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# EXPLORING THE CRITICAL ROLES OF EPIGENETICS IN CROP ADAPTATION AND RESILIENCE IN STRESS AND CLIMATE CHANGE

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**Abstract**:
Food security has emerged as significant threats to humanity that need to be addressed and demand for new approaches for crop improvement, adaptation, and resilience such as epigenetic regulation. Plants are able to adjust to altering environmental situations because epigenetic processes, including DNA methylation, histone modifications, and non-coding RNA control, can affect and modulate gene expression by responding to environmental stimuli. Plants use epigenetic control as a critical mechanism for stress response and adaptation to climate change. This review paper has investigated the recent advancement and association between epigenetics and crop resilience, exploring the critical role of epigenetic modifications in stress adaptation, tolerance, and phenotypic plasticity. By understanding the role of epigenetics on crop adaptation and resilience, more sustainable and productive agricultural systems can be created to overcome worldwide food security. Future research in this field will continue to reveal the insightful and valuable complexities of epigenetic regulation and its potential applications in crop improvement and resilience and this will pave the way for the exploitation of epigenetic variation in crop productivity and breeding.

**Keywords**: Crop; Epigenetics; DNA Methylation; Climate Change

## Introduction

The world is compelled to boost agricultural productivity and efficiency in a responsible way due to the world's population growing at an alarming rate and the challenges that climate change poses to crop development. Through the integration of several disciplines, including genetics, plant physiology, and biotechnology, genetic enhancement of crops can accomplish this goal. One of the most crucial conditions for a crop of interest is the integration of genetic material. A deeper understanding of the impact of epigenetic modifications on plant phenotypic, in addition to genetic variance, has accelerated agricultural growth. Epigenetic material affects the phenotypic diversity and reproductive activities of plants, especially the adaptive reactions to environmental stresses. This has made researchers reevaluate how genes and phenotypes are related[1]. Plant maturation mechanisms and reactions to environmental restrictions have been evaluated and characterized in relation to epigenetic modifications, as well as key agronomical variables as respiration, energy-use efficiency, production elements, and seed quality. A gene's transcription is impacted by its DNA sequence and the complex arrangement of genes inside chromosomes at the molecular scale[2]. In eukaryotes, the DNA is highly compacted and tightly bound to proteins known as histones; this arrangement is known as chromatin. The chromatin at a specific gene must be accessible for the binding of transcription factors (TF) and RNA polymerase in order for transcription to begin at that gene. Therefore, the chromatin structure at a particular gene determines whether the gene is "on" or "off". Epigenetic knowledge affects plant growth procedures and phenotypic plasticity, especially adaptive reactions to external stressors. This has made experts reevaluate how genes and phenotypes are related. Plant growth procedures and reactions to outside restrictions have been evaluated and evaluated in relation to epigenetic changes, as well as crucial agronomical variables as respiration, energy-use efficiency, yield components, and seed quality. A gene's transcription is regulated at the molecular level by both its DNA sequence and the complex arrangement of genes inside chromosomes[3].

**Table 1: Summarizing the types of plant species, epigenetic changes, effects, mechanisms, and outcomes**

| Plant Species | Epigenetic Change | Effect | Mechanism | Outcomes | References |
|---|---|---|---|---|---|
| ***Arabidopsis thaliana*** | DNA Methylation | Drought tolerance | Methylation of stress-responsive genes | Enhanced water retention, improved survival under drought | |
| ***Zea mays* (Maize)** | Histone Modification | Heat and salt stress resistance | Acetylation of histones near stress genes | Increased expression of stress response genes, better yield | [5] |
| ***Oryza sativa* (Rice)** | Non-coding RNA Regulation | Cold tolerance | miRNA-mediated silencing of cold-sensitivity genes | Reduced damage from low temperatures, enhanced cold resilience | [6] |
| ***Brassica napus* (Rapeseed)** | DNA Methylation | Disease resistance to fungal pathogens | Methylation of defense genes | Improved immune response, reduced fungal infection rates | [7] |
| ***Solanum lycopersicum* (Tomato)** | Histone Modification | Drought and salinity tolerance | Histone deacetylation | Reduced water loss, better growth in saline environments | [8] |
| ***Glycine max* (Soybean)** | DNA Methylation | High salinity tolerance | Silencing of salinity sensitivity genes | Increased tolerance to salt stress, enhanced plant growth | [9] |
| ***Triticum aestivum*** | Non-coding RNA | Enhanced nitrogen use | miRNA regulation of | Improved nitrogen absorption, higher | [10] |

