Proceedings of the 4th International Conference on Biological Engineering and Medical Science
DOI: 10.54254/2753-8818/63/2024.17986

Molecular Mechanisms of Plant Response to Abiotic Stresses and Breeding for Stress Tolerance

Jingxi Lin

College of Life Sciences, Yunnan University, Yunnan, China

48911404@qq.com

Abstract. Major threats to global food security are abiotic stresses like salinity, drought, extreme temperatures and hypoxia. Comprehending plant responses' molecular mechanisms to these stresses is essential for stress-tolerant crops. This article provides a comprehensive overview of plant abiotic stress responses, focusing on stress signal perception and transduction, gene expression regulation, cellular and physiological adaptation mechanisms. It emphasizes advancements in identifying key factors for stress tolerance and in omics technologies facilitating these. The article also discusses applying this knowledge to develop stress-tolerant crops via genetic engineering and other means. However, it acknowledges challenges in translating molecular knowledge into practical breeding outcomes, such as stress tolerance trait complexity, genotype-by-environment interactions, and trade-offs with other agronomic traits. The article emphasizes the need for a multidisciplinary approach integrating molecular biology, genomics, biotechnology and traditional breeding to address these challenges. It also highlights the importance of exploring and using genetic diversity in wild relatives and landrace collections, and the potential of emerging technologies like systems biology and AI in speeding up stress-tolerant crop development. The review concludes by calling for continued investment in R&D, capacity building, and collaboration among researchers, breeders, policymakers and stakeholders to ensure a food-secure future faced with global climate change.

Keywords: Abiotic stress, Molecular mechanisms, Stress tolerance, Crop improvement, Sustainable agriculture.

1. Introduction

Plants, as immobile organisms, constantly face a multitude of environmental stresses throughout their life cycle. Plant growth, development, and productivity are notably impacted by these abiotic stresses such as salinity, drought, extreme temperatures, and hypoxia [1]. As the impacts of global climate change intensify, the intensity and frequency of these stresses are predicted to increase, presenting a grave danger to global food security [2]. To fulfill the rising demand for food, feed, and fiber, it is essential to cultivate stress-resistant crops capable of withstanding unfavourable environmental circumstances [3].

In recent years, there have been significant progressions in understanding the molecular mechanisms beneath plant reactions to abiotic stresses. Plants have developed intricate sensing and signaling networks to detect environmental cues and trigger appropriate defense mechanisms [4]. These include the modulation of gene expression, alteration of metabolic pathways, and activation of protective mechanisms such as antioxidant systems and osmolyte accumulation [5]. By unraveling these complex networks, researchers have pinpointed key genes, proteins, and metabolites that play a role in stress tolerance of plants. [6].

The evolution of proteomics, metabolomics, genomics and transcriptomics has significantly promoted the identification of stress-responsive genes and pathways. High-throughput sequencing technologies have enabled the genome-wide detection of stress-responsive genes and regulatory components [7]. Transcriptome profiling has revealed the dynamic changes in gene expression under stress conditions, while proteomic and metabolomic analyses have given a glimpse into the functional roles of proteins and metabolites in stress adaptation [8]. The knowledge gained from these studies has laid the foundation for developing stress-tolerant crops through approaches like genetic engineering and molecular breeding. Transgenic plants overexpressing stress-responsive genes have demonstrated increased resistance to a diverse range of abiotic stresses [3]. As potent tools for accurately modifying stress-related genes and characteristics, genome editing technologies, such as CRISPR/Cas9, have arisen [9]. Moreover, marker-assisted selection and genomic selection have facilitated the introgression of stress tolerance traits into elite crop varieties [10]. However, translating the knowledge from model plants to crop species remains a challenge. The complexity of stress responses, genotype-by-environment interactions, polygenic nature of stress tolerance traits have hindered the progress of developing stress-tolerant crops [11]. Therefore, the molecular mechanisms underlying stress tolerance in crops must be comprehensively understood as it is essential for designing effective breeding strategies and improving crop resilience to abiotic stresses.

This review article aims to provide an in-depth analysis of the current knowledge on plant responses to abiotic stresses at the molecular level, with a focus on crop species. It will discuss the latest findings on stress perception, signal transduction, gene regulation, and adaptation mechanisms. The article will also highlight the challenges and opportunities in translating this knowledge into breeding stress-tolerant crops, considering the complex interactions between genotypes, environments, and management practices. Finally, the review will outline future research directions and strategies for harnessing the potential of molecular breeding and biotechnology to develop climate-resilient crops for sustainable agriculture.

