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Genetic "Face-Lifting": Applications and Prospects of Epigenetic Modifications in Stress Response of Trees

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Abstract Trees play a critical role in ecosystems and human life, serving as essential components of biodiversity and providing numerous ecological and economic benefits. However, various stress factors, such as climate change and pollutants, pose significant threats to tree health and survival. Epigenetics, encompassing mechanisms like DNA methylation, histone modification, and RNA-associated silencing, offers insights into how trees adapt to these stressors at a molecular level. This study delves into the basics of epigenetic mechanisms in trees, highlighting their role in gene regulation during stress responses and evolutionary adaptations. We explore environmental stressors, such as drought, temperature extremes, and pollution, and their corresponding epigenetic responses in trees. Case studies provide detailed examinations of epigenetic changes under specific conditions, including drought, air pollution, and cold tolerance in alpine species. Advancements in technology, such as genomic sequencing and bioinformatics, have revolutionized epigenetic research in trees, allowing for more precise analysis and potential applications in epigenetic editing. The influence of epigenetics on tree development, reproduction, and intergenerational patterns is also examined, emphasizing its impact on forestry practices and conservation strategies. The study concludes with a discussion on the ethical and policy considerations of epigenetic applications, public perception, and future research directions. By integrating epigenetic knowledge with traditional genetic research, this study aim to enhance tree resilience and contribute to sustainable forestry management.

Keywords Epigenetics; Environmental stress; Tree adaptation; Forestry conservation; Sustainable management

1 Introduction

Trees are indispensable to both ecosystems and human society, serving as the backbone of forest environments, providing habitat for countless species, and playing a crucial role in carbon sequestration. Beyond their ecological importance, trees contribute significantly to human well-being through resources such as timber, food, and medicinal compounds. Additionally, urban trees enhance the quality of life by improving air quality, providing shade, and reducing the urban heat island effect (Locosselli et al., 2020).

However, trees face an array of stress factors that threaten their health and longevity. Climate change, with its associated temperature extremes, altered precipitation patterns, and increased frequency of extreme weather events, poses one of the most significant challenges (Marzano and Urquhart, 2020; Jia et al., 2020). Furthermore, pollutants, such as heavy metals, ozone, and particulate matter, contribute to the degradation of tree health, impacting growth, reproduction, and resistance to pests and diseases. Understanding how trees respond to these stressors is critical for developing strategies to protect and sustain forests (Linnakoski et al., 2019; Locosselli et al., 2019).

Epigenetics, a field studying heritable changes in gene expression that do not involve alterations to the DNA sequence, offers profound insights into how trees can adapt to environmental stresses. Epigenetic mechanisms, including DNA methylation, histone modification, and RNA-associated silencing, play pivotal roles in regulating gene expression in response to external stimuli. These modifications can lead to changes in phenotype without altering the underlying genetic code, enabling trees to rapidly adjust to changing environments. This study aims to explore the applications and prospects of epigenetic modifications in enhancing the stress response of trees. By understanding these mechanisms, we can potentially develop innovative approaches to improve tree resilience, contributing to more effective conservation and sustainable forestry practices.

2 Basics of Epigenetic Mechanisms in Trees

2.1 Understanding epigenetic changes: DNA methylation, histone modification, RNA-associated silencing

Epigenetic changes are crucial for the regulation of gene expression in trees, particularly in response to environmental stress. DNA methylation, histone modification, and RNA-associated silencing are the primary mechanisms through which these changes occur. DNA methylation involves the addition of a methyl group to the DNA molecule, typically at cytosine bases, which can suppress gene expression. Histone modifications, such as acetylation and methylation, alter the chromatin structure, thereby influencing gene accessibility and transcription. RNA-associated silencing involves small RNA molecules that can degrade mRNA or inhibit its translation, thus regulating gene expression post-transcriptionally (Narasimhan et al., 2015; Wan et al., 2015).

