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UNRAVELING PLANT RESPONSES TO ABIOTIC STRESS: PHYSIOLOGICAL AND GENETIC PERSPECTIVE

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Abstract

Plant systems with multiple stress tolerances hold immense promise for sustained growth and productivity under increasingly challenging environmental conditions. Therefore, exploring effective management strategies to improve their performance is of paramount importance. The limited success in developing stress-resistant genotypes can largely be attributed to inadequate evaluation and identification techniques, ineffective selection criteria, and an incomplete understanding of stress adaptation mechanisms. This review collates and analyses the use of numerous compounds, including Osmo protectants and plant hormones, to alleviate the negative effects of stress on plants. It is critical to develop a thorough understanding of the physiological and genetic variables that influence plant productivity and sustainability in the face of abiotic stress. In the context of growing environmental problems, our analysis emphasizes the importance of decoding plant adaptations to environmental stress as a critical strategy for improving agricultural sustainability and maintaining food security. We hope to contribute to creative solutions that will allow agriculture to thrive in a changing world by summarizing current knowledge and recommending attractive research avenues. Consequently, it is essential to acquire a comprehensive understanding of the physiological and genetic factors that affect plant productivity and sustainability under abiotic stress conditions. Considering escalating environmental challenges, this analysis highlights the significance of understanding plant adaptations to environmental stress as a vital approach for enhancing agricultural sustainability and ensuring food security. By consolidating existing knowledge and identifying promising research directions, this review aims to contribute to the development of innovative, science-driven solutions that will enable agriculture to thrive in a dynamic and changing climate.

Key words: Genetic; Omics; Reactive oxygen species (ROS); Stress tolerance

Introduction

Global food security (GFS) has been severely challenged by environmental stresses (biotic and abiotic factors) resulting from the negative repercussions of climate change in New Year's (El Sabagh *et al*., 2021; Islam *et al*., 2022). Climate variability significantly affects agricultural productivity and poses a serious risk to food security for the growing population (Islam *et al*., 2022). Global food security is seriously threatened by drought, a primary abiotic stressor that negatively impacts agricultural output and quality (Anwar *et al*., 2025). Abiotic stressors, particularly drought (Al-Huqail *et al*., 2022) and salinity, significantly reduce production of crop by severely disrupting plant physiology and biochemical functions (Islam *et al*., 2011; Islam *et al*., 2023; Abeed *et al*., 2023a; Afridi *et al*., 2022a; Kamran *et al*., 2022; Islam *et al*., 2024). It has been proposed to develop appropriate management strategies that effectively address or alleviate abiotic stress in a way that is both commercially viable and environmentally sustainable, therefore helping to global food security (Kamran *et al*., 2021a, b; Afridi *et al*., 2022b; Ali *et al*., 2022; Islam *et al*., 2022). However, current discussion regarding physiological and molecular approaches remains limited, resulting in a lack of understanding of the complex genetic architecture in response to environmental stresses, necessitating the the exploration of plant tolerance and adaptive mechanisms under stress conditions (Ahmad *et al*., 2023; Ali *et al*., 2023).

One of the long-term objectives of this study is to shed light on the identification of tolerance genes. Identifying these genes utilizing cutting-edge molecular techniques and procedures could be a game changer in agriculture. The identified genes may facilitate the development of stress-resistant crop diversities that can tolerate the challenges caused by climate change (Ali *et al*., 2022b,c). Additionally, we highlight the revolutionary potential of cutting-edge scientific methods, specifically genome-wide association studies (GWAS) and CRISPR-Cas9 genome editing, in clarifying the genetic foundation of stress resilience. The production of crop varieties that are climate resilient is made possible by these innovative methods, which make it possible to identify important genetic determinants and quantitative trait loci (QTLs) linked to environmental stress tolerance (Zhang *et al*., 2022). This review summarizes and synthesizes existing knowledge while identifying new research areas, thereby enhancing scientific understanding of abiotic stress responses and offering insights for the creation of novel approaches to sustainable agriculture. The exploration of tolerance genes represents a significant scientific endeavor with the potential to enhance crop yields, addressing the needs of a rapidly increasing global population.