2. Theoretical Research

Plant responses to abiotic stresses involve a complex network of molecular mechanisms that enable them to perceive, transduce, and adapt to adverse environmental conditions. At the forefront of this response are the stress detection and signal transmission pathways. Plants have evolved a diverse array of sensors and receptors that can detect changes in the environment, such as osmotic stress, ionic imbalance, and temperature fluctuations [1]. These sensors include membrane-bound receptor-like kinases (RLKs), ion channels, and cytosolic calcium sensors, among others [4].

Upon stress perception, the signals are transduced through a network of second messengers and protein phosphorylation cascades. Calcium is of central importance in stress signaling, with stress-induced calcium influx activating various calcium-binding proteins and downstream signaling components [6]. Stress signal transduction involves other key players such as reactive oxygen species (ROS), mitogen-activated protein kinases (MAPKs), and phytohormones like abscisic acid (ABA), ethylene, and jasmonic acid(JA) [12].

The signals that are transduced eventually bring about alterations in gene expression, a vital element in plant stress responses. Transcription factors (TFs) play a pivotal role in regulating stress-responsive gene expression. Several families of transcription factors, including NAC, WRKY, bZIP, and MYB, are involved in abiotic stress responses [7]. These TFs attach to particular cis-regulatory elements in the promoters of genes responsive to stress, activating or repressing their expression. In addition to transcriptional regulation, post-transcriptional mechanisms, including alternative splicing, mRNA stability, and microRNA-mediated gene silencing, also contribute to the fine-tuning of stress-responsive gene expression [8].

DOI: 10.54254/2753-8818/63/2024.17986

The products of stress-responsive genes, including functional proteins and metabolites, constitute the cellular defense mechanisms against abiotic stresses. These consist of enzymes taking part in the biosynthesis of osmoprotectants (like proline and glycine betaine), antioxidants (such as glutathione and ascorbate), and protective proteins (for instance, late embryogenesis abundant proteins and heat shock proteins) [5]. The accumulation of these protective molecules helps to maintain cellular homeostasis, stabilize proteins and membranes, and scavenge ROS under stress conditions.

In addition to these cellular-level responses, plants also employ morphological and physiological adaptations to cope with abiotic stresses. These include changes in root architecture, leaf morphology, stomatal regulation, and photosynthetic efficiency [2]. The coordination of these responses across different scales, from molecular to whole-plant levels, is crucial for the successful adaptation of plants to abiotic stresses.

3. Problems in Research Objects

Despite the significant progress made in understanding the molecular mechanisms of plant abiotic stress responses, there are still several challenges in applying this knowledge to develop stress-tolerant crops. One major obstacle is the complexity of stress tolerance traits, which are polygenic and influenced by multiple genes and their interactions [11]. This complexity makes it hard to recognize and control the key genes that underlie stress tolerance in crops.

Moreover, stress tolerance traits often exhibit significant genotype-by-environment (G×E) interactions. The performance of a genotype under stress conditions can vary widely depending on the specific environment and management practices [4]. This variability poses challenges in designing and implementing effective breeding strategies for stress tolerance. The lack of consistent phenotyping protocols and high-throughput screening methods further complicates the evaluation and selection of stress-tolerant genotypes.

Another challenge lies in the trade-offs between stress tolerance and other agronomic traits. In many cases, stress tolerance is associated with reduced growth and yield under optimal conditions. This phenomenon, known as the "cost of tolerance," can limit the adoption of stress-tolerant varieties by farmers [3]. Balancing stress tolerance with yield stability and other desirable traits is a critical consideration in crop breeding programs.

The limited genetic diversity within elite crop germplasm is another constraint in breeding for stress tolerance. Modern crop varieties have undergone intensive selection for yield and quality traits, resulting in a narrow genetic base. This narrow genetic diversity limits the available sources of stress tolerance alleles and hinders the development of resilient crop varieties [10]. Exploring and harnessing the genetic diversity present in wild relatives and landrace collections is crucial for broadening the gene pool and improving stress tolerance in crops.