2.2 Role of epigenetics in gene regulation during stress responses

Epigenetic modifications play a significant role in how trees respond to various stressors, such as drought, salinity, and pathogen attacks. These modifications can activate or repress specific genes that are involved in stress responses, enabling trees to adapt to changing environmental conditions. For instance, during drought stress, DNA methylation patterns can change to regulate genes involved in water conservation and root growth. Similarly, histone modifications can activate defense-related genes in response to pathogen attacks, enhancing the tree's ability to resist infections (Ozdemir et al., 2002; Jones and Grover, 2004).

2.3 Evolutionary implications of epigenetic modifications in trees

The evolutionary implications of epigenetic modifications in trees are profound. These modifications can be heritable, meaning that they can be passed down to subsequent generations, thereby influencing the evolutionary trajectory of tree populations (Kurpisz and Pawłowski, 2022). Epigenetic changes can provide a rapid response mechanism to environmental changes, offering a form of plasticity that genetic mutations alone cannot provide. This ability to quickly adapt to environmental stressors through epigenetic mechanisms can enhance the survival and reproductive success of trees, contributing to their long-term evolutionary fitness (Stuzin et al., 2000; Kang et al., 2020).

3 Environmental Stressors and Epigenetic Responses

3.1 Types of environmental stresses affecting trees

Trees are subjected to a variety of environmental stressors that can significantly impact their growth, development, and survival. These stressors include abiotic factors such as drought, extreme temperatures, and pollution, as well as biotic factors like pests and diseases. Each type of stress can trigger specific physiological and molecular responses in trees, which are often mediated by epigenetic modifications.

3.2 Epigenetic adaptations to drought and water scarcity

Drought and water scarcity are among the most critical environmental stressors affecting trees. Epigenetic mechanisms, such as DNA methylation, histone modifications, and non-coding RNAs, play a crucial role in enabling trees to adapt to these conditions. For instance, DNA methylation patterns can change in response to water deficit, leading to the activation or repression of genes involved in water use efficiency and stress tolerance. Histone modifications can also alter chromatin structure, thereby regulating the expression of drought-responsive genes. These epigenetic changes can be stable and heritable, allowing trees to "remember" past drought events and respond more effectively to future water scarcity (Narasimhan et al., 2015; Wan et al., 2015).

3.3 Responses to temperature extremes and pollution

Temperature extremes, including both high and low temperatures, pose significant challenges to tree survival (Figure 1) (Kurpisz and Pawłowski, 2022). Epigenetic modifications are essential for trees to cope with these stresses. For example, histone acetylation and methylation can regulate the expression of heat shock proteins and other stress-responsive genes, enabling trees to withstand high temperatures. Similarly, cold stress can induce changes in DNA methylation and histone modifications, which help in the activation of cold-responsive genes and the stabilization of cellular structures (Ozdemir et al., 2002; Jones and Grover, 2004). Pollution, particularly from heavy metals and other toxic compounds, also exerts stress on trees. Epigenetic responses to pollution include changes in DNA methylation and histone modifications that can either protect the genome from damage or activate detoxification pathways. These modifications can help trees to tolerate and survive in polluted environments, although the long-term effects of such epigenetic changes are still under investigation (Stuzin et al., 2000).

