

# DNA Methylation Changes in Crops in Response to Drought Stress

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## Introduction

Drought stress is one of the most significant environmental challenges faced by crops worldwide, threatening food security and agricultural productivity. The increasing frequency and severity of drought events due to climate change further exacerbate this problem, making it crucial to understand how crops respond to such stresses. One of the key mechanisms through which plants adapt to environmental stresses like drought is through epigenetic modifications, particularly DNA methylation. DNA methylation, a covalent modification of the DNA molecule, involves the addition of a methyl group to the 5' position of cytosine residues, usually occurring in the context of cytosine-guanine (CpG) dinucleotides. This modification can influence gene expression without altering the underlying DNA sequence, making it a vital player in the regulation of stress responses. Recent studies have increasingly focused on the dynamics of DNA methylation in crops under drought stress, as it offers promising insights into how plants can adapt to water scarcity at the molecular level. This commentary explores the role of DNA methylation in plant responses to drought stress, highlighting its potential for improving drought tolerance in crops.

## Description

Plants are highly sensitive to drought stress, and this sensitivity can vary significantly across different species and varieties. The ability of a plant to cope with drought involves complex physiological, biochemical, and molecular responses, including changes in water uptake, transpiration, and cellular homeostasis. At the molecular level, drought stress triggers a cascade of signaling events that affect gene expression, activating pathways involved in stress response, osmotic regulation, and protective protein synthesis. DNA methylation plays a central role in modulating the expression of these stress-responsive genes, helping plants adapt to changing environmental conditions. DNA methylation is part of a broader group of epigenetic modifications, which also include histone modifications and non-coding RNAs. These modifications collectively contribute to the regulation of gene expression, controlling which genes are turned on or off in response to environmental cues. In the case of drought stress, DNA methylation has been shown to alter the expression of key genes involved in water conservation, osmotic adjustment, and the synthesis of stress-related proteins. This epigenetic regulation provides plants with a flexible and reversible mechanism to fine-tune their responses to fluctuating environmental conditions [1].

Unlike genetic mutations, which are permanent and passed on to offspring, DNA methylation changes can be reversible, allowing plants to adapt to transient stress conditions and recover when the stress is alleviated. Recent studies have shown that drought stress induces changes in DNA methylation patterns in a wide range of crops, including maize, rice, wheat, and barley. These changes are often tissue- and time-dependent, with distinct methylation patterns observed in roots, leaves, and other plant tissues. In some cases, DNA methylation changes are associated with specific stress-responsive genes.

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For example, genes involved in the production of osmolytes, such as proline and sugars, often show altered methylation patterns under drought conditions. These molecules play a crucial role in maintaining cellular water balance and protecting cells from damage caused by dehydration. DNA methylation may also regulate the expression of transcription factors that coordinate the overall stress response, influencing the plant's ability to tolerate drought [2].

The dynamics of DNA methylation in response to drought stress are not entirely understood, but several mechanisms have been proposed. One possibility is that drought stress may activate DNA methyltransferases, the enzymes responsible for adding methyl groups to DNA. These enzymes could then target specific regions of the genome, leading to changes in the methylation status of stress-responsive genes. Another possibility is that drought-induced changes in gene expression may be driven by the removal or redistribution of DNA methylation marks, possibly through the action of DNA demethylases. This process can lead to either the silencing or activation of specific genes, depending on the location of the methylation marks and the associated chromatin context. In addition to direct changes in DNA methylation patterns, drought stress may also induce changes in the expression of genes involved in the DNA methylation machinery itself. For example, the expression of DNA methyltransferases and demethylases may be modulated by drought-induced signaling pathways, such as those involving abscisic acid (ABA), a plant hormone that plays a central role in the response to water stress. ABA is known to activate a range of genes involved in stress tolerance, and recent research suggests that it may also influence the expression of genes involved in DNA methylation. By modulating the DNA methylation landscape, ABA could help fine-tune the plant's response to drought, enhancing its ability to survive periods of water scarcity [3].

The relationship between DNA methylation and drought tolerance is particularly intriguing in the context of crop improvement. One of the main challenges in breeding drought-tolerant crops is the complexity of the traits involved. Drought tolerance is a polygenic trait, meaning it is controlled by multiple genes that interact with one another and with the environment. Traditional breeding methods often face limitations in selecting for drought tolerance due to the time required for phenotypic selection and the difficulty in identifying all of the genes involved. However, by focusing on the epigenome, and specifically on DNA methylation patterns, researchers may be able to identify new markers for drought tolerance that are more accessible and faster to detect. One promising approach is the use of epigenetic markers to predict drought tolerance in crops. DNA methylation patterns can be stable over generations, making them ideal candidates for use in marker-assisted selection. In some cases, DNA methylation changes may be heritable, allowing them to be passed on to offspring and influencing the drought tolerance of future generations. Epigenetic markers could complement traditional genetic markers, providing additional information about the stress tolerance potential of a crop. Additionally, DNA methylation could be used to monitor the effects of drought stress on plants in real-time, providing insights into how crops are responding to water scarcity and allowing for more precise management of irrigation practices [4].

In recent years, several studies have explored the potential for manipulating DNA methylation to improve drought tolerance in crops. One approach involves using chemicals or genetic engineering to modify the activity of DNA methyltransferases and demethylases, thereby altering the DNA methylation landscape of drought-responsive genes. For example, overexpression of specific DNA methyltransferases in rice has been shown to increase the methylation of certain stress-responsive genes, leading to improved drought tolerance. Similarly, genetic modification of genes involved in DNA demethylation has been found to enhance stress tolerance in plants by activating specific stress-responsive pathways. Another strategy is to focus

on the use of epigenetic priming to enhance drought tolerance. Epigenetic priming involves exposing plants to mild stress conditions, which induces changes in DNA methylation that prepare the plant for future stress events. This approach has been shown to improve drought tolerance in some crops by pre-conditioning the plant to respond more effectively to water scarcity. By leveraging the dynamic nature of DNA methylation, plants can 'remember' past stress experiences and activate appropriate defense mechanisms when faced with subsequent challenges [5].

## Conclusion

Despite these promising findings, there are still many unanswered questions regarding the role of DNA methylation in drought tolerance. The complexity of the epigenome and the interaction between genetic and environmental factors make it difficult to fully understand how DNA methylation regulates drought responses in plants. Furthermore, the potential for unintended effects when manipulating DNA methylation raises concerns about the safety and long-term stability of such interventions. As research continues, it will be important to carefully evaluate the benefits and risks of using epigenetic approaches in crop improvement. DNA methylation plays a crucial role in the molecular response of crops to drought stress. By regulating the expression of stress-responsive genes, DNA methylation helps plants adapt to fluctuating environmental conditions, offering a flexible mechanism for drought tolerance. Understanding the dynamics of DNA methylation in response to drought stress is essential for developing strategies to improve crop resilience in the face of climate change. Through the use of epigenetic markers, manipulation of the DNA methylation machinery, and epigenetic priming, researchers are paving the way for innovative approaches to enhance drought tolerance in crops. As we move forward, the integration of DNA methylation studies with traditional breeding methods and modern genetic tools will be key to ensuring food security in a changing climate.

## Acknowledgement

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## Conflict of Interest

None.

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