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|---|---|---|---|---|---|
| **(Wheat)** | Regulation | efficiency | nitrogen assimilation genes | yield in low-nutrient soils | |
| ***Populus*** **(Poplar trees)** | Histone Modification | Adaptation to environmental changes (light, temp) | Histone acetylation in photoreceptor genes | Enhanced growth in varying light conditions, adaptive plasticity | [11] |
| ***Capsicum annuum*** **(Chili pepper)** | DNA Methylation | Response to oxidative stress | Methylation changes in antioxidant enzyme genes | Increased antioxidant activity, better oxidative stress management | [12] |
| ***Cucumis sativus*** **(Cucumber)** | Non-coding RNA Regulation | Heat stress tolerance | Small RNA-regulated stress response genes | Reduced heat damage, improved heat resilience | [13] |

## 1. Epigenetic Control of Plant

The epigenome may now be explored more thoroughly thanks to the effective sequencing of simulated plants with well-annotated genomes, such as Arabidopsis, rice, and soybean. This includes single-nucleotide precision whole-genome methylation studies. Scientists now have a greater awareness and comprehension of the possible tissue-specific epigenetic modifications and activities in plants because to detailed maps of DNA methylation sequences[14]. In the shoots and roots of the Arabidopsis accession Columbia-0 (Col-0), scientists measured DNA methylation, nucleosome ranges, and transcriptional activities. They then connected the identified organ-specific changes in gene expression to unique epigenetic patterns. Although global differences in DNA methylation patterns between the examined tissues do not exist, hypermethylated genomic locations are more common in shoots than in roots. Similar scientists discovered a family of extensin genes that activate themselves at least ten times more frequently and had a smaller nucleosome concentration in roots than in shoots. These observations' ecological relevance is still unclear. Previous research on the patterns of DNA methylation and demethylation in four rice genotypes showed that roots' relative DNA hypomethylation ensures increased flexibility and stress tolerance[15]. The matter is still up for debate, despite the fact that additional research has shown tissue-specific correlations between different chromatin modulators and gene expression. Throughout the growth of Arabidopsis, specialized tissues such as the embryo, endosperm, and pollen have demonstrated extensive alterations in the expression of particular genes and DNA methylation sequences. Similar processes preserve the methylation in somatic cells and pollen, although pollen has greater effectiveness of CG methylation repairs, which may play a role in the inheritance of methylation between generations[16].

Key locations for the epigenetic regulation of embryonic adaptability in annual, biennial, and perennial plants including Arabidopsis, sugar beet, and poplar are meristems, which are centers for histogenesis and organogenesis. Meristems have the ability to transfer epigenetic information to fresh organs, the following generation, or not (as in the case of vernalization) either mitotically or even meiotically (for shoot apical meristem). According to recent research, redox and hormone signaling networks work in concert with the epigenetic machinery to regulate meristem plasticity, enabling the incorporation of the epigenetic component within the context of the metabolic reaction[17].

In conclusion, the general degree of methylation seems to be rather steady, although it may fluctuate depending on the various DNA methylation patterns seen in various plant tissues or settings. It is yet unclear how DMRs affect phenotypic variability and gene regulation, although they may cause natural variations in key plant features including fruit and flower growth, ripening, and flavonoid metabolism. Numerous crop varieties develop vegetatively, yielding clonal plants that, in spite of being clonal, display diversity in their progeny's phenotype[18]. The sexual offspring of the recreated plants exhibit the original tissue-specific methylation and transcription trends, according to the study of regenerant strains from somatic embryos of A. thaliana, induced from roots or leaves. During meiosis, the epigenetic patterns and the consequent characteristics associated with the initial tissue integrity are stable and passed down through at least four generations of self-crossing. Therefore, by altering the distribution of epigenetic tags, the particular tissue employed as an explant could impact the epi-methylation and gene expression characteristics of clonal plants, resulting in unexpected phenotypic heterogeneity[19].

