

Review

Molecular Plant Physiology for Model Plants under Abiotic Stress Conditions

Babak Sokouti *

Biotechnology Research Center, Tabriz University of Medical Sciences, Tabriz, Iran; E-Mails: b.sokouti@gmail.com; sokoutib@tbzmed.ac.ir

* **Correspondence:** Babak Sokouti; E-Mails: b.sokouti@gmail.com; sokoutib@tbzmed.ac.ir

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Abstract

Extreme temperatures, drought, and high soil salinity are some of the significant abiotic stresses that can severely impact crop yields, posing a threat to global food production. Comprehensive studies on model plant species are crucial for understanding their biochemical, physiological, and molecular responses to abiotic stresses. Identifying stress response mechanisms and potential targets can aid in developing stress-tolerant crop varieties. Additionally, elucidating the functions of reactive oxygen species is essential for this research area. In model plants, the perception of abiotic stresses is a complex phenomenon that entails intricate interactions between hormones, gene regulation, and physiology. The presence of specific stress receptors and sensors contributes to this perception. Activating signaling pathways involves a cascade of events, starting with generating reactive oxygen species, then calcium signaling and MAP kinase signaling. Because of these processes, transcription factors and genes susceptible to stress are ultimately activated in the latter stages. It starts with a series of physiological and biochemical modifications, which entail adjustments in photosynthesis and the accumulation of osmoprotectants. We have gained significant insights from studying model plant stress responses, but there remain considerable challenges in effectively applying these findings to enhance crop resilience. These challenges contribute to



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reproducing the results across various species. These difficulties arise because of phenotypes, molecular mechanisms, and genetic differences. The utilization of model plants will persist in their crucial role as essential systems for unraveling the complexities of plant stress responses. They will play a vital role in overcoming present constraints, particularly in areas such as the mathematical modeling of plant physiology. The exploration of gene function across species can significantly contribute to efforts aimed at improving crops. The key to addressing threats to global food security and promoting crop stress resilience lies in adopting a multi-pronged approach that uses model plant systems.

Keywords

Abiotic stress; model plants; stress signaling; reactive oxygen species; crop resilience

1. Introduction

In molecular plant physiology for model plants, considering the abiotic stress conditions, the intricate interplay between plants and their environment unfolds, revealing a delicate balance challenged by various abiotic stressors. These stressors, ranging from drought and salinity to high temperatures, floods, and the pervasive influence of climate change, cast a shadow over global agricultural sustainability. Recent research, as exemplified by the work of Francini & Sebastiani, underscores the profound impact of these stressors, with reports indicating substantial yield reductions of 50% to 70% in crops [1, 2]. The far-reaching consequences extend to rural areas, where agricultural production grapples with staggering losses, reaching up to 50% [3, 4]. Moreover, the convergence of multiple stress factors amplifies the challenges faced by agricultural systems worldwide, underscoring the urgent need for comprehensive understanding and strategic interventions [5-12].

Studying how model plant species react to abiotic stress has become increasingly important for several reasons. Studying how model plant species respond to abiotic stress has gained increasing importance for several reasons. First, abiotic stresses, including drought, extreme heat, salt, and their combinations, threaten agricultural output significantly [13-15]. Understanding how plants respond to these stressors is crucial for developing strategies to enhance crop resilience and ensure food security [16, 17]. In addition, plants may respond favorably or adversely to abiotic stress by increasing their production of reactive oxygen species (ROS), affecting their stress tolerance [18, 19]. Studying ROS's function in abiotic stress responses is crucial to comprehend how plants adapt fully.

To further understand how plants react to abiotic stress, researchers must first discover the distinct regulatory transcripts, metabolites, and proteins each stress combination produces [20]. To help plants better withstand a variety of stresses, this information is crucial for creating tailored treatments. Further, by studying how plants naturally react to abiotic stress, we may find the genes and alleles that help plants survive in harsh environments [21]. Such insights are valuable for breeding stress-tolerant crop varieties that thrive under challenging growing conditions.

Furthermore, improving crop stress tolerance requires knowledge of how plants control gene expression, use antioxidants, and handle oxidative damage in abiotic stress [22, 23]. Researchers can identify potential targets for genetic engineering to develop stress-resistant plant varieties by

studying the molecular mechanisms underlying plant responses to abiotic stress. Overall, the multifaceted nature of plant responses to abiotic stress underscores the importance of continued research in this field to address global challenges related to climate change and food security.

Amidst these challenges, model plant species emerge as invaluable allies in unraveling the mysteries of plant adaptation to abiotic stresses [18, 24, 25]. Through meticulous study, researchers have peeled back the layers of complexity, delving into the molecular, physiochemical, and biochemical mechanisms that enable plants to navigate adverse environmental conditions [13]. These investigations have yielded crucial insights into regulatory transcripts, metabolites, and proteins intricately linked to stress responses, laying the groundwork for innovative strategies to enhance crop resilience [26, 27].