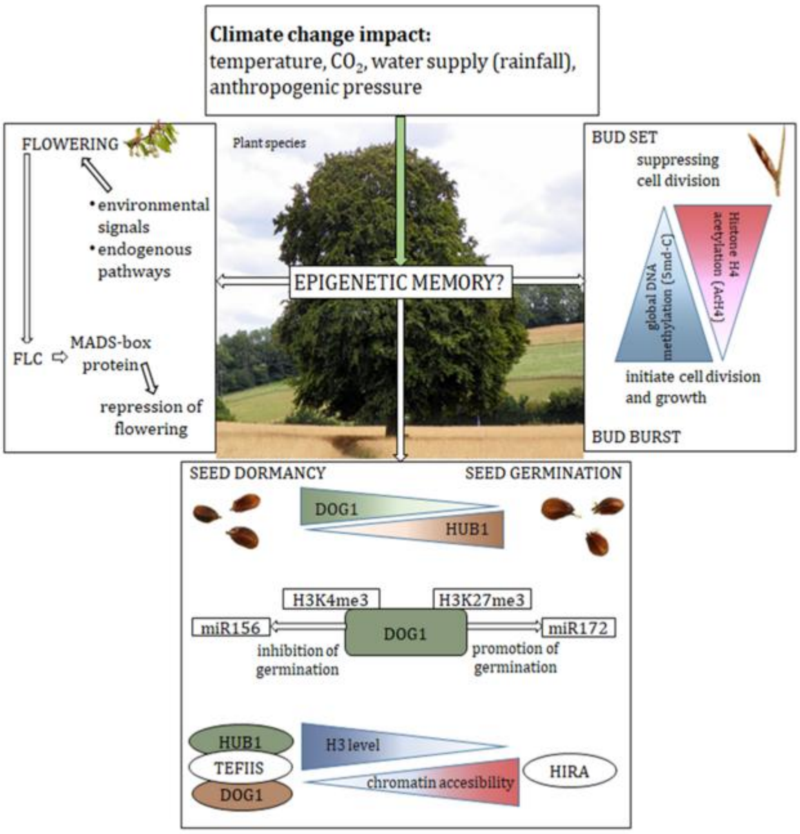

Figure 1 Epigenetic factors in the adaptive strategies of trees under the influence of environmental changes (Adopted from Kurpisz and Pawłowski, 2022)

Image caption: Climate change caused by environmental factors such as temperature, CO_2 concentration, water supply, etc., can influence epigenetic regulations in the plant. This, in turn, may result in the adjustment of the mechanisms responsible for flowering or the seed germination and bud burst. FLC, Flowering Locus C; DOG1, Delay of Germination 1; TEFIIS, Translational Elongation Factor 2; HUB1, Histone Mono-ubiquitination 1; HIRA, Histone Regulator A; H3K4me3, trimethylation of lysine 4 on histone H3; and H3K27me3, trimethylation of lysine 27 on histone H3 (Adopted from Kurpisz and Pawłowski, 2022)

4 Case Studies: Epigenetic Responses to Environmental Stresses

4.1 Detailed examination of epigenetic changes under drought conditions

Drought stress represents one of the most significant challenges for tree survival and productivity. Trees respond to drought through various physiological and molecular mechanisms, including epigenetic modifications. Studies have shown that drought conditions can lead to alterations in DNA methylation patterns, histone modifications, and changes in non-coding RNA expression (Figure 2) (Sow et al., 2021). One notable example is the response of oak (*Quercus* spp.) to prolonged drought periods. Research has demonstrated that drought stress induces hypermethylation at specific gene loci associated with water use efficiency and stress response pathways. These epigenetic changes are thought to contribute to the activation of genes involved in stomatal closure, osmotic adjustment, and antioxidative defense mechanisms. Furthermore, these modifications can be inherited, suggesting a potential role for epigenetic memory in drought resilience. Another case study involves poplar (*Populus* spp.), where drought conditions led to significant changes in histone acetylation levels at stress-responsive genes. These histone modifications facilitate a more open chromatin structure, promoting the rapid activation of genes essential for drought tolerance. This adaptive response underscores the dynamic nature of the epigenome in facilitating tree survival under water-limited conditions (Singh and Prasad, 2021; Kurpisz and Pawłowski, 2022).