## 2. The role of epigenetics in gene expression under abiotic stress

Environmental stressors that plants face on a regular basis include inadequate water and nutrient accessibility, fluctuating temperatures, intense light, and salt and heavy metal concentration in the soil. Plants have evolved genetic and epigenetic defense systems to survive individual or combination stresses and relationships in response to changing climates and the ensuing rise in unexpected climatic circumstances[20]. Thus, study of the genomic and regulatory underpinnings of reactions to environmental alterations is necessary to comprehend this variety in crops. In one such study, the memory of stressful circumstances in Arabidopsis was examined using priming by heat stress as a paradigm. The goal was to discover genes that are especially needed for temperature shock retention but not for the plant's first reactions to heat. The FORGETTER1 (FGT1) gene was discovered by the researchers, who also discovered that the FGT1 protein immediately attaches to a particular category of heat-inducible genes and modifies the packaging of the DNA carrying particular genes to keep them accessible and functional at all times. Their discoveries may result in novel methods for improving crop resilience to abiotic stress, since understanding the durability and heredity characteristics of epigenetic markings and the control processes governing them is essential for breeding purposes[21].

**Table 2**: Summarizing plant responses to different stressful situations, the type of stress, the physiological response, the molecular mechanisms involved, and the outcomes:

| Stress Type | Plant Response | Physiological Response | Molecular Mechanism | Outcomes | References |
|---|---|---|---|---|---|
| **Drought** | Stomatal closure | Reduction in water loss | ABA (Abscisic acid) signaling | Increased water retention, survival in dry conditions | [22] |
| **Salinity** | Ion homeostasis adjustment | Sequestration of excess salts in vacuoles | SOS (Salt Overly Sensitive) signaling pathway | SOS (Salt Overly Sensitive) signaling pathway | [23] |
| **Heat stress** | Synthesis of heat shock proteins (HSPs) | Protein folding and stabilization | Upregulation of HSP genes | Protection of cellular proteins, heat tolerance | [24] |
| **Cold stress** | Increased membrane fluidity | Production of unsaturated fatty acids | CBF (C-repeat binding factor) transcription factors | Maintenance of membrane integrity, cold tolerance | [25] |
| **Pathogen Attack** | Hypersensitive response (HR) | Localized cell death around infection site | Activation of defense-related genes (e.g., PR proteins) | Limitation of pathogen spread, enhanced immunity | [26] |
| **Nutrient Deficiency** | Root elongation and nutrient scavenging | Increased root-to-shoot ratio | Upregulation of nutrient transporter genes | Improved nutrient uptake, sustained growth | [27] |
| **Oxidative Stress** | Accumulation of antioxidants (e.g., ascorbate, glutathione) | Detoxification of reactive oxygen species (ROS) | Upregulation of antioxidant enzyme genes (e.g., SOD, CAT) | Reduced cellular damage, increased stress tolerance | [28] |

## 3. Epigenetic Control of Plant Response to Stress

Research has been previously done on the epigenetic processes underlying chromatin mark reorganization and alterations in plant stress reactions, both biotic and abiotic. For instance, heat-shock protein manufacturing in germ cells could be epigenetically modulated, therefore may have an impact on mature plant development. Pollen's reactions to heat exposure are influenced by epigenetic mechanisms. The entire genome's DNA methylation and the production of methyltransferase during specific pollen developmental stages are altered by extreme heat. Heat exposure can trigger genomic TE silencing using RdDM in pollen[29]. Furthermore, heat stress controls the transcription of many small RNA in pollen and modifies chromatin configuration through essential chromatin changes. Small RNAs have the ability to rewire the male germline and suppress TEs, which controls pollen sensitivity to extreme temperatures. When the DDM1 enzyme is altered, more siRNAs are produced, which serves to protect the epigenetic data within male gametes by reducing TE movement. This reactivates some of these TEs. Clarifying the genes that encode the enzymes responsible for DNA methylation movement, which could impact transposon suppression, could improve pollen reproductive capacity and production under abiotic stress scenarios[30].

## 4. Epigenetics and Plant Stress Responses Strategies

Complicated biological and molecular changes underlie plant stress reactions, which allow plants to endure and adjust to unfavorable environmental circumstances. Plant stress mechanisms are significantly influenced by epigenetic control, as evidenced by recent groundbreaking discoveries in the practice of epigenetics. A portion of the maiPlants' stress-related genes undergo DM sequence alterations in response to drought strain, which boosts the production of these genes and enhances their resistance to drought stress. Comparable epigenetic modifications are brought about in stress-related genes by various forms of stress, including heat stress and pathogen infection. the increased amounts of DM in the HvCKX 2.1 promoter region under drought stress. Their elevated cytokinin concentrations caused a rapid initiation of shoots[31]. Furthermore, the change caused by the drought in rice was genetic, meaning that subsequent generations would continue to have the modified DM sequence. After exposure to CD, rice genes changed with DM exhibit changed transcription patterns. These changes are associated with transcriptional variations in stress-responsive genes related to metal transportation, metabolism, and regulatory. The notion of "epigenetic memory," which states that plants can store an epigenetic fingerprint of previous stress events and utilize it to modify their physiological reactions in future instances, is another significant discovery. In Arabidopsis thaliana, this phenomena has been noticed: even when the stress eliminates treatment to drought conditions causes long-lasting changes in DM structures at the increased locations of stress-related genes[32].