Furthermore, the significance of model plants transcends mere academic inquiry, extending into the realm of biotechnological advancement. Researchers have unearthed key genetic pathways and regulatory networks pivotal in conferring stress tolerance by leveraging the knowledge gained from studying model woody plants and other model species [17, 28]. Research into model plants is essential for creating robust crop types because it paves the way for designing crops with increased tolerance to several abiotic stressors simultaneously. This understanding serves as a springboard for developing genetically modified crops engineered to withstand the rigors of abiotic challenges, thereby bolstering agricultural productivity and resilience [29, 30].

Moreover, as the climate change spectre looms, the imperative to decipher the molecular underpinnings of plant stress responses becomes ever more pressing [31, 32]. Model plant species offer a gateway to understanding the dynamic interactions between plants and their environment, particularly in the context of ROS and their pivotal role in stress responses [33]. Through rigorous molecular investigations, researchers are unravelling plant physiology's complexities and charting a course toward sustainable agriculture in a changing world [24].

Plants' molecular responses to abiotic stress have been the subject of much research, which has led to new ideas on how to lessen the impact of this kind of stress on plants. Emphasizing their interactions with phytohormone signaling pathways, Samanta et al. examine the involvement of ROS and reactive nitrogen species (RNS) in plant responses to drought stress. Investigating the molecular model of plant stress responses is the focus of this reference [34]. Mariyam et al. explore the application of nanotechnology in agricultural science for managing abiotic stress. An overview of nanotechnology's potential for stress management provides a futuristic perspective on alleviating plant stress, possibly combined with medical advancements [35]. The authors investigate how circadian rhythms affect *Spinacia oleracea*'s physiological and phytochemical responses under salinity stress and light. Timing and environmental factors have been analyzed to understand how stress affects plant molecular physiology [36]. Choudhary et al. review the effects of hydrogen peroxide and hydrogen sulfide on seed priming. It discusses drought, temperature, UV radiation, and ozone stress using hydrogen peroxide and hydrogen sulfide treatments. An overview of historical perspectives and current applications is included in this comprehensive reference, which explores the molecular mechanisms underlying stress tolerance [37].

To suppress plant diseases, Kim et al. utilize nanocomposites and silver nanoparticles. This study provides insight into the interactions between nanoparticles and plants, which may help develop strategies to improve plant health under stressful conditions [38]. Kumar et al. review the interactions between nanomaterials and phytohormones, presenting novel perspectives on leveraging nanotechnology to mitigate environmental challenges. It highlights the molecular-level

interactions that can influence plant responses to stress [39]. Kim et al. delve into the use of alginic acid-functionalized silver nanoparticles for quickly detecting tellurium, a technology-critical element [40]. While the primary focus is not on plant physiology under abiotic stress conditions, the research offers valuable insights into the application of nanotechnology for environmental monitoring and the detection of specific elements. The study highlights the potential versatility of nanomaterials across various fields, including environmental science and technology.

Using drought, salt, heat, heavy metals, and other environmental stressors as case studies, this research examines how these factors affect model plant species' biochemistry, physiology, and molecular biology. A wide range of molecular components will be discussed in the review, including citric acid, transcription factors, anthocyanins, root system architecture, and receptor-like protein kinases. Studying various molecular components is highly relevant for understanding plant responses to abiotic stresses. These components include citric acid (involved in metal stress tolerance), transcription factors (key regulators of stress-responsive genes), anthocyanins (antioxidants mitigating oxidative damage), root system architecture (crucial for water/nutrient acquisition under stress), and receptor-like protein kinases (perceiving and transducing stress signals). Plants have devised complex ways to deal with abiotic challenges, including drought, salt, high temperatures, and lack of nutrients. In order to combat food insecurity and increase agricultural yields, it is essential to learn how to modify crops to withstand abiotic stress genetically. The review will further focus on how these molecular responses affect plant development, growth, and resiliency to stress. The study will focus on strategies for enhancing plant resilience to stress and their implications for improving crop resilience in light of changing environmental conditions.

2. Perception Mechanisms

As a result of evolution, plants have developed elaborate mechanisms to detect and respond to abiotic stress, such as drought and salinity. They must detect the signals of stress and then react to it. These stress signals are believed to be seen by plants through a complex interaction of hormones, gene regulation, and physiological changes.

When plants are threatened by drought, they activate many signaling pathways. Plants respond to drought stress by triggering a cascade of signaling channels. During drought, many important signaling pathways are activated, including the mitogen-activated protein kinase (MAPK), abscisic acid (ABA), brassinosteroids (BRs), sugar, and specific transcription factors pathways [41]. These pathways are critical for controlling how plants react to drought stress by controlling physiology, gene expression, and stress tolerance mechanisms. The ABA signaling pathway is well-studied and essential for plant responses to drought stress [42-44]. ABA is a drought-inducible phytohormone that helps plants regulate stomatal closure, osmotic adjustment, and other adaptive responses to conserve water and enhance stress tolerance.