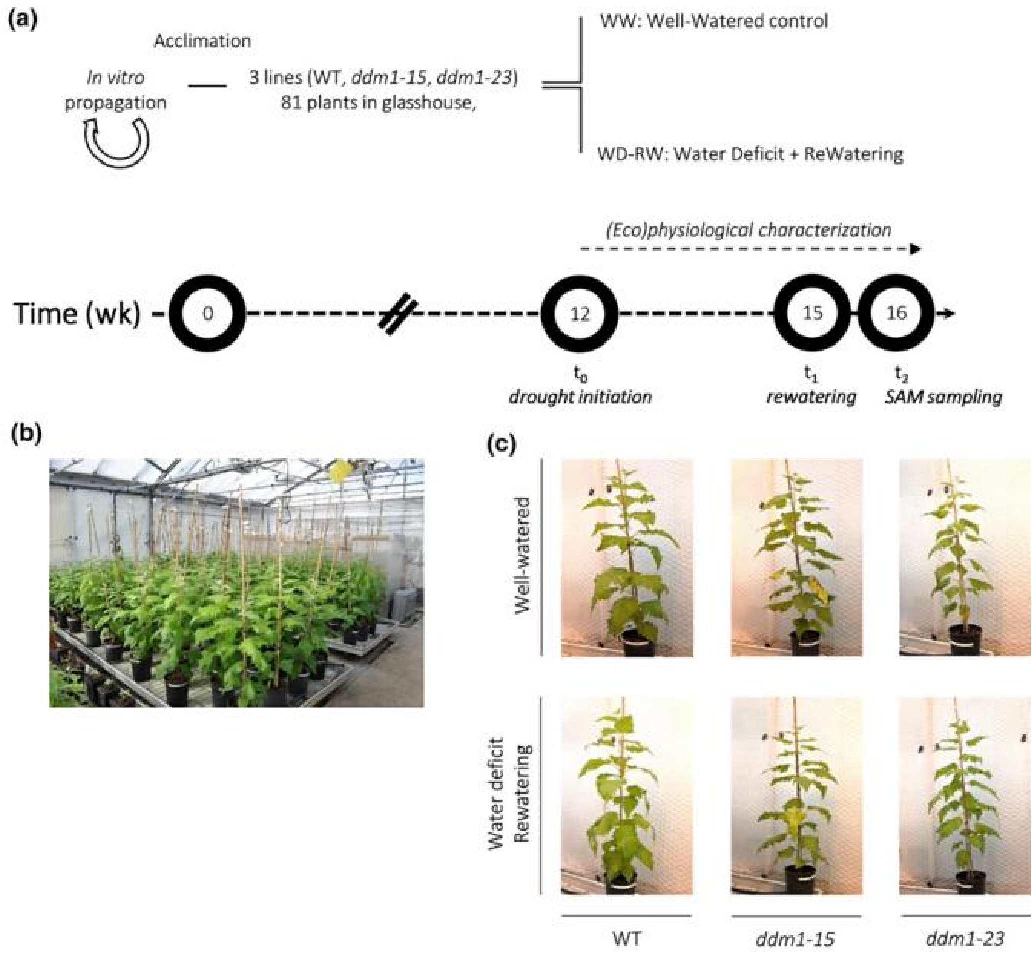

Figure 2 General overview of the drought experiment on poplars (*Populus tremula* × *Populus alba*) (Adopted from Sow et al., 2021)
Image caption: (a) Timeline of the experiment. Propagated *in vitro* plantlets from the wild-type (WT) and the two RNAi-*ddm1* transgenic lines were acclimated in a heated glasshouse, transferred into 4 L pots and kept under control conditions until they were 3-months-old. At that time (t_0), a waterd eficit was initiated for the plants assigned to the water deficit/rewatering treatment (WD-RW), while control plants were kept well-watered (WW). After 3 wk of water deficit (t_1), plants of the WD-RW condition were rewatered to field capacity for 1 wk, after which the experiment ended (t_2). The ecophysiological characterization of plant material was performed between t_0 and t_2. Sampling of shoot apical meristems (SAMs)for molecular analysis was performed at t_2. (b) Overview of the plants in the glasshouse. (c) Examples of plant phenotypes at t_2 under WW and WD-RW conditions for WT and RNAi-*ddm1* lines (Adopted from Sow et al., 2021)

