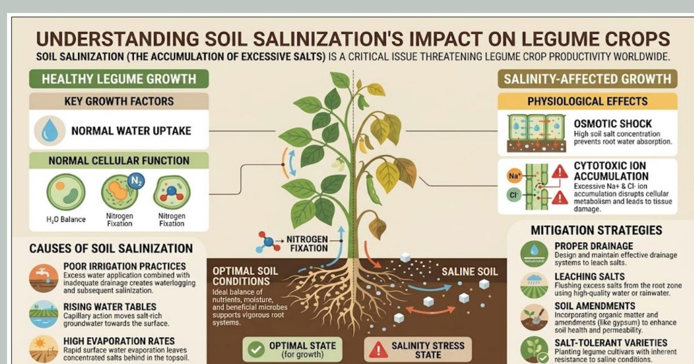
ABSTRACT

Common bean (Phaseolus vulgaris L.) represents one of the most critical grain legumes for direct human consumption, providing vital dietary protein, micronutrients, and calories worldwide. However, as an extreme glycophyte, Phaseolus vulgaris exhibits pronounced sensitivity to soil salinization, suffering severe yield penalties at electrical conductivity levels exceeding standard agricultural thresholds. Soil salinity inflicts primary osmotic shock and secondary cytotoxic ionic accumulation, which collectively compromise cell division, tissue elongation, photosynthetic efficiency, and membrane stability. Salinity also triggers excessive production of reactive oxygen species (ROS), causing lipid peroxidation, protein carbonylation, and premature organ senescence. Furthermore, the Rhizobium–legume symbiosis and biological nitrogen fixation apparatus within root nodules are exceptionally vulnerable to hyperosmotic and saline environments. This review synthesizes empirical findings across morphological, physiological, biochemical, transcriptomic, and genomic layers of salt stress responses in Phaseolus vulgaris. Furthermore, comprehensively evaluates salinity-induced perturbations in water relations, photosynthetic carbon assimilation, ion transport kinetics, antioxidant defenses, and nodulation biology, alongside modern genetic mapping and agronomic mitigation approaches.

Graphical Abstract



Keywords: Common Bean, Phaseolus Vulgaris, Salinity, Salt Stress, Oxidative Stress, Antioxidant Defense, Nodulation, Nitrogen Fixation, ION Transport, Salt Tolerance

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INTRODUCTION

AGRONOMIC IMPORTANCE AND THE SALINITY BOTTLENECK

Soil salinization is an escalating abiotic stress that threatens global agricultural sustainability and crop productivity across arid and semi-arid cropping systems Atta, K., et al. (2023). Common bean (*Phaseolus vulgaris* L.) constitutes roughly half of all grain legumes directly consumed by humans across Latin America, Africa, and the Mediterranean basin Hiz et al. (2014). The species supplies plant-based protein, dietary fiber, essential amino acids, iron, and zinc to food-insecure populations Senousy et al. (2023). Despite its agronomic importance, *Phaseolus vulgaris* is classified as one of the most salt-susceptible grain legumes, exhibiting marked yield declines even under moderate salinity levels below 2 dS/m Garcia et al. (2019). The onset of salinity stress exposes root systems to two distinct phases of physiological disruption: an immediate osmotic phase driven by lowered soil water potential, followed by a slower, cumulative ionic phase caused by intracellular sodium (Na^+) and chloride (Cl^-) accumulation Atta et al. (2023). These dual stresses alter primary metabolic networks, destabilize cellular membranes, disrupt mineral transport, and depress reproductive development Shahid et al. (2020). Deciphering the mechanistic basis of salinity damage and tolerance in *Phaseolus vulgaris* is essential for modern crop improvement programs Raggi et al. (2024).