The MAPK signaling pathway also converts extracellular drought stress signals into intracellular signals, contributing to plant defense mechanisms against drought [45, 46]. Moreover, the activation of autophagy-related pathways, such as those regulated by the gene *COST1*, has been linked to plant drought tolerance [43]. For plants to adapt to drought, autophagy is essential for cellular homeostasis maintenance and stress adaption promotion. Additionally, transcription factors' interactions with ABA signaling pathways are critical for plants to reduce drought stress [47].

When plants experience drought stress, transcription factors control gene expression, affecting how the plants respond.

Overall, activating multiple signaling pathways, including ABA, MAPK, autophagy-related, and transcription factor-mediated pathways, collectively enhances plant resilience and survival under drought-stress conditions. Understanding the intricate network of signaling pathways involved in plant responses to drought is essential for developing strategies to improve crop productivity and sustainability in changing environmental conditions.

In response to drought stress, multiple sensors sense molecular patterns generated by abiotic stress, relaying to various parallel signaling networks and resulting in downstream responses. In addition to stomatal closure, stomatal proteins and metabolites are synthesized under the influence of stress [48]. The abscisic acid (ABA) hormone is crucial among the many stress responses to drought. Research has shown a correlation between root-to-shoot peptide signals and leaf ABA accumulation. These signals are critical for plant survival under drought stress when they cause ABA accumulation in leaves [49, 50]. Furthermore, Xiong et al. showed that crucial variables affecting plant drought tolerance could be identified by a genetic study of the roots' reaction to drought stress and their absorption of ABA [51]. There has also been a growing body of evidence suggesting that genes involved in drought stress are needed to regulate gene expression, including genes from the NAC family [52].

Furthermore, plants can detect the stress signal by exhibiting specific mechanisms when they are stressed by salinity. Salt stress hinders plants' capacity to swiftly adjust to changing environmental circumstances by causing them to accumulate osmolytes, such as proline, and activate stress signaling pathways [53, 54]. It is well-established that ethylene regulates the response of other phytohormones to salt stress, keeping plants' resistance to salt stress intact [55]. Also, Tao et al. discovered that ethylene helps plants deal with salt, drought, and heat stress by integrating signals from JA and ABA [56]. Plants enhance xylem aphid absorption to help with osmoregulation in drought-stricken plants and ABA signaling pathways in salt-stressed plants [57].

Studying histidine kinases involved in *Arabidopsis thaliana* abiotic stress signaling pathways is crucial to comprehending the molecular mechanisms that control plant responses to environmental stresses. Specifically, several histidine kinases have been identified, including AHK1/ATHK1, AHK2, AHK3, and CRE1, which exhibit distinct expression patterns under water deficiency conditions. Furthermore, the overexpression of ARGOS genes, encoding ethylene receptors, significantly enhances drought tolerance in *Arabidopsis* and *Zea mays* (maize). These results implicate a critical role for ethylene signaling in plant adaptation to drought stress. *Arabidopsis* transgenic with the ABA receptor gene GhPYL9-11A demonstrated enhanced drought resistance, demonstrating that ABA receptors play a critical role. VaPYL4 (the grape ABA receptor gene) is overexpressed, which increases *Arabidopsis*'s ability to withstand a variety of abiotic stimuli. It suggests these receptors may influence the plant's reaction to those conditions. AITR genes are implicated in drought tolerance, as shown by the fact that the whole family of AITR genes has been shown to control drought stress responses in *Arabidopsis* by deletion. In the study of *Arabidopsis* plants containing the wheat gene TaVQ14, salt and drought tolerance were demonstrated, suggesting a potential role for the gene as an environmental sensor. Furthermore, it has been found that *Arabidopsis* contains a novel drought-sensing gene, the DUF569 gene, which could serve as an indicator of drought stress [58].

Researchers conducted comprehensive phenotypic analyses to study *rice* salinity tolerance mechanisms. A study has also found that salinity tolerance can be improved by overexpressing OsGF14C in *rice*. The findings indicate that OsGF14C may be able to detect salinity stress and may improve salinity tolerance. It is possible that bZIP45, a transcription factor from grapevines known as bZIP, is an essential marker of drought stress in *Arabidopsis* since it regulates VvANN1, which in turn affects *Arabidopsis*'s response to drought. In addition, a study of *rice* plants' response to these stresses has proposed theoretical support for generating *rice* germplasm tolerant of both saline and alkali stresses. The methods through which *rice* plants react to salt must be understood, as noted by Tran et al. [58].

Through perception systems, stressors affect plants, including heat, heavy metals, drought, and salt. It is crucial to have a thorough grasp of how plants detect and react to heat and heavy metal stress. The references provide insight into many elements of plant perception, but there is still a lot to discover about how plants perceive and respond to heat and heavy metals.

There are several processes by which plants detect and react to heat stress. Research has linked specific plant temperature-sensing processes to histones, heat-shock proteins, and nucleosomes [59, 60]. Furthermore, when plants sense heat stress, they undergo a series of reactions, including early blooming, leaf hyponasty, and quick axe extension [61]. Understanding the molecular pathways involved in heat perception and response is crucial for developing strategies to enhance plant resilience to high-temperature conditions.