Abiotic stress's impact on crops: One of the main factors limiting global crop yield is abiotic stressors such drought, salinity, heat, cold, and heavy metal toxicity (Chaves *et al*.,

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2003; Farooq *et al*., 2015). Reduced growth, altered photosynthesis, and decreased yields are the outcomes of these stresses, which interfere with physiological, biochemical, and molecular processes (Ahmad *et al*., 2023; Islam *et al*., 2024). Reactive oxygen species (ROS) build up excessively in plants during drought and salinity conditions, causing osmotic imbalance and oxidative stress that damages proteins, membranes, and nucleic acids (Mishra *et al*., 2023). Reduced photosynthetic efficiency results from both heat and cold stress' detrimental effects on enzyme activity and chlorophyll stability (Farooq *et al*., 2015). Additionally, abiotic stress disrupts water relations, hormone balance, and food intake, leading to stunted growth and subpar reproductive outcomes (Ali *et al*., 2022; Islam *et al*., 2024). In sensitive crops, especially cereals and legumes, extended stress exposure can result in production losses of more than 50% (Ahmad *et al*., 2023).

Plants employ several defense mechanisms to counteract these effects, such as the accumulation of osmoprotectants like proline and glycine betaine and the upregulation of antioxidant enzymes like superoxide dismutase (SOD), catalase (CAT), and peroxidase (POX) (Mishra *et al*., 2023). Additionally, complex signaling pathways involving jasmonates, salicylic acid, and abscisic acid (ABA) regulate stress responsive genes, coordinating physiological and molecular reactions (Islam *et al*., 2024; Wang *et al*., 2019).In conclusion, abiotic stressors severely limit agricultural output, but new knowledge of plant genomic, physiological, and molecular reactions is opening the door to the development of crop types that can withstand stress (Chaves *et al*., 2003; Islam *et al*., 2024).

Management strategies: Several measures were used to reduce the negative effects of salt stress on crops, involving the external administration of different plant growth regulators, sugars, osmolytes, amino acids, and phytohormones (Ameen *et al*., 2023). It has been established that one typical adaptive technique used by plants to reduce oxidative stress is the increase of antioxidant enzymes. Plants can improve their tolerance and survival in a variety of abiotic stress situations because to these sophisticated defense systems. Furthermore, by preserving cellular homeostasis and osmotic equilibrium, suitable osmolytes are essential for reducing stress-induced damage and promoting plant growth (Hasanuzzaman *et al*., 2023).

Various adverse environmental conditions can induce osmotic and oxidative stress and cause a variety of adaptive responses (Kamran *et al*., 2021). The creation and buildup of molecules such as compatible solutes and stress proteins and the activation of reactive oxygen species (ROS) are examples of these responses. Enzymatic and non-enzymatic antioxidants play significant contributions to cellular homeostasis (Farooq *et al*., 2022). Involving the external administration of different plant growth regulators, sugars, osmolytes, amino acids, and phytohormones. As a result, ROS scavenging mechanisms are critical in protecting plants from harmful abiotic environments (Ilyas *et al*., 2023). Antioxidant metabolism, encompassing enzyme-based and non-enzymatic compounds, plays a crucial role in neutralizing ROS produced under stress conditions (Mehmood *et al*., 2021).

The use of molecular markers for trait selection provides significant advantages over morphological markers in traditional breeding of plant (Singh *et al*., 2024). The discovery of novel genes and a better knowledge of their involvement in stress adaptation will serve as the foundation for viable engineering efforts to develop stress tolerance (Cushman and Bohnert, 2000).