4.2 Effects of air pollution on epigenetic patterns in urban trees

Urban environments expose trees to various pollutants, including particulate matter, heavy metals, and volatile organic compounds, all of which can impact their growth and health. Epigenetic modifications play a crucial role in enabling trees to cope with these stresses (Katsidi et al., 2023). A study on London plane trees (*Platanus* × *acerifolia*) in high-traffic urban areas revealed significant changes in DNA methylation patterns in response to air pollution. Increased methylation levels were observed at genes involved in detoxification and stress response pathways, suggesting an epigenetic mechanism for enhanced tolerance to pollutants. This epigenetic reprogramming allows urban trees to mitigate the detrimental effects of air pollution by modulating gene expression profiles in favor of stress adaptation and detoxification processes. In addition, research on black poplar (*Populus nigra*) exposed to industrial pollutants demonstrated alterations in histone modification patterns (Mukherjee et al., 2019). Specifically, histone methylation at stress-responsive gene promoters was increased, leading to the upregulation of genes involved in metal ion binding and oxidative stress defense. These findings highlight the importance of histone modifications in the epigenetic regulation of gene expression in response to environmental pollution (Locosselli et al., 2019).

4.3 Cold tolerance and epigenetic adaptations in alpine tree species

Cold stress is a critical factor limiting the distribution and survival of tree species in alpine and boreal regions. Epigenetic modifications have been shown to play a vital role in enhancing cold tolerance in these extreme environments. In Norway spruce (*Picea abies*), exposure to low temperatures resulted in significant changes in DNA methylation and histone acetylation at genes associated with cold response and metabolic adjustment. These epigenetic changes facilitate the activation of cold-responsive genes, enabling the trees to adjust their metabolism and cellular processes to withstand freezing temperatures. Importantly, some of these epigenetic modifications were retained across growing seasons, suggesting a form of epigenetic memory that enhances cold tolerance in subsequent winters (Syngelaki et al., 2020; Syngelaki et al., 2021).

Similarly, research on silver birch (*Betula pendula*) in alpine regions revealed that cold stress induces specific patterns of non-coding RNA expression. These non-coding RNAs regulate the expression of key genes involved in cold acclimation, such as those controlling membrane fluidity and antifreeze protein production. The regulation of gene expression by non-coding RNAs highlights another layer of epigenetic control contributing to the cold tolerance of alpine tree species. In conclusion, these case studies underscore the significant role of epigenetic modifications in enabling trees to adapt to various environmental stresses (Ebrahimi et al., 2023). Understanding these mechanisms not only provides insights into tree resilience but also offers potential applications in forestry and conservation practices aimed at enhancing stress tolerance in tree populations (Yu et al., 2020).

5 Technological Advances in Epigenetic Research

5.1 Emerging technologies for studying epigenetics in trees

Recent advancements in technology have significantly enhanced our ability to study epigenetic modifications in trees. High-throughput sequencing technologies, such as whole-genome bisulfite sequencing (WGBS), have become pivotal in mapping DNA methylation patterns across entire genomes. These technologies allow for the comprehensive analysis of methylation landscapes, providing insights into how environmental stressors influence epigenetic modifications in trees (Sinno et al., 2015). Additionally, chromatin immunoprecipitation followed by sequencing (ChIP-seq) has been instrumental in identifying histone modifications and their role in gene regulation under stress conditions (Narasimhan et al., 2015). The integration of these technologies with advanced bioinformatics tools has enabled researchers to dissect complex epigenetic networks and their functional implications in tree physiology and stress responses (Floyd et al., 2019).