In terms of heavy metal stress, plants have systems that can detect and lessen the harmful impacts of environmental heavy metals. While the references provided do not directly address heavy metal perception mechanisms, studies have highlighted the role of ion channels, membrane potentials, and signal transduction pathways in early defense signaling against herbivorous insects, which may share some commonalities with responses to heavy metal stress [62]. Plant reactions to heavy metal stress also include modifications to ion transport, detoxifying mechanisms, and gene expression regulation.

As a result of the references provided, it is clear that further research is needed to understand plant perception mechanisms in response to heat and heavy metal stress in plant models better to identify specific signaling pathways and molecular mechanisms. In addition to improving our understanding of plant stress responses, understanding these mechanisms will help us develop strategies to enhance plant tolerance to environmental stresses (Figure 1).

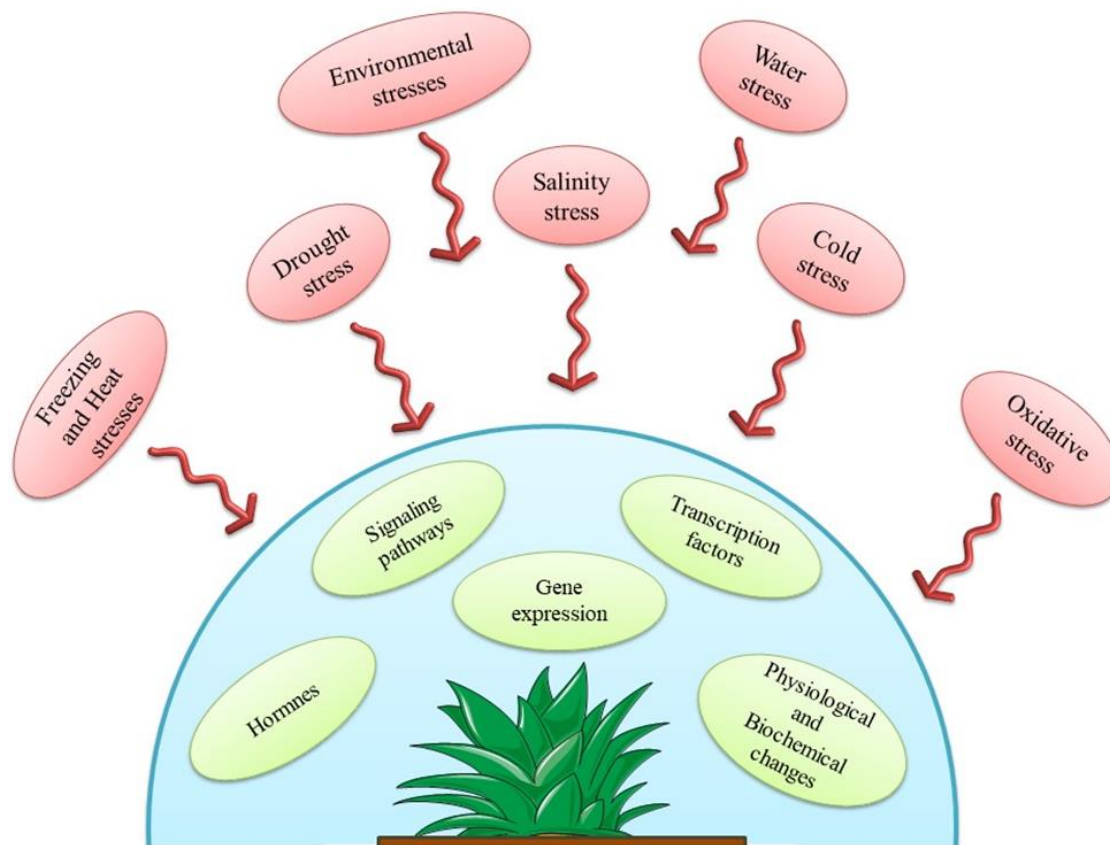


Figure 1 Various environmental stresses threaten the plants and their protective function.

Finally, rice and *Arabidopsis* contain several receptors and sensors that can detect abiotic stress, including salt, drought, and other similar conditions. These results may lighten the molecular processes underpinning plants' reactions to biotic stress and identify possible targets for enhancing plant stress tolerance; abiotic stress is very stressful for plants.

3. Overview of Signaling Pathways

In plant models like *Arabidopsis* and *rice*, it is clear that stress perception initiates early signaling processes, such as ROS production, calcium signaling, and MAP kinase activation, all of which are necessary for the stress response. Plants address both biological and environmental stressors via these signaling pathways [63]. They trigger a series of molecular events when they perceive stress, which triggers a series of defense mechanisms and adaptive responses in the plant [64]. Research has shown that ROS signaling is crucial in how plants respond to stress. Plant ROS molecules regulate physiological reactions, such as dehydration and oxidative stress [64].