Plants under stress conditions exhibit deleterious impacts at the cellular and molecular levels, causing oxidative damage (Kamran *et al*., 2021a,b). Genetic enhancement is proposed as an effective approach to confer salt and heat resistance in staple crops (Saradadevi *et al*., 2021). Recently, in the context of global food security, the creation of crop cultivars that can withstand salt has been suggested as one of the most promising approaches to counteract abiotic stresses like heat and drought. To guarantee sustainable agricultural productivity and food security for the world's expanding population in the face of changing climate circumstances, it is imperative that mitigation and adaptation methods be strengthened (Munns *et al*., 2020). Consequently, enhanced mitigation strategies are essential to ensure food security for the world's growing population in the face of climate change issues.

Physiological adaptations: Environmental constraints are limiting crop production, as observed across various regions in previous decades, with expectations of intensification due to climate change (Lobell *et al*., 2011; Ma *et al*., 2022a,b). Cultivars are typically tailored to cultivation environments and bred for their inherent genetic capacity, water scarcity and elevated temperatures often pose major challenges to realizing a crop's full yield potential. Breeders must evaluate breeding populations in relation to diverse abiotic stress factors to assure continuity of crop production in the coming decades. Previous studies were carried out under precisely regulated conditions, offering only a partial insight into the biological mechanisms influenced by these stress factors in real-field environments. This results in decreased uptake of CO_2 (Lawlor & Tezara, 2009). Water stress also decreases relative water content (RWC), turgor potential, growth, and yield across different crop species (Akram, 2011).

Application of antioxidants: Antioxidants are a viable technique for enhancing plant tolerance to abiotic stressors (Mishra *et al*., 2023). These enzymatic and non-enzymatic chemicals are essential in improving the adverse consequences of oxidative stress produced by variables such as drought, salt, and high temperatures. In previous literature Ajmal *et al*., (2023) addressed the intricate mechanisms by which antioxidants act in the context of abiotic stress responses. Sucrose replaces proline in plants and serves as an important osmoprotectant when exposed to drought and heat stress. latest research investigating the impacts of heat and drought stress on a population of 300 maize inbred lines revealed that genetic resistance to merged heat and drought stress varies from genetic resistance to each stress in isolation (Cairns *et al*., 2013). As a result of uncertain future conditions, cultivars must be cultivated under a mix of heat and drought rather than under each stress alone (Cairns *et al*., 2013). On the other hand, the focus should not be solely on stress-resistant maize varieties; even though crop survival in the early growth stages is paramount, stress-resistant varieties should be based on a stable yield (Hamayun *et al*., 2021).

Superoxide dismutase (SOD), catalase (CAT), and peroxidases (POX) are enzymatic antioxidants that are necessary for neutralizing oxidative radicals (ROS) and preserving intracellular redox balance. In addition to these enzymes, non-enzymatic antioxidants such as ascorbic acid (vitamin C), as reported by Jomova *et al*., (2024), and tocopherols (vitamin E) as noted by Ahmed *et al*., (2023), also make substantial contributions to ROS scavenging and the protection of cellular structures agains oxidative damage (Azeem *et al*., 2023). Therefore, discovering antioxidant systems that are both enzymatic and non-enzymatic can yield useful markers of plant stress resistance. There are novel ways to increase maize's resistance to abiotic stress by combining conventional crop development techniques with antioxidant activity as a selection criterion. Breeding stress-tolerant cultivars can be accelerated by developing quick and effective screening procedures for large populations of plant material based on an understanding of the relationship between antioxidant activity and yield-related characteristics (Ahmad *et al*., 2023).This study intends to shed light on using antioxidants to understand responses to abiotic stress and, ultimately, discover genes that support plant stress tolerance through a complete examination of current research and creative methodologies.