5.2 The role of genomic sequencing and bioinformatics in epigenetic analysis

Genomic sequencing and bioinformatics have revolutionized the field of epigenetics by providing robust platforms for data analysis and interpretation. Next-generation sequencing (NGS) technologies, such as RNA-seq and ATAC-seq, have facilitated the exploration of transcriptomic and chromatin accessibility changes in response to environmental stressors (Sinno et al., 2015; Narasimhan et al., 2015). Bioinformatics tools and pipelines, such as those for differential methylation analysis and motif discovery, have been developed to handle the vast amounts of data generated by these sequencing technologies. These tools enable the identification of key regulatory elements and epigenetic markers associated with stress tolerance in trees (Floyd et al., 2019). Moreover, the integration of multi-omics data, including genomics, transcriptomics, and epigenomics, through bioinformatics approaches has provided a holistic view of the molecular mechanisms underlying stress responses in trees (Narasimhan et al., 2015).

5.3 Innovations in epigenetic editing: potential and challenges

Epigenetic editing technologies, such as CRISPR/dCas9-based systems, have opened new avenues for precise manipulation of epigenetic marks in trees. These tools allow for targeted modifications of DNA methylation and histone marks, enabling researchers to study the causal relationships between specific epigenetic changes and phenotypic outcomes (Sinno et al., 2015). Despite their potential, the application of these technologies in trees faces several challenges. The complexity of tree genomes, long generation times, and the need for efficient delivery systems for epigenetic editors are significant hurdles that need to be addressed (Narasimhan et al., 2015). Additionally, the off-target effects and long-term stability of induced epigenetic changes remain areas of concern.

Nevertheless, ongoing research and technological advancements hold promise for overcoming these challenges and harnessing the full potential of epigenetic editing in improving stress resilience in trees (Floyd et al., 2019).

6 Epigenetics in Tree Development and Reproduction

6.1 Influence of epigenetics on tree growth and developmental processes

Epigenetic mechanisms play a crucial role in the regulation of tree growth and developmental processes. These mechanisms, including DNA methylation, histone modification, and non-coding RNAs, can alter gene expression without changing the underlying DNA sequence. This allows trees to adapt to environmental changes and stress conditions more efficiently. For instance, DNA methylation patterns have been shown to influence the expression of genes involved in growth regulation and stress responses, thereby affecting overall tree development and resilience (Wan et a., 2015; Narasimhan et al., 2015).

6.2 Role of epigenetic mechanisms in tree reproduction and seed development

Epigenetic modifications are also pivotal in tree reproduction and seed development. These modifications can regulate the expression of genes critical for flowering, fruiting, and seed maturation. For example, histone modifications and DNA methylation can control the timing of flowering and the development of reproductive organs, ensuring successful reproduction under varying environmental conditions. Additionally, epigenetic changes in seeds can influence germination rates and seedling vigor, which are essential for the propagation and survival of tree species (Jones and Grover, 2004).

6.3 Impact of environmental changes on epigenetic patterns across generations

Environmental changes can induce epigenetic modifications that are heritable across generations, allowing trees to pass on adaptive traits to their offspring. This transgenerational epigenetic inheritance can be crucial for the survival of tree populations in changing climates. For instance, exposure to drought or extreme temperatures can lead to epigenetic changes that enhance stress tolerance in subsequent generations. These heritable epigenetic patterns ensure that progeny are better equipped to cope with similar environmental stresses, thereby contributing to the long-term resilience and adaptability of tree species (Ozdemir et al., 2002).

7 Implications for Forestry Practices and Conservation

7.1 Utilizing epigenetic knowledge for tree breeding and conservation

The application of epigenetic knowledge in tree breeding and conservation offers promising avenues for enhancing the resilience and adaptability of tree species. Epigenetic modifications, such as DNA methylation and histone modifications, can influence gene expression without altering the underlying DNA sequence, thereby enabling trees to respond dynamically to environmental stresses. By understanding and harnessing these epigenetic mechanisms, forestry practices can be improved to develop tree varieties that are better equipped to withstand biotic and abiotic stresses, such as pests, diseases, and climate change (Narasimhan et al., 2015; Sinno et al., 2015; Wan et al., 2015).