Plants rely on ROS to react to stresses like dehydration and salt. Various physiological responses in plants, including oxidative stress and dehydration, are regulated by ROS molecules, which also function as signaling molecules [65]. While ROS can damage cells in certain situations, new evidence shows they are crucial as signal transduction molecules mediating reactions to pathogen infection, environmental stress, programmed cell death, and other developmental cues [65].

According to studies, ROS is necessary for many essential biological processes, such as cell growth and division [66]. As crucial signaling molecules, ROS also play a role in acclimatization responses to

various abiotic stressors [67]. Plants may be helped to survive by controlling genes involved in stress defense pathways and keeping ROS generation below a certain threshold level [68].

In addition, nitric oxide (NO) and reactive oxygen species (ROS) assume pivotal functions in regulating various physiological processes such as transpiration, hormonal balance, germination, stomatal gaseous exchange, fruit maturation, blossoming, defense mechanisms, and programmed cell death [69]. ROS generated in response to stress can act as long-distance signals to alert plants for stress adaptation [63]. The interplay between ROS and NO is essential for maintaining ROS homeostasis and coordinating various physiological processes in plants [70].

A similar role has been recognized for calcium signaling in plant cells, one of the most important ones in signaling. Its effect on our knowledge of cell signaling is influenced by its participation in cell signaling in plants and its many functions in stress responses [71]. When plants experience stress from their surroundings, MAP kinase cascades are activated. These cascades regulate stress responses and affect core body temperature under cold and dry conditions [72]. The context suggests that MAP kinase signaling cascades in plants mediate stress responses to environmental stressors like drought and cold. Still, they also influence the regulation of the plant's internal temperature or heat levels during exposure to these temperature extremes.

Plants do not have a constant internal body temperature like warm-blooded animals. However, their temperature can fluctuate based on the ambient temperature conditions. During heat or cold stress, plants must modulate their internal temperatures through various mechanisms to prevent damage. So, in this context, "the body's temperature" refers to the internal heat levels or thermal regulation mechanisms within the plant body that are influenced by MAP kinase signaling during temperature stress conditions like drought (which can cause heat stress) and cold temperatures.

Several studies have shown that *Arabidopsis* and rice show similarly recognized and transduced signals when exposed to cold stress but in different ways. Cold stress responses, phospholipid signaling, MAPK cascade signaling, ROS generation, and ICE-CBF (inducer of CBF expression -C-repeat binding factor) pathways have been extensively studied [73]. Studies on transgenic rice have shown that stress caused by DREB1a improves stress tolerance, lessens stress-related negative consequences, and decreases stress sensitivity [74].

Plants employ calcium signaling as a versatile signaling mechanism in response to drought stress or limited soil water availability. Three calcium sensors mainly regulate Drought-stress signaling in plants [75], highlighting its importance in plant stress responses. Plants have also been found to boost their immune system with calcium and interact with plant microbes [76]. It is thought that plant calcium signaling is regulated by calcium-dependent protein kinases (CDPKs), calcium-modules (CaMs), and calcineurin B-like proteins (CBLs). Several target proteins, such as transcription factors and metabolic enzymes, interact with and are modulated by CaMs, which bind calcium and undergo conformational changes. Protein kinases with calmodulin-like domains and kinase domains are CDPKs. The CDPK becomes activated when it binds to calcium and phosphorylates downstream targets, triggering signaling cascades. The calcium sensor protein CBL interacts with CBL-interacting protein kinases (CIPKs) in a calcium-dependent manner and activates them. In turn, CBL-CIPK complexes regulate a variety of proteins that are involved in development and stress.

Several signaling pathways trigger early signaling events when the body perceives stress. Such pathways include ROS signaling, calcium signaling, and MAP kinase cascades. Plant stress signaling involves intricate, interconnected pathways determining how plants respond to different stresses.

Numerous transcription factors have been discovered and shown via research using *Arabidopsis* and rice plants as models. Activation of transcription factors in response to stress signals alters gene expression.

Studies on *Arabidopsis* and *rice* MYB transcription factors are numerous. In plants, MYB transcription factors promote various physiological activities, including secondary metabolism, disease resistance, abiotic stress tolerance, secondary metabolism, and hormone signal transduction. According to the findings of Katiyar et al., MYB transcription factors affect plants' growth [77]. Also, drought response pathways may include MYB transcription factors, highlighting their role in post-drought gene expression regulation [78].

Concerning *Arabidopsis*, a transcription factor known as DREB2A has been recognized as a dual-functional transcription factor. It has been revealed that this transcription factor is engaged in both heat stress-induced transcription and water stress-induced transcription. In response to extreme dryness and high salt levels, this gene may control the expression of genes involved in these physiological responses by interacting with a cis-acting dehydration-responsive element (DRE) sequence [79].