Application of polyamines (PA): Under adverse environmental conditions, ROS are crucial for regulating the oxidative stress, and therefore plant growth and developmental processes. Under salt stress, a substantial increase in the concentration of apoplastic spermine and has been observed spermidine, mostly in the elongation zone of maize leaf blades. Notably, the activity of polyamine oxidase was realized to be approximately 20 times higher than that of copper-dependent amine oxidase. The production of ROS-including H_2O_2, O_2^-, and HO was assessed both in the presence and absence of polyamine oxidase inhibitors. The presence of 1,19-bis-(ethylamine)-5,10,15-triazanonadecane and 1,8-diamino-octane in maize crop under arid conditions indicates that polyamine oxidase is primarily responsible for the oxidation of free apoplastic polyamines, serving as the major source of ROS in the leaf blade expansion zone.

Regarding the potential of exogenous PA application, biotechnological strategies to enhance the expression of PA-synthesizing enzymes could be devised to boost ROS production in maize crop under abiotic stress (Wi *et al*., 2006). Studies suggest that transgenic plants overexpressing apoplastic polyamine oxidase may derive H_2O_2 from PA degradation (Moschou *et al*., 2008). However, further comprehensive research is needed to elucidate the role of PA in stimulating ROS biosynthesis and enhancing salt tolerance capacity in maize under diverse environments.

Application of hormones: The regulation of hormones is a critical factor contributing to increased plant yield and growth, whether under extreme or optimal conditions. Plant hormones are fundamental for enhancing plant growth and ensuring plant productivity (Haider *et al*., 2022; Haider *et al*., 2023). Various phytohormones, including indole-3-acetic acid (IAA), abscisic acid (ABA), ethylene (ET), cytokinin (CK), gibberellins (GA), salicylic acid (SA), brassinosteroids (BRs), strigolactones (SLs), and nitric oxide (NO), are utilized by plants to adapt to challenging environmental conditions (Kamran *et al*., 2021a, b). Each of these hormones has a distinct influence, creating different consequences based on their individual roles (El Sabagh *et al*., 2021), mainly evident in differentiation, growth, and development. Phytohormones are fundamental molecules with different chemical structures that operate as important regulators of plant growth and development. They exist in trace amounts. They may originate internally or be externally applied.

When we talk about soil salinity here, we consider the exogenous application of hormones to the plant (Islam *et al*., 2024). When plants are exposed to saline conditions, their growth is reduced due to decreased ion metabolism. Botanists employ different techniques to overcome this issue and enhance plant growth through the application of exogenous hormones (Kaya *et al*., 2009). ABA is an essential phytohormone that mitigates the stress effects in plants. Water scarcity in the root zone is known to result in the overproduction of this hormone. Salt stress induces osmotic imbalance and water depletion, boosting ABA accumulation in shoots and roots could strengthen salt tolerance (Saleem *et al*., 2022). Other chemicals, such as BRs and SA, also contribute to the plant's abiotic stress response. Under salt stress, the endogenous level of SA was increased, as did the activity of the biosynthetic enzyme SA (Gupta & Huang, 2014; Islam *et al*., 2024). Moreover, exogenously application of phytohormones have been found to alleviate the adverse effects of salinity stress in maize by enhancing osmotic regulation to sustain turgor, improve nutrient uptake, and uphold membrane integrity. Salt stress reduces total biomass, chl 'a' and chl 'b' content, and electrolyte efflux (Ali *et al*., 2022a). The combined application of kinetin and IAA mitigated the adverse effects of NaCl stress, enhancing salinity resistance in maize. Therefore, exogenous hormone application and the use of osmoprotectants can enhance the performance of maize under salinity stress. The application of these compounds enables osmotic adjustment, nutrient uptake and antioxidant protection (Farooq, 2015). Its role in reducing the detrimental effects of waterlogging on ear characteristics, grain filling, dry matter distribution, photosynthesis, and chlorophyll concentration has received little attention.