7.2 Impacts of epigenetic understanding on sustainable forestry management

Sustainable forestry management can greatly benefit from the insights provided by epigenetic research. Epigenetic markers can serve as indicators of tree health and stress levels, allowing for more precise monitoring and management of forest ecosystems. This knowledge can inform practices such as selective breeding, habitat restoration, and the implementation of adaptive management strategies that take into account the epigenetic profiles of tree populations. By integrating epigenetic data into forestry management plans, it is possible to enhance the resilience and sustainability of forests, ensuring their long-term health and productivity (Trepsat, 2001; Castello et a., 2011).

7.3 Strategies for enhancing tree resilience through epigenetic interventions

To enhance tree resilience through epigenetic interventions, several strategies can be employed. One approach is the use of epigenetic priming, where trees are exposed to mild stressors to induce beneficial epigenetic changes that prepare them for future stress events. Another strategy involves the selection and propagation of tree genotypes with favorable epigenetic traits, thereby creating populations that are more resilient to environmental challenges. Additionally, biotechnological tools such as CRISPR/Cas9 can be utilized to target specific epigenetic modifications, enabling precise manipulation of gene expression to enhance stress tolerance. These strategies, grounded in a deep understanding of tree epigenetics, hold significant potential for improving the resilience and adaptability of forest ecosystems (Moody and Sengelmann, 2004; Derby and Codner, 2017; Floyd et al., 2019).

8 Ethical and Policy Considerations in Epigenetic Applications

8.1 Ethical implications of manipulating epigenetic information

The manipulation of epigenetic information in trees raises significant ethical concerns. One primary issue is the potential for unintended consequences on ecosystems. Altering the epigenetic makeup of trees to enhance stress responses could inadvertently affect other species that rely on these trees for habitat or food, leading to a cascade of ecological impacts (Wan et al., 2015). Additionally, there is the question of whether it is morally acceptable to modify the genetic and epigenetic makeup of living organisms for human benefit, especially when the long-term effects are not fully understood (Narasimhan et al., 2015). The potential for creating "designer trees" that are optimized for specific conditions also raises concerns about biodiversity and the natural evolution of species (Wan et al., 2015; Narasimhan et al., 2015).

8.2 Policy frameworks needed for epigenetic research and application

To address these ethical concerns, robust policy frameworks are essential. These frameworks should include guidelines for conducting epigenetic research responsibly and transparently. Policies should mandate comprehensive environmental impact assessments before the release of epigenetically modified trees into the wild (Wan et al., 2015). Additionally, there should be regulations to ensure that the benefits of such technologies are equitably distributed and do not disproportionately favor certain groups or industries (Narasimhan et al., 2015). International cooperation is also crucial, as the effects of epigenetic modifications can cross national borders, necessitating a coordinated global approach to regulation (Wan et al., 2015; Narasimhan et al., 2015).

8.3 Public perception and legal aspects of epigenetic modification in trees

Public perception plays a critical role in the acceptance and success of epigenetic modifications in trees. There is often a gap between scientific advancements and public understanding, which can lead to resistance or fear of new technologies (Wan et al., 2015). Effective communication strategies are needed to educate the public about the benefits and risks of epigenetic modifications, fostering informed and balanced opinions (Narasimhan et al., 2015). Legally, there must be clear definitions and regulations regarding the ownership and patenting of epigenetically modified organisms. This includes addressing issues of intellectual property rights and ensuring that indigenous and local communities are not exploited or marginalized in the process (Wan et al., 2015; Narasimhan et al., 2015).