Various environmental stressors, both biotic and abiotic, may trigger WRKY transcription factors to activate in plants. Several plant biological processes rely on them. Abiotic, developmental, and hormonal variables have been the focus of substantial research on how these proteins work in various plant species, including *Arabidopsis*, *rice*, potatoes, and parsley [80, 81]. Also, *Arabidopsis*'s cold stress response relies heavily on the transcription factors CBF and DREB1A, which boost oxidative stress tolerance in plants [82-84]. Research has also shown that melatonin significantly influences the transcription of specific transcription factors. Evidence suggests that the *Arabidopsis* transcription factors ZAT6 and HSFA1 are pivotal in controlling the heat stress and cold stress signaling pathways, respectively [85-87].

Arabidopsis and *rice* are model plants that control gene expression by mediating certain transcription factors in response to stress signals. Researchers have shown that plants are essential for abiotic survival and adaptation because of their capacity to respond to a wide range of environmental conditions, including heat, cold, drought, and oxidative stresses [67].

Plants rely on protective signaling pathways to lessen the effect of abiotic stresses. In response to different types of stress, complex processes are engaged along these routes. To help plants adapt and survive in harsh environments, the signaling pathways are interrelated and comprise a network of responses. Plant responses to abiotic stress are regulated by phytohormones such as JA and ABA [88, 89]. Inducing defensive reactions in plants, these hormones work by interacting with different signaling pathways. In addition, polyamines have protective functions in abiotic stress responses; improving stress tolerance in plants is possible via polyamine pathway manipulation [85]. Nitrogen and polyamines are two signaling molecules that interact to modulate plant responses to stress and protect them from damage [90]. Additionally, ABA, MAPK, and ROS signaling work together to improve plant defense systems and adapt to biotic and abiotic challenges [91].

As abiotic stress combinations are prevalent in plants, it has also been shown that systemic signaling is essential [92]. Various stressors elicit distinct systemic signaling reactions in plants, which result in the accumulation of transcripts and metabolites specific to the stressors and facilitate the process of stress adaptation (Table 1).

Table 1 The list of involved signaling pathways in various model plants in abiotic stress.

Pathway	Model Plant	Components	Function
Abscisic Acid (ABA) signaling	Arabidopsis	AREB1/ABF2, AREB2/ABF4, ABF3	Regulates responses to drought, salinity, and cold stresses
Mitogen-Activated Protein Kinase (MAPK)	Arabidopsis Rice	MKK, MPK proteins	Mediates responses to various abiotic stress factors, including cold stress
Reactive Oxygen Species (ROS) signaling	Various	NADPH oxidases, antioxidant enzymes (e.g., SOD, CAT)	Involved in oxidative stress response
Calcium (Ca ²⁺) signaling and Calcium Sensors	Wheat	Ca ²⁺ channels, calmodulin, protein kinases	Regulates responses to multiple abiotic stresses, including cold
Ethylene (ET) signaling	Arabidopsis Rice	EIN2, EIN3 transcription factor	Involved in responses to drought and other stresses
Heat Shock Factor (HSF) pathway	Arabidopsis	HSF, Heat Shock Proteins (HSPs)	Response to heat stress and other proteotoxic stresses
C-repeat Binding Factors (CBF)	Various	CBF like genes and DREB1A	Response to low-temperature stress and cold stress
CBL-CIPK System	Various	CIPK genes	Response to cold stress

By elucidating these pathways and their interactions, researchers can identify potential targets for genetic manipulation to enhance plant resilience to environmental challenges (Figure 2).



Figure 2 A schematic illustration of protective signaling pathways in abiotic stress.

4. Physiological and Biochemical Changes

Upon abiotic stress, plants upregulate stress-response and tolerance genes. Several methods have been used to study this process, including gene upregulation. Dehydration, excessive salinity, and ABA treatment stimulate AREB1/ABF2, AREB2/ABF4, and ABF3. It demonstrates the significance of these proteins and ABA in reacting to abiotic stress [93]. Under biotic and abiotic stress, the WRKY transcription factors are among the most important regulators of the plant hormone signal transduction system [94]. OsNAC6, a NAC-type transcription factor specific to plants that respond to biotic and abiotic stimuli, potentially controls the expression of genes involved in these responses [95].

Stress caused by abiotic factors may also be managed and mediated by JA, which is thought beneficial for plant regulation [89]. Recently, it has become apparent that many heat stress transcription factors (HSFs) regulate the expression of stress-responsive genes, including heat shock proteins. These HSFs influence plants' responses to different abiotic stressors (HSPs). Plants are continuously exposed to numerous stimuli via the endoplasmic reticulum, crucial in integrating biotic and abiotic signals [96].

The *rice* plant overexpressing OsNAC5, a plant transcription factor that responds to abiotic stresses, regulates genes that are inducible by stress and improves its stress tolerance. The stabilization of EIN3/EIL1 in *Arabidopsis* has also been shown to help it tolerate salinity, which suggests that ethylene signaling is crucial to adapting to abiotic stresses [97]. Furthermore, B-BOX genes exert considerable influence over plant development, growth, and stress response; thus, they might assist the plant in managing stress more effectively [98].