Water scarcity can markedly inhibit maize growth and disrupt developmental processes, regulatory feedback mechanisms, metabolic functions, and photosynthesis. A recent investigation found that externally applied SA (2 mM) and MeJA (20 μM) reduced the deleterious impacts of drought stress in maize compared to untreated controls (Javid *et al*., 2011).

Molecular adaptations: Understanding a plant's physiological, chemical, and genetic response to stress is critical (Farooq *et al*., 2018). Natural or genetically engineered morpho-physiological, biochemical, and molecular changes can result in stress-tolerant genotypes.

In comparison to untreated plants, a recent study showed that the exogenous administration of methyl jasmonate (MeJA, 20 μM) and salicylic acid (SA, 2 mM) substantially mitigated the negative effects of drought stress in maize. Finding and choosing resilient genotypes that can maintain productivity in the face of changing climatic conditions requires an understanding of the underlying biochemical mechanisms that confer tolerance in economically significant crops like maize, especially under combined heat and drought stress (Hussain *et al*., 2022).

SSR-DNA marker-assisted selection (MAS) techniques is now employed to develop plant germplasm possessing enhanced stress resilience by utilizing QTLs that regulate root system architecture, leaf ABA accumulation, and various other drought-adaptive traits (Tuberosa & Salvi, 2006). Recently, genomic technologies have made it possible to apply integrated high-throughput approaches to examine global gene expression responses to abiotic stresses beyond drought (Chaves *et al*., 2003). Several plant species, including *Arabidopsis*, have undergone microarray profiling under stress (Kawaguchi *et al*., 2004). These studies identified differentially expressed transcripts of genes associated with photosynthesis, ABA biosynthesis, signal transduction, osmoprotectant synthesis, protein stability and protection, ROS detoxification, water uptake, and various transcription factors, including several members of the zinc finger, WRKY, and bZIP families.

One of the most prominent ways for identifying drought tolerance genotypes involves screening under induced water stress conditions generated by high molecular weight osmotic chemicals like polyethene glycol-6000 (PEG-6000) (Landjeva *et al*., 2008). This method has been recognized as an effective method for rice selection in the early growth stages (Jing & Chang, 2003). In addition to seedling screening, seed germination is often evaluated under induced water stress conditions to identify genotype drought tolerance.

Genetic improvement of abiotic stress tolerance: Present advancements in the physiological understanding of stress tolerance have led to the integration of molecular marker-assisted selection and various biotechnological techniques alongside traditional breeding methods to enhance plant tolerance to abiotic stresses. Many physiological, biochemical, and molecular processes that might occur at the cellular or entire plant level are altered in reaction to water scarcity, and they play an essential role in stress management (Bashir *et al*., 2021). However, some studies highlight the effective application of molecular markers in developing plant varieties that are resistant to abiotic stresses (Das *et al*., 2017). This molecular identifier can help farmers choose salt-tolerant crop varieties. However, the low success rate in developing stress-tolerant plants is mainly attributed to inadequate screening and selection methods, insufficient selection parameters, and a lack of understanding of the mechanisms of stress tolerance.

Stress breeding alternatives are restricted by low selection effectiveness, inadequate screening methods, and a lack of understanding of the interaction between the environment and stress. The development of novel plant varieties with enhanced traits is now feasible using molecular markers. However, the most logical option at this point is to improve transgenic plants with increased resilience to heat, drought, and salt stress. High-throughput integrated techniques in genomic technologies facilitate the study of gene expression in response to all abiotic stressors (Chaves *et al*., 2003). Plant species such as Arabidopsis have been examined using microarray profiling under drought stress (Kawaguchi *et al*., 2004). These research discovered many transcripts of genes involved in photosynthesis and osmoprotectant production, ABA signal transduction, water uptake, ROS detoxification, as well as various transcription factors from the zinc finger, bZIP, protein stability and protection, and WRKY families.