Furthermore, the complex interactions between multiple abiotic stresses pose additional challenges. In natural environments, plants are often exposed to a combination of stresses, such as drought and heat or salinity and nutrient deficiency. These combined stresses can have synergistic or antagonistic effects on plant performance, making it difficult to predict and breed for multi-stress tolerance [1]. Comprehending the molecular mechanisms that underlie plant responses to multiple stresses and their interactions is crucial for creating crops with broad-spectrum stress tolerance.

Lastly, the gap between laboratory research and field application is a significant hurdle in translating molecular knowledge into practical breeding outcomes. Many stress tolerance studies are conducted under controlled conditions using model plants, which may not accurately reflect the complex field environments encountered by crops [2]. Bridging this gap requires robust field testing, validation of stress tolerance mechanisms, and collaboration between researchers, breeders, and farmers.

4. Problem-Solving Methods

To address the challenges in developing stress-tolerant crops, a multidisciplinary approach integrating molecular biology, genomics, biotechnology, and traditional breeding is necessary. One promising strategy is the identification and utilization of stress-reactive genes and regulatory elements derived

DOI: 10.54254/2753-8818/63/2024.17986

from diverse genetic resources. This can be achieved through comparative genomics, transcriptomics, and functional characterization of stress-related genes from wild relatives, landraces, and stress-tolerant crop genotypes [7]. By mining these genetic resources, novel stress tolerance alleles and mechanisms can be discovered and introduced into elite crop varieties through genetic engineering or marker-assisted breeding.

Genome editing technologies, particularly CRISPR/Cas9, offer unprecedented opportunities for precise manipulation of stress-related genes in crops. By targeting specific genes or regulatory elements, researchers can create desirable allelic variations or knock out undesirable alleles associated with stress susceptibility [9]. This targeted approach can help to minimize the trade-offs between stress tolerance and other agronomic traits. Moreover, genome editing can accelerate the development of crops with stress tolerance by reducing the time and resources required for conventional breeding.

Molecular breeding approaches, like marker-assisted selection (MAS) and genomic selection (GS), are potent instruments for enhancing stress tolerance in crops. MAS involves the use of molecular markers linked to stress tolerance QTLs (quantitative trait loci) to select superior genotypes in breeding populations. GS, on the other hand, utilizes genome-wide markers to forecast the breeding values of individuals according to their genomic profiles [10]. These approaches can improve the efficiency and accuracy of selecting stress-tolerant lines, especially for complex traits controlled by multiple genes.

In addition to genetic approaches, advances in phenomics and high-throughput screening methods are crucial for evaluating stress tolerance in crops. Remote sensing technologies, such as drone-based imaging and hyperspectral sensors, enable non-destructive and large-scale phenotyping of plant reactions to non-biological stresses. [4]. Machine learning algorithms can be applied to analyze the vast amounts of phenotypic data generated, allowing for the recognition of stress-tolerant genotypes and the dissection of complex stress tolerance traits.

Integrating multi-omics data, including genomics, transcriptomics, proteomics, and metabolomics, can provide a systems-level comprehension of plant stress reactions. By merging these various datasets, researchers can identify key regulatory networks, metabolic pathways, and molecular markers associated with stress tolerance [1]. This knowledge can direct the creation of targeted breeding approaches and the selection of candidate genes for genetic modification.

Lastly, collaborative efforts among researchers, breeders, and farmers are essential for successful translation of molecular knowledge into stress-tolerant crops. Field trials and on-farm evaluations are necessary to validate the performance of stress-tolerant varieties under real-world conditions. Engaging farmers in participatory breeding and variety selection can ensure the adoption and widespread dissemination of stress-tolerant crops [3]. Furthermore, capacity building and technology transfer to developing countries, where the influence of abiotic stresses on crop production is extremely severe, should be prioritized to promote global food security.

5. Conclusions

Developing stress-tolerant crops is a vital challenge for ensuring food security amid global climate change. Progress in molecular biology, genomics, and biotechnology has significantly improved our comprehension of the intricate mechanisms underlying plant responses to non-biological stresses. This knowledge has opened up new avenues for improving stress tolerance in crops by means of genetic engineering, molecular breeding, and targeted gene manipulation [1, 7, 9].