Various molecular mechanisms and pathways can be upregulated due to abiotic stress signaling in plant models, including hormone-mediated gene expression, transcription factor activity, and stress regulation. The upregulation of functional genes in response to this signaling encompasses various molecular pathways and mechanisms. In plants, responses to abiotic stress are complicated and coordinated, which is evident in these examples.

Abiotic stress induces various physiological adaptations in plant models through molecular, biochemical, and developmental processes. Adaptability is an essential component of plant growth and survival under adverse conditions. Numerous investigations have shown the various physiological processes by which plants adapt to abiotic stress, such as alterations in development, photosynthesis, stomatal behavior, etc.

Abiotic stresses, like high temperatures, salinity, and droughts, necessitate physiological adaptations that mitigate their effects on growth, reproduction, and survival. When stress signals are converted into ABA, some physiological and developmental processes in plants are activated, acquiring the adaptations necessary for survival [99]. In addition, plants' remarkable ability to survive in these environments and adapt to changes in their environment is fundamental to their evolutionary success, demonstrating that physiological adaptations are essential for plant survival and resilience [100].

Stress has been shown to alter plant physiological, biochemical, and molecular processes. Plants can change their photosynthetic apparatus, membrane lipid compositions, and calcium flux to cope with stress conditions and accumulate antioxidants and osmoprotectants [101]. Moreover, plant adaptation to stress is multifaceted since plants respond to environmental stress using highly

complex, integrated, and multidimensional means involving various molecular, physiological, and biochemical processes [102].

It is also essential to consider that plant hormones facilitate physiological adaptations to abiotic stress. To adjust to external challenges, including water stress and events crucial to their development and growth, vegetative tissues rely on ABA, a fundamental regulator of physiological pathways involving these cells [103]. In addition, zeatin (ZA), a member of the cytokinin family, interacts extensively with ABA during stress adaptation [104].

To understand the physiological and biological alterations that transpire in plants due to environmental stresses, including oxidative stresses, heat, cold, and drought, it is imperative to contemplate the complex molecular processes and signaling pathways at play. Devireddy et al. significantly contribute to understanding how plant hormones and ROS mediate response to temperature changes [67]. The research emphasizes that plant hormones control thermotolerance by increasing ROS generation, activating NADPH oxidases, and changing redox signaling, among other cellular and physiological reactions.

Rapid systemic signaling in plants is also covered by Waszczak et al., who discuss how electric, calcium, ROS, and hydraulic signals are integrated [105]. The research highlights the importance of fluctuations in membrane potentials, calcium levels, reactive oxygen species waves, and hydraulic pressure as essential to plants' fast, long-distance signal transmission processes. In order to fully understand the complex processes involved in plant physiological changes, one must grasp the interaction and influence of signals on how plants react to environmental challenges. Researchers have also illuminated the collaboration between ROS and ABA in regulating plants' rapid systemic adaptation in terms of both time and space [106, 107]. The study sheds insight into the complex signaling pathways and gene reprogramming in plant systemic tissues when exposed to abiotic stress, demonstrating the pivotal role played by ROS and ABA in mediating these processes. The extensive data in the study highlights the key role of ROS, plant hormones, calcium signaling, and other molecular components in regulating plant physiological responses to stress. Due to the interaction between these compounds and signaling pathways, a complicated network of both is formed. This network regulates the plant's ability to survive, adapt, and tolerate stress in response to environmental stresses. In their investigation of fast systemic communication in plants, Fichman and Mittler look at how electric, calcium, ROS, and hydraulic signals work together [106]. This research sheds light on the complex interplay of various signaling components, including receptors, glutamate, NADPH oxidases, calcium, plasmodesmata, membrane proteins, and Arabidopsis proteins, in orchestrating rapid systemic responses essential for plant survival. By investigating the mechanisms through which these signals propagate through plant vascular bundles at fast rates, the study provides valuable insights into the coordination of systemic processes in plants in response to environmental challenges.

Plant models undergo a wide range of physiological adaptations when subjected to abiotic stress, such as changes in growth, photosynthesis, stomatal behavior, hormonal regulation, and the outcome of physiological responses. The complex, multifaceted nature of the system within which plants deal with abiotic stress illustrates how adaptation to adverse environmental conditions is crucial to plant survival and productivity during unfavorable climatic conditions.

5. Outlook and Future Directions

Arabidopsis and *rice* are crop plants that share the same gene space, but translating knowledge from model plant systems poses several challenges and gaps in understanding. Although model plants and crops share the same gene space, translating their molecular mechanisms remains challenging [108, 109]. While genome sequences and genomic tools are available, phenotypic traits can still be quantified in significant crop species using high-throughput methods [110]. Several studies have uncovered epigenetic mechanisms in plant defenses, but most of these discoveries were made by studying model plants like *Arabidopsis*, resulting in challenges for application [111, 112].

Translational approaches in plant biology have been advocated to enhance understanding of how knowledge is translated from model plants to crops [113]. Using crop simulation models allows for predicting plant growth and development under diverse circumstances and investigating the relationships between these scenarios [114]. The complexity of plant systems may be represented in mathematical models and models developed using machine learning [115, 116]; however, the complexity may not be accurately represented.