SEED GERMINATION, VEGETATIVE GROWTH, AND BIOMASS PENALTIES

Seed germination and early seedling establishment represent the initial developmental bottlenecks when common bean encounters saline soils Borromeo et al. (2024). Elevating sodium chloride (NaCl) concentrations reduces the external osmotic potential, restricting imbibition and delaying water uptake by dry bean cotyledons Atta et al. (2023). Osmotic restriction combined with Na^+ toxicity suppresses key hydrolytic enzymes, such as α-amylase, thereby limiting the mobilization of endospermic starch reserves needed for embryonic axis development Bouzroud et al. (2023). Consequently, both germination percentage and seedling emergence speed decline steeply in salt-exposed bean seeds Borromeo et al. (2024). During vegetative stages, salinity leads to significant reductions in plant height, stem caliper, leaf expansion rate, and total canopy area Ekinci et al. (2023). Diminished cell division and compromised turgor-driven cell elongation in expanding leaves restrict total vegetative biomass accumulation in both shoot and root systems Alzahrani et al. (2024). Salinity decreases shoot fresh weight, root fresh weight, and dry matter accumulation in common bean seedlings Ekinci et al. (2023). High external salinity also modifies cell wall architecture, suppresses root elongation, and accelerates root cortical tissue senescence Zhang et al. (2022). Furthermore, progressive salt exposure leads to marginal leaf necrosis, chlorosis, and premature defoliation, severely reducing crop harvest index and pod yields Youssef et al. (2023).

OSMOTIC IMBALANCE, WATER RELATIONS, AND PHOTOSYNTHETIC IMPAIRMENT

The immediate consequence of rhizosphere salinization is the induction of physiological drought, which depresses root hydraulic conductivity and leaf relative water content Rady et al. (2021). Plants respond to this sudden osmotic drop by rapidly synthesizing endogenous abscisic acid (ABA), which signals guard cells to trigger rapid stomatal closure Ekinci et al. (2023). While stomatal closure curbs transpirational water loss, it simultaneously restricts internal sub-stomatal carbon dioxide (Ci) availability within the mesophyll Senousy et al. (2023). This reduction in Ci impairs the carboxylation efficiency of ribulose-1,5-bisphosphate carboxylase/oxygenase (RuBisCO) in common bean foliage Ekinci et al. (2023). Prolonged salinity also damages photosynthetic machinery through non-stomatal biochemical limitations Senousy et al. (2023). Excessive Na^+ accumulation within the chloroplast stroma destabilizes thylakoid membrane integrity and degrades light-harvesting pigment–protein complexes Acosta-Motos et al. (2020). Salt-stressed common bean leaves show consistent declines in chlorophyll a, chlorophyll b, and carotenoid concentrations Youssef et al. (2023). Over-excitation of the photosynthetic electron transport chain in damaged chloroplasts generates excess excitation energy, exacerbating photosystem II (PSII) photoinhibition and depressing net carbon assimilation Hasanuzzaman et al. (2013).

ION HOMEOSTASIS, TOXIC ION COMPARTMENTALIZATION, AND OSMOREGULATION

Cytosolic ion toxicities occur when large amounts of Na^+ and Cl^- enter the root xylem via non-selective cation channels and transpire into aerial bean tissues Shahid et al. (2020). High cytosolic Na^+ levels disrupt potassium (K^+) uptake and compete directly with K^+ for functional binding sites on key metabolic and protein-synthesis enzymes Sulthana Jafarullakhan et al. (2024). As a result, maintaining a high cytosolic K^+/Na^+ ratio is crucial for salt tolerance in glycophytic legumes Bouzroud et al. (2023). To prevent intracellular dehydration without causing enzymatic inhibition, common bean cells accumulate compatible, low-molecular-weight organic osmolytes in their cytoplasm El-Gazzar et al. (2020). Endogenous proline accumulation acts as a primary osmoprotectant, stabilizing native protein conformations, scavenging hydroxyl radicals, and buffering cytosolic pH Sulthana Jafarullakhan et al. (2024). Glycine betaine and soluble sugars likewise accumulate under hyperosmotic stress, helping preserve membrane structure, maintain ionic selectivity, and stabilize cellular turgor under salinity regimes Zhu et al. (2022).

Table 1

Table 1 Summary of Primary Physiological and Biochemical Responses of Phaseolus Vulgaris L. Under Salinity Stress.