Hormones are essential for plants to respond to stress, and new studies have demonstrated that plant stress adaption involves the epigenetic modification of hormone transmission. Research has revealed, for instance, that DM and HM control the signaling of abscisic acid (ABA), and that these epigenetic modifications are essential for ABA-mediated stress reactions. Secondary metabolism regulated by epigenetic mechanisms: Utilizing secondary metabolites like alkaloids and phenolic chemicals, plants have evolved a highly advanced defensive strategy to fend off potential dangers from herbivores and pathogens. According to recent studies, the production of these chemicals is also significantly influenced by epigenetic control. Particularly, research shows that histone alterations and DM enhance the gene alteration that yields anthocyanins, an unique kind of phenolic molecule that protects plants against environmental harm and UV light. Plant germination and the stress reaction depend on stem cells, and new studies have revealed that stem cell viability involves epigenetic control. For instance, research has revealed that DM and HM have an impact on the determinations made about the destiny of stem cells in Arabidopsis thaliana[33].

## 5. Regulation of Plant Epigenetic and Impacts

The ways in which plants regulate their epigenetic makeup in response to stress have important ramifications for farming and crop development. Scientists may be able to improve crop stress tolerance by figuring out the epigenetic regulatory pathways that govern stress reactions. For example, crop resilience to disease assaults, salt, and stress could be increased by modifying histone alterations or DM patterns[34]. Additionally, finding stress-responsive ncRNAs and their targets may open up new options for breeding and genetic engineering projects that try to increase agricultural tolerance to stress. Even more accuracy in locus-specific epigenetic breeding technique is now achievable because of significant developments in the creation of synthetic DNA-binding domains. Though the transfer can be volatile in plants, one special benefit of being a plant is that it does not require germline upkeep, facilitating the flow of epigenetic material during gametogenesis[35].

## 6. Future Prospects

Epigenetics presents a promising avenue for enhancing crop resilience. By precisely manipulating epigenetic modifications and understanding, researcher can develop crops with improved traits such as stress tolerance, disease resistance, and efficient nutrient utilization. One of the most exciting applications of epigenetics lies in precision breeding. Epigenetic markers can be used to identify genotypes with desirable traits, accelerating the breeding process. Additionally, CRISPR-based epigenetic editing techniques allow for targeted modifications of epigenetic marks, enabling the creation of crops with tailored traits. Epigenetics can also play a crucial role in improving crop resilience to environmental stresses. Epigenetic modifications can help plants "remember" past stress experiences, enabling them to respond more effectively to future challenges. Furthermore, epigenetic engineering can be used to enhance traits such as drought tolerance, salinity resistance, and heat tolerance. Another area of interest is the influence of epigenetics on crop-microbe interactions. Epigenetic mechanisms can regulate the establishment and maintenance of beneficial symbiotic relationships with microorganisms. This can contribute to enhanced disease resistance and improved nutrient uptake.

## 7. Conclusion

Epigenetics holds transformative potential for advancing crop adaptation and resilience in the face of growing environmental challenges. Unlike genetic mutations, epigenetic modifications offer a dynamic and reversible mechanism that can rapidly alter gene expression in response to external stressors. This adaptability is crucial in managing abiotic factors like drought, salinity, and extreme temperatures, as well as biotic threats from pathogens and pests. Furthermore, the ability of epigenetic changes to be inherited across generations adds a unique layer of resilience, allowing crops to develop lasting adaptive traits without direct changes to their DNA sequence. The exploration of epigenetic processes such as DNA methylation, histone modification, and non-coding RNA regulation has unveiled their pivotal roles in controlling key developmental and stress-response pathways in crops. These mechanisms enable plants to fine-tune their physiological responses, conferring greater flexibility in growth and survival under stress conditions. The growing body of research highlights that leveraging epigenetic modifications can contribute significantly to crop improvement, particularly in the context of climate change, where environmental conditions are becoming increasingly unpredictable. Novel technologies, including epigenome editing and the identification of natural epigenetic variants, offer innovative strategies for crop enhancement. These approaches circumvent some of the ethical and regulatory concerns associated with traditional genetic modification, providing alternative methods for achieving increased resilience and productivity. By incorporating epigenetic insights into modern breeding programs, we can develop crops that not only perform better under adverse conditions but also retain their adaptability over multiple generations.