Understanding how plants respond to their environment and what variables affect root growth and development is crucial for managing plant interactions under multispecific canopies and maximizing soil resource absorption by related crops. Plant translational genomics, or simply translational genomics in plants, represents the ultimate challenge to extending these applications to crops. Translating gene functions from model plants into yields is a very challenging endeavor. It is a challenging endeavour to translate gene functions from model plants into yields [117].

Transferring knowledge from model plant systems to crops presents some challenges due to the difficulty in translating molecular mechanisms, quantitative methods for phenotypic traits, epigenetic knowledge, and translational methods for solving knowledge from model plant systems into crops. Further, it is important to note that plant biology and crop improvement are experiencing significant gaps and challenges in abstracting dynamic plant physiological mechanisms into mathematical models, understanding plant root development, and translating gene functions from model plants to crops.

The cold stress-induced physiological and biochemical alterations in *Arabidopsis* result from an intricate interplay between numerous molecular pathways. Several studies have shed light on the mechanisms underlying these responses. For instance, the overexpression of transcription factors like MbMYBC1, TaABC1, VvWRKY28, and GmDREB3 has been shown to enhance cold stress tolerance in *Arabidopsis* by modulating physiological and biochemical indicators [118-121]. These factors regulate stress-responsive genes and pathways, improving plant resilience to cold stress.

Additionally, RNA-binding proteins such as GRP2, AtGRP7, and TaRZ2 have been implicated in affecting mitochondrial respiration, catalase, and peroxidase activities, and mRNA export under cold stress conditions, respectively, in *Arabidopsis* [122-124]. These proteins contribute to the regulation of gene expression and cellular processes essential for cold stress adaptation.

Furthermore, the involvement of specific transcription factors like NIZAT12 and ICE1/ICE2 from *Vitis amurensis* in enhancing cold tolerance in *Arabidopsis* has been demonstrated [125, 126]. Plants can withstand cold stress better because these transcription factors control the expression of genes sensitive to cold. Moreover, studies have highlighted the role of secondary metabolites, chlorophyll content, and α -tocopherol in mediating responses to cold stress in *Arabidopsis* [127, 128]. These

compounds protect plants from oxidative damage and maintain cellular homeostasis under cold stress conditions. The physiological and biochemical changes in various stresses involve a sophisticated network of molecular pathways and regulatory elements. Improving productivity in agriculture in adverse circumstances and increasing plant stress tolerance both need an understanding of these systems (Table 2).

Table 2 Lists physiological and biochemical changes, including stress factors, etc.

Stress Factor	Physiological Changes	Biochemical Changes	Model Plant
Drought	Reduced stomatal conductance, wilting	Increased production of abscisic acid (ABA), osmoprotectants	Arabidopsis Rice
Salinity	Ion toxicity, osmotic stress	Increased synthesis of compatible solutes, ion compartmentalization	Arabidopsis
Heat Stress	Altered growth rates, heat shock response	Induction of heat shock proteins (HSPs), changes in membrane fluidity	Arabidopsis
Oxidative Stress	Cell damage, lipid peroxidation	Activation of antioxidant enzymes (SOD, CAT), accumulation of ROS	Arabidopsis
Cold Stress	Mitochondrial respiration, catalase and peroxidase activities, and mRNA export	RNA-binding proteins and overexpression of transcription factors	Arabidopsis

6. Conclusions

In summary, studying model plants like Arabidopsis and rice has provided invaluable insights into the molecular mechanisms, signaling pathways, and physiological adaptations involved in plant responses to abiotic stresses. These model systems have shed light on stress perception mechanisms, early signaling events such as ROS production and calcium signaling, activation of MAP kinase cascades, the roles of transcription factors, hormone-mediated regulation, and various biochemical and physiological adjustments plants undergo to adapt to environmental challenges. However, translating this knowledge from model plants to crop species remains a significant challenge due to differences in phenotypes, molecular mechanisms, and genetic backgrounds. Addressing this translational gap is crucial for developing stress-tolerant crop varieties that can withstand the impacts of climate change and ensure global food security. Future research should focus on creating integrated approaches that combine cutting-edge technologies, such as high-throughput phenotyping, epigenetic studies, translational genomics, and advanced mathematical modeling, to bridge the gap between model plant systems and crop species. Furthermore, exploring the potential of emerging fields like nanotechnology and its applications in agriculture could provide novel strategies for mitigating abiotic stress in plants. Ultimately, a multi-pronged approach that leverages the knowledge gained from model plant studies, advances in biotechnology, and interdisciplinary collaborations will be essential to overcome the challenges posed by abiotic stresses and promote crop resilience in the face of changing environmental conditions.

Author Contributions

BS - Conceptualization; Data curation; Formal analysis; Investigation; Methodology; Project administration; Supervision; original draft; review & editing. The author read and approved the final manuscript.

Competing Interests

The author has declared that no competing interests exist.

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