Physiological/ Biochemical Parameter	Response under Salinity in P. vulgaris	Primary Functional Consequence
Shoot & Root Biomass	Severe Reduction (20–60%)	Inhibition of cell elongation and division
Photosynthetic Pigments	Chlorophyll a & b Breakdown	Degradation of light-harvesting complexes
Stomatal Conductance (gs)	Rapid Decrease via ABA Signaling	Conserves water but restricts carbon assimilation
Cellular K^+/Na^+ Ratio	Marked Decrease	Enzyme inhibition and metabolic disruption
Proline & Soluble Sugars	Significant Accumulation	Osmotic adjustment and subcellular hydration
Lipid Peroxidation (MDA)	Elevated Membrane Peroxidation	Loss of plasma membrane selective permeability
Nodule Formation & BNF	Severe Attrition	Impaired rhizobial infection and nitrogenase arrest

OXIDATIVE STRESS CASCADES AND ANTIOXIDANT ENZYME MODULATION

Secondary oxidative stress is a hallmark of salinity damage in *Phaseolus vulgaris* tissues Rady et al. (2021). Impairments in photosynthetic electron flow promote univalent metabolic reduction of molecular oxygen, forming reactive oxygen species such as superoxide radicals ($O_2\bullet^-$), hydrogen peroxide (H_2O_2), and hydroxyl radicals (•OH) Hasanuzzaman et al. (2021). Uncontrolled ROS accumulation triggers lipid peroxidation of polyunsaturated fatty acids in membrane bilayers, leading to structural leakage and elevated malondialdehyde (MDA) concentrations Ekinci et al. (2023). Exogenous application of nitric oxide donors and protective amino acid intermediates modulates reactive oxygen species networks to alleviate salt-induced oxidative injuries across crop species Ragaey et al. (2022). To mitigate oxidative damage, common bean activates a coordinated network of enzymatic and non-enzymatic antioxidant scavengers Youssef et al. (2023). Superoxide dismutase (SOD) provides the first line of enzymatic defense by dismutating $O_2\bullet^-$ into oxygen and H_2O_2 Hasanuzzaman et al. (2021). Catalase (CAT) subsequently decomposes toxic H_2O_2 into water and molecular oxygen within peroxisomes Sulthana Jafarullakhan et al. (2024). Concurrently, the ascorbate–glutathione (AsA-GSH) pathway—driven by *ascorbate peroxidase (APX)* and *glutathione reductase* (GR) removes cytosolic and chloroplastic peroxides while maintaining cellular redox balance Senousy et al. (2023). Non-enzymatic antioxidants, including ascorbate, glutathione, α-tocopherol, and polyphenols, further protect vulnerable cellular macromolecules Youssef et al. (2023).

SALINITY IMPACTS ON NODULATION AND SYMBIOTIC NITROGEN FIXATION

As a legume, *Phaseolus vulgaris* relies heavily on symbiotic association with nitrogen-fixing soil rhizobia (such as Rhizobium tropici, Rhizobium etli, and Rhizobium leguminosarum) to satisfy its nitrogen requirements Aserse et al. (2024). However, the legume–rhizobium symbiosis is significantly more sensitive to salinity stress than either host plant vegetative growth or free-living bacterial survival alone Bouzroud et al. (2023). Saline environments inhibit the early biochemical dialogues between plant roots and rhizobia, suppressing flavonoid secretion by bean roots and interfering with rhizobial Nod-factor synthesis Del Cerro et al. (2017). High salinity also restricts root hair curling, impairs infection thread formation, and reduces the total number and mass of functional nodules per plant Faghire et al. (2011). Inside established nodules, salinity disrupts symbiosome membrane integrity and downregulates leghemoglobin biosynthesis, leading to oxygen inactivation of catalytic nitrogenase enzyme complexes Bouhmouch et al. (2005). Furthermore, salt stress reduces the activities of carbon-metabolizing nodular enzymes, such as *phosphoenolpyruvate carboxylase* (PEPC) and *malate dehydrogenase (MDH)*, depriving bacteroids of respiratory dicarboxylates needed to sustain biological nitrogen fixation Faghire et al. (2011). Inoculation with specialized, osmotolerant rhizobial strains can mitigate some of this damage by supplying antioxidant enzymes and compatible solutes to root tissues under stress Wekesa et al. (2022). Specifically, indigenous stress-adapted rhizobial biostimulant strains demonstrate high efficacy in boosting nodule vigor and metabolic recovery in stressed common bean cultivars Del-Canto et al. (2023).