However, translating molecular knowledge into practical breeding outcomes requires a multidisciplinary approach that integrates cutting-edge technologies with traditional breeding practices. The identification and utilization of novel stress tolerance genes and alleles from diverse genetic resources, combined with precise genome editing tools, can accelerate the development of stress-tolerant crops [4, 10]. Molecular breeding approaches like marker-assisted selection and genomic selection, can improve the efficiency and accuracy of selecting superior genotypes.

Advances in phenomics and high-throughput screening methods are crucial for evaluating stress tolerance in crops under field conditions [2]. The integration of multi-omics data can offer a comprehensive understanding of plant stress responses at a systems level, guiding the development of targeted breeding strategies [1]. Collaborative efforts among researchers, breeders, and farmers are essential for successful translation of molecular knowledge into stress-tolerant crops and their adoption by end-users [3].

Despite the progress made, several challenges remain in developing crops with durable and broad-spectrum stress tolerance. The complex nature of stress tolerance traits, genotype-by-environment interactions, and trade-offs with other agronomic traits require further research and innovative solutions [11]. Exploring the genetic diversity present in wild relatives and landrace collections is crucial for broadening the gene pool and improving stress tolerance in crops [10].

Looking ahead, the integration of emerging technologies like genome editing, systems biology, and artificial intelligence, will have a crucial role in accelerating the development of stress-tolerant crops [1, 9]. Continued investment in research and development, as well as capacity building and technology transfer to developing countries, is necessary to harness the entire potential of these technologies for worldwide food security.

In conclusion, the promotion of stress-tolerant crops is a crucial necessity for sustainable agriculture in the age of climate change. By harnessing the power of molecular biology, genomics, and biotechnology, and integrating them with traditional breeding practices, we can create resilient crop varieties that can withstand the challenges posed by abiotic stresses [3]. This will demand a joint effort from researchers, breeders, policymakers, and stakeholders to prioritize research, investment, and collaboration in this vital area. With the right tools, knowledge, and commitment, we can ensure a food-secure future for generations to come.

References

[1] Zhu, J. K. (2016). Abiotic Stress Signaling and Responses in Plants. Cell, 167(2), 313-324.

[2] Bailey-Serres, J., Lee, S. C., & Brinton, E. (2012). Waterproofing crops: effective flooding survival strategies. Plant Physiology, 160(4), 1698-1709.

[3] Hu, H., & Xiong, L. (2014). Genetic engineering and breeding of drought-resistant crops. Annual Review of Plant Biology, 65, 715-741.

[4] Roy, S. J., Negrão, S., & Tester, M. (2014). Salt resistant crop plants. Current Opinion in Biotechnology, 26, 115-124.

[5] Munns, R., & Tester, M. (2008). Mechanisms of salinity tolerance. Annual Review of Plant Biology, 59, 651-681.

[6] Ji, H., Pardo, J. M., Batelli, G., Van Oosten, M. J., Bressan, R. A., & Li, X. (2013). The Salt Overly Sensitive (SOS) pathway: established and emerging roles. Molecular Plant, 6(2), 275-286.

[7] Fang, Y., & Xiong, L. (2015). General mechanisms of drought response and their application in drought resistance improvement in plants. Cellular and Molecular Life Sciences, 72(4), 673-689.

[8] Liu, Q., Zhang, Y. C., Wang, C. Y., Luo, Y. C., Huang, Q. J., Chen, S. Y., \... & Chen, Y. Q. (2017). Expression analysis of phytohormone-regulated microRNAs in rice, implying their regulation roles in plant hormone signaling. FEBS Letters, 583(4), 723-728.

[9] Zhang, Z., Li, J., Pan, Y., Li, J., Zhou, L., Shi, H., \... & Shang, H. (2019). Correction: Natural variation in CTB4a enhances rice adaptation to cold habitats. Nature Communications, 10(1), 1-14.

[10] Shi, Y., Ding, Y., & Yang, S. (2018). Molecular Regulation of CBF Signaling in Cold Acclimation. Trends in Plant Science, 23(7), 623-637.

[11] Thomashow, M. F. (1999). Plant cold acclimation: freezing tolerance genes and regulatory mechanisms. Annual Review of Plant Biology, 50(1), 571-599.

[12] Yoshida, T., Mogami, J., & Yamaguchi-Shinozaki, K. (2014). ABA-dependent and ABA-independent signaling in response to osmotic stress in plants. Current Opinion in Plant Biology, 21, 133-139.