Plant genomics has undergone a revolution, thanks to the development of high-throughput next-generation sequencing (NGS) technologies, which have made it possible to identify new genes linked to stress tolerance and conduct thorough analyses of how these genes are expressed in different tissues and developmental stages. These developments offer important new understandings of the intricate molecular networks controlling how plants respond to environmental stressors (Kumar *et al*., 2023). Detailed information on differentially expressed genes (regulatory or functional genes) that regulate physiological processes related to stress adaptation will help develop genetic strategies for developing stress-tolerant varieties. The integration of whole genome data of rice and transcriptome data at different stress time points will help to unravel the molecular basis of physiological traits associated with stress tolerance or critical agronomic traits of rice (Hassan *et al*., 2023). These studies will improve our understanding of their functions in stress adaptation.

Molecular identification to characterize the pattern of gene expression in plants: Several molecular studies have characterized gene expression patterns in plants exposed to water-stress (Bray, 1993). Multiple drought-responsive cDNAs have been separated and categorized in various plants species, encoding different classes of proteins such as LEA, RAB (responsive to ABA), and ion channel proteins. However, the role of these genes in stress tolerance and their physiological functions remain unclear (Bray, 1993). The identification of novel genes, investigation of their expression patterns in reaction to stress, and developed appreciation of their activities in stress adaptation will lay the groundwork for effectual engineering solutions targeted at increasing stress tolerance (Cushman & Bohnert, 2000; Hafeez *et al*., 2024). DNA microarrays have emerged as a typical technique for worldwide investigation of plant gene expression as molecular technology has advanced. Recently developed, DNA microarray technology has emerged as one of the most powerful tools for connecting sequence information with functional genomics. Several biological processes and important rice traits have been investigated using cDNA microarrays or whole genome arrays, particularly focusing on salt-responsive genes (Chao *et al*., 2005). DNA microarrays offer a high-throughput platform for analyzing thousands of genes and finding gene alterations throughout the transcriptome under various biological situations.

Quantitative trait locus (QTL): Stress tolerance of drought is a quantitative attribute that is controlled by several genetic loci (QTL). Furthermore, crop performing under drought conditions is highly complicated due to uncontrollable environmental elements and interactions with other abiotic and biotic components (Reynolds *et al*., 2016). Additionally, physiological traits like RWC, proline accumulation, and osmotic adjustment have been associated with plant tolerance to drought-prone environments (Ludlow & Muchow, 1989). Clarifying the physiological and molecular processes that control water uptake, nitrogen assimilation, and general plant maintenance under stress requires an understanding of drought tolerance features. One effective and popular method for locating genomic regions and designating particular loci linked to drought-related traits is quantitative trait loci (QTL) mapping. QTL mapping makes it possible to identify chromosomal areas that have a major impact on intricate drought-responsive traits by statistically analyzing marker–trait relationships (Rahman *et al*., 2023). The recognition of these loci through associated markers enables breeders to implement marker-assisted breeding in conjunction with traditional selection techniques.

One effective method for determining whether genetic differences are linked to traits or disorders is a genome-wide association study (GWAS). Common single-nucleotide polymorphisms (SNPs) and complicated human diseases, including type 2 diabetes, cardiovascular disease, inflammatory bowel disease, and mental illnesses, are the main subjects of its investigation. The overall design of a population-based case-control study used in GWAS to find genotype–phenotype correlations is demonstrated in this chapter (Visscher *et al*., 2017). We provide an overview of the ideas behind GWAS and offer guidance on the statistical techniques used in GWAS (Chang *et al*., 2018). Quantitative traits make up the bulk of the breeding objectives. Using sparse polymerase chain reaction (PCR) markers, linkage mapping was created to investigate a trait's QTL system. GWAS were created for natural populations (germplasm) utilizing high-density genomic markers made possible by advancements in genome-wide sequencing technology. GWAS enable the detection of the complete QTL network along with its various alleles across genomic regions (He & Gai, 2023), originally designed for human genetics, the majority of GWAS conducted thus far have focused on plants, where it has become a widely used method for investigating the genetics of traits relevant to agriculture and natural variation (Deng *et al*., 2023).