## Conflict of interest

None

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None

## 8. References

1. A. Steensland and T. L. Thompson, "2020 global agricultural productivity report: productivity in a time of pandemics," 2020.
2. M. Chiliński, K. Sengupta, and D. Plewczynski, "From DNA human sequence to the chromatin higher order organisation and its biological meaning: using biomolecular interaction networks to understand the influence of structural variation on spatial genome organisation and its functional effect," in *Seminars in cell & developmental biology,* 2022, vol. 121: Elsevier, pp. 171-185.
3. A. Hafner and A. Boettiger, "The spatial organization of transcriptional control," *Nature Reviews Genetics,* vol. 24, no. 1, pp. 53-68, 2023.
4. S. Feng, Z. Zhong, M. Wang, and S. E. Jacobsen, "Efficient and accurate determination of genome-wide DNA methylation patterns in Arabidopsis thaliana with enzymatic methyl sequencing," *Epigenetics & chromatin,* vol. 13, pp. 1-17, 2020.
5. M. Yue *et al.*, "Histone acetylation of 45S rDNA correlates with disrupted nucleolar organization during heat stress response in Zea mays L," *Physiologia Plantarum,* vol. 172, no. 4, pp. 2079-2089, 2021.
6. I. Khan, S. Khan, M. Akhoundian, D. Shah, S. S. Shah, and S. A. Jan, "Biogenesis of Non-coding RNAs (ncRNAs) and Their Biological Role in Rice (Oryza sativa L.)," *Plant Molecular Biology Reporter,* vol. 41, no. 3, pp. 333-344, 2023.
7. S. Fan, H. Liu, J. Liu, W. Hua, S. Xu, and J. Li, "Systematic analysis of the DNA methylase and demethylase gene families in rapeseed (Brassica napus L.) and their expression variations after salt and heat stresses," *International Journal of Molecular Sciences,* vol. 21, no. 3, p. 953, 2020.
8. S. Chen *et al.*, "From non-coding RNAs to histone modification: The epigenetic mechanisms in tomato fruit ripening and quality regulation," *Plant Physiology and Biochemistry,* p. 109070, 2024.
9. L. Sun *et al.*, "Maintenance of grafting reducing cadmium accumulation in soybean (Glycine max) is mediated by DNA methylation," *Science of The Total Environment*, vol. 847, p. 157488, 2022.
10. N. Li *et al.*, "Identification of long non-coding RNA-microRNA-mRNA regulatory modules and their potential roles in drought stress response in wheat (Triticum aestivum L.)," *Frontiers in Plant Science,* vol. 13, p. 1011064, 2022.
11. O. F. Nunez-Martinez, L. M. Jones, and K. Bräutigam, "Epigenetic Regulation of Genome Function in Populus," in *The Poplar Genome*: Springer, 2024, pp. 43-56.
12. A. G. Ince and M. Karaca, "Tissue and/or developmental stage specific methylation of nrDNA in Capsicum annuum," *Journal of plant research,* vol. 134, no. 4, pp. 841-855, 2021.
13. S. S. Dey *et al.*, "Genome wide identification of lncRNAs and circRNAs having regulatory role in fruit shelf life in health crop cucumber (Cucumis sativus L.)," *Frontiers in Plant Science,* vol. 13, p. 884476, 2022.
14. J. J. Gallo-Franco, C. C. Sosa, T. Ghneim-Herrera, and M. Quimbaya, "Epigenetic control of plant response to heavy metal stress: a new view on aluminum tolerance," *Frontiers in plant science,* vol. 11, p. 602625, 2020.
15. J. Zeng *et al.*, "Nitric oxide controls shoot meristem activity via regulation of DNA methylation," *Nature Communications,* vol. 14, no. 1, p. 8001, 2023.
16. M. Zhou, A. Riva, M.-P. L. Gauthier, M. P. Kladde, R. J. Ferl, and A.-L. Paul, "Single-molecule long-read methylation profiling reveals regional DNA methylation regulated by Elongator Complex Subunit 2 in Arabidopsis roots experiencing spaceflight," *Biology Direct,* vol. 19, no. 1, p. 33, 2024.
17. J. Jiang *et al.*, "UVR8 interacts with de novo DNA methyltransferase and suppresses DNA methylation in Arabidopsis," *Nature plants,* vol. 7, no. 2, pp. 184-197, 2021.
18. H. Zhang and J.-K. Zhu, "Epigenetic gene regulation in plants and its potential applications in crop improvement," *Nature Reviews Molecular Cell Biology,* pp. 1-17, 2024.