MOLECULAR DYNAMICS, TRANSCRIPTOMICS, AND GENOMIC ARCHITECTURE

High-throughput transcriptomic sequencing has clarified the molecular networks underlying salinity responses in common bean Hiz et al. (2014). Genome-wide expression profiling shows widespread transcriptional changes in root and shoot tissues exposed to salinity stress Hiz et al. (2014). Differentially expressed genes (DEGs) in salt-tolerant bean genotypes are enriched in transmembrane transport systems, energy metabolism, secondary metabolite biosynthesis, and hormonal signaling pathways Hiz et al. (2014). Specific transcription factor families—including *WRKY, bZIP, MYB, NAC*, and *AP2/ERF*—act as central regulatory switches controlling stress-responsive downstream regulons Sulthana Jafarullakhan et al. (2024). Recent genome-wide association studies (GWAS) on diverse *Phaseolus vulgaris* panels have begun uncovering the genomic regions that govern salt tolerance at early vegetative stages Raggi et al. (2024). Significant single-nucleotide polymorphism (SNP) associations on chromosomes 5 and 11 link candidate genes—such as chloroplastic-related proteins and membrane transporters—to shoot dry weight retention under saline conditions Raggi et al. (2024). In addition, genes involved in cell wall remodeling and secondary cell wall deposition are strongly upregulated during salt-stress acclimation in common bean sprouts Zhang et al. (2022).

EXOGENOUS ALLEVIATION STRATEGIES AND SUSTAINABLE INTERVENTIONS

Multiple agronomic, chemical, and biological approaches have been developed to enhance salinity resilience in *Phaseolus vulgaris* cropping systems Bouzroud et al. (2023). Seed priming and foliar application of exogenous phytohormones represent effective, low-cost intervention strategies Youssef et al. (2023). Exogenous salicylic acid (SA) application upregulates endogenous antioxidant defenses, preserves photosynthetic pigment concentrations, and improves K^+/Na^+ selectivity in salt-treated common bean seedlings Youssef et al. (2023). Similarly, exogenous melatonin treatment promotes cell wall biosynthesis, maintains sprout elongation, and limits intracellular sodium buildup under salinity Zhang et al. (2022). Gasotransmitters like hydrogen sulfide (H_2S) also counter salt toxicity by boosting photosynthetic carbon assimilation and reducing membrane lipid peroxidation Ekinci et al. (2023). Biological approaches utilizing beneficial soil microorganisms offer additional paths to stress mitigation Acosta-Motos et al. (2020). Co-inoculation with arbuscular mycorrhizal fungi (AMF) and drought/salt-tolerant Rhizobium strains stimulates glomalin-related soil protein (GRSP) synthesis, enhances root nutrient uptake, and improves common bean pod yield under saline irrigation Garcia et al. (2019). Furthermore, combining Funneliformis mosseae mycorrhizal colonization with nanoparticle supplementation enhances water uptake, mineral balance, and vegetative vigor in *Phaseolus vulgaris* under salt stress El-Gazzar et al. (2020). Halotolerant endophytic fungi, such as Cladosporium halotolerans, colonize the bean root cortex, reduce MDA accumulation, and support shoot and root growth in saline soils Alzahrani et al. (2024). Microalgae-derived biostimulant extracts also enhance chlorophyll retention, stomatal conductance, and antioxidant gene expression in salt-stressed bean crops Senousy et al. (2023). Advanced nanotechnology approaches, including foliar-applied nano-selenium dioxide and biological silicon nanoparticles, also alleviate ionic toxicity and restore membrane stability in salt-stressed *Phaseolus vulgaris* Rady et al. (2021), El-Saadony et al. (2021).

CONCLUSION AND FUTURE SCOPE

Salinity stress limits *Phaseolus vulgaris* production worldwide through combined osmotic shock, intracellular ion toxicities, oxidative damage, photosynthetic collapse, and symbiotic nodule disruption. While common bean possesses endogenous adaptation mechanisms including osmolyte synthesis, selective ion exclusion, and antioxidant enzyme upregulation, these intrinsic defenses are often overwhelmed by severe salinity regimes. Accelerating future progress requires integrating forward-genomics, GWAS, and marker-assisted selection to introgress stable salt-tolerant alleles from wild bean relatives and resilient landraces into high-yielding commercial cultivars. Combining stress-tolerant genotypes with targeted agronomic interventions such as halotolerant microbial bio-inoculants, hormone seed priming, and nano-nutrient delivery offers a practical path toward sustaining common bean productivity across salt-affected agricultural lands.

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