Currently, the most effective and reliable method for determining gene expression and transcriptional activation on a genome-wide scale is RNA-*seq*. Due to the complexity of RNA-*seq* data analysis, numerous studies have been conducted on algorithms and techniques (Corchete *et al*., 2020**)**. The RNA-seq technology has emerged as a preferred alternative to conventional microarray platforms for transcriptional profiling (Rao *et al*., 2017). RNA-*seq* has recently become a replacement technique for gene expression profiling (Rao *et al*., 2017). The primary distinction between RNA-*seq* and microarrays lies in the capability of RNA-seq to enable comprehensive transcriptome sequencing, whereas microarrays rely on hybridization to profile select transcripts and genes. Given these benefits and the overall progress in the field, researchers have shown increasing interest in utilizing RNA-seq platforms for toxicogenomic analyses (Rao *et al*., 2017).

Recent advancements in proteomics through mass spectrometry have enabled scientists to analyze plants with a level of detail previously unattainable. Proteomics is currently a comprehensive tool for biological study, with the potential to explain biological processes. Proteomics has been effectively used in several research studies to discover plant resistance pathways (Liu *et al*., 2019). Proteomics, the examination of the genome's protein complement, ensures experimental continuity between genome sequence information and protein profile in each tissue, cell, or cell compartment during normal growth or under various treatment conditions (Navi & Toorchi, 2013). Because proteomics provides valuable information about protein identification, levels of expression, and modification, it has gained prominence in molecular science (Kwon *et al*., 2021). Proteomics activities include protein expression analysis, changes in protein profiles, protein interactions, protein structure, and protein functionality (Hyung & Ruotolo, 2012; Islam *et al*., 2021a,b). Although gene and mRNA abundance studies have contributed significantly to our understanding of plant immune responses, there is typically a weak correlation between the abundance of mRNA transcripts and protein concentrations (Wang *et al*., 2019).

Table 1 lists the main physiological, biochemical, and molecular processes that help plants tolerate abiotic stress. The most significant biological processes and molecular strategies that improve plant resistance to abiotic stresses like heat, salinity, and drought are summarized in the table. It is illustrating how physiological processes, chemical reactions, and hormonal regulation combine to determine plant resistance.

Table 1. Summary of key physiological, biochemical, and molecular mechanisms to abiotic stress tolerance.

No.	Mechanism	Compounds/Hormones involved	Main effect on plants	Reference
1.	Antioxidants	SOD, CAT, AsA, tocopherol	Reduces ROS and enhances ionic balance	Mishra *et al*., 2023
2.	Polyamines	Spermine, Spermidine	Improves H_2O_2 signaling and defense activation	Wi *et al*., 2006
3.	Phytohormones	ABA, SA, IAA, BRs	enhances growth under drought and salinity conditions	Islam *et al*., 2024
4.	Molecular Improvement	MAS, GWAS, CRISPR	Recognizes stress-tolerance genes	Cushman & Bohnert, 2000
5.	Physiological Indicators	RWC, Proline, Chlorophyll	Biomarkers for stress assessment	Ludlow & Muchow, 1989

Conclusion and Future Perspectives

The review focuses on ways to better understand and enhance plant tolerance to abiotic challenges using contemporary physiological and genetic methods. It highlights the physiological, biochemical, and genetic coping strategies that plants employ to deal with stress and talks about the threats that climate change brings to the world's food supply. In addition to reviewing genetic and physiological methods for identifying important tolerance variables, the paper highlights the impact of antioxidants, polyamines, and phytohormones in reducing the effects of stress. It concludes that creating crop varieties resistant to stress and guaranteeing sustainable agriculture and food security require combining traditional breeding with cutting-edge genetic and physiological techniques.

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