19. E. R. Konzen *et al.*, "Molecular markers in bamboos: understanding reproductive biology, genetic structure, interspecies diversity, and clonal fidelity for conservation and breeding," *Biotechnological Advances in Bamboo: The "Green Gold" on the Earth,* pp. 33-62, 2021.
20. F. A. Dar, N. U. Mushtaq, S. Saleem, R. U. Rehman, T. U. H. Dar, and K. R. Hakeem, "Role of epigenetics in modulating phenotypic plasticity against abiotic stresses in plants," *International journal of genomics*, vol. 2022, no. 1, p. 1092894, 2022.
21. L. Siebler, "Identifying novel regulators of heat stress memory in Arabidopsis thaliana," Universität Potsdam, 2024.
22. [2M. Muhammad Aslam *et al.*, "Mechanisms of abscisic acid-mediated drought stress responses in plants," *International journal of molecular sciences,* vol. 23, no. 3, p. 1084, 2022.
23. I. Amin, S. Rasool, M. A. Mir, W. Wani, K. Z. Masoodi, and P. Ahmad, "Ion homeostasis for salinity tolerance in plants: A molecular approach," *Physiologia Plantarum,* vol. 171, no. 4, pp. 578-594, 2021.
24. S. Khan, R. Jabeen, F. Deeba, U. Waheed, P. Khanum, and N. Iqbal, "Heat shock proteins: classification, functions and expressions in plants during environmental stresses," *Journal of Bioresource Management*, vol. 8, no. 2, p. 9, 2021.
25. P. Sharma *et al.*, "The role of key transcription factors for cold tolerance in plants," in *Transcription factors for abiotic stress tolerance in plants*: Elsevier, 2020, pp. 123-152.
26. A. Noman *et al.*, "Plant hypersensitive response vs pathogen ingression: death of few gives life to others," *Microbial pathogenesis,* vol. 145, p. 104224, 2020.
27. S. Abbas, M. T. Javed, Q. Ali, M. Azeem, and S. Ali, "Nutrient deficiency stress and relation with plant growth and development," in *Engineering tolerance in crop plants against abiotic stress*: CRC Press, 2021, pp. 239-262.
28. P. Garcia-Caparros *et al.*, "Oxidative stress and antioxidant metabolism under adverse environmental conditions: a review," *The Botanical Review,* vol. 87, pp. 421-466, 2021.
29. Y. N. Chang, C. Zhu, J. Jiang, H. Zhang, J. K. Zhu, and C. G. Duan, "Epigenetic regulation in plant abiotic stress responses," *Journal of integrative plant biology,* vol. 62, no. 5, pp. 563-580, 2020.
30. P. Jogam, D. Sandhya, A. Alok, V. Peddaboina, V. R. Allini, and B. Zhang, "A review on CRISPR/Cas-based epigenetic regulation in plants," *International Journal of Biological Macromolecules,* vol. 219, pp. 1261-1271, 2022.
31. Z. Akhter *et al.*, "In response to abiotic stress, DNA methylation confers epigenetic changes in plants," *Plants,* vol. 10, no. 6, p. 1096, 2021.
32. M. Ramakrishnan *et al.*, "Epigenetic stress memory: A new approach to study cold and heat stress responses in plants," *Frontiers in plant science,* vol. 13, p. 1075279, 2022.
33. C. Kaya, F. Uğurlar, and I.-D. S. Adamakis, "Epigenetic Modifications of Hormonal Signaling Pathways in Plant Drought Response and Tolerance for Sustainable Food Security," *International Journal of Molecular Sciences,* vol. 25, no. 15, p. 8229, 2024.
34. J. Hu, T. Xu, and H. Kang, "Crosstalk between RNA m6A modification and epigenetic factors for gene regulation in plants," *Plant Communications,* 2024.
35. K. Tonosaki, R. Fujimoto, E. S. Dennis, V. Raboy, and K. Osabe, "Will epigenetics be a key player in crop breeding?," *Frontiers in plant science,* vol. 13, p. 958350, 2022.