9 Future Research Directions in Tree Epigenetics

9.1 Unexplored areas in epigenetic studies of tree stress responses

Despite significant advancements in understanding the role of epigenetics in plant stress responses, there remain several unexplored areas, particularly in trees. One critical area is the identification and functional analysis of specific epigenetic modifications that contribute to stress resilience in different tree species. Current research has primarily focused on model plants and annual crops, leaving a gap in our knowledge regarding perennial woody plants like trees (Narasimhan et al., 2015; Sinno et al., 2015). Additionally, the long-term stability and heritability of these epigenetic changes under natural environmental conditions are not well understood. Studies have shown that epigenetic modifications can be transient or stable, but the factors influencing their persistence in trees, which have long lifespans, require further investigation (Gordon and Adam, 2015; Floyd et al., 2019).

9.2 Potential for integrating epigenetics with other genetic research

Integrating epigenetic research with other genetic approaches holds great potential for advancing our understanding of tree biology and improving stress resilience. For instance, combining epigenetic profiling with genome-wide association studies (GWAS) can help identify epigenetic markers linked to stress tolerance traits. This integrative approach can provide a more comprehensive understanding of the genetic and epigenetic networks involved in stress responses (Stuzin et al., 2000; Stuzin, 2007). Moreover, the use of CRISPR/Cas9 technology to edit epigenetic marks offers a promising avenue for functional validation of candidate epigenetic modifications and their roles in stress adaptation (Bayraktar and Sîrbu, 2012). Such integrative strategies can accelerate the development of tree varieties with enhanced resilience to environmental stresses.

9.3 Future prospects for epigenetic research in forest and urban environments

The application of epigenetic research in forest and urban environments presents exciting future prospects. In forest ecosystems, understanding the epigenetic mechanisms underlying tree responses to climate change, pests, and diseases can inform conservation strategies and forest management practices. For example, identifying epigenetic markers associated with drought tolerance can aid in selecting and breeding tree species better suited to changing climatic conditions (Stuzin, 2008; Narasimhan et al., 2015). In urban environments, where trees face unique stressors such as pollution and limited space, epigenetic studies can help develop urban forestry practices that enhance tree health and longevity. Additionally, exploring the potential for epigenetic memory in trees to retain stress adaptation traits across generations could have significant implications for both natural and managed ecosystems. By addressing these future research directions, we can harness the power of epigenetics to improve tree resilience and sustainability in diverse environments.

10 Concluding Remarks

Epigenetic modifications play a pivotal role in the ability of trees to respond to various environmental stresses. These modifications, which include DNA methylation, histone modification, and non-coding RNA activity, enable trees to dynamically regulate gene expression in response to changing environmental conditions. By facilitating rapid and reversible changes in gene activity without altering the underlying DNA sequence, epigenetic mechanisms provide trees with a flexible and adaptive strategy to cope with stresses such as drought, air pollution, and extreme temperatures. The evidence presented in this study underscores the importance of epigenetic processes in enhancing the resilience and adaptability of trees, which is crucial for their survival in an increasingly variable and challenging climate.

This study has highlighted the multifaceted role of epigenetic modifications in the stress responses of trees, offering a comprehensive synthesis of current knowledge in this rapidly evolving field. By examining case studies across different environmental stresses, we have illustrated the diverse ways in which trees utilize epigenetic mechanisms to enhance their survival and adaptability. This study contributes to tree biology by elucidating the specific molecular pathways through which epigenetic changes influence physiological responses and stress tolerance. Additionally, it bridges a critical gap in environmental sciences by linking molecular epigenetic processes with ecological outcomes, thereby providing a holistic understanding of how trees interact with and adapt to their environments. Our findings emphasize the significance of epigenetics in forest management and conservation strategies, highlighting its potential to inform practices aimed at improving tree resilience and ecosystem stability.

Future research should aim to further elucidate the specific molecular mechanisms underlying epigenetic modifications in trees, particularly in response to a broader range of environmental stresses. Longitudinal studies are needed to assess the heritability and long-term impacts of these epigenetic changes across generations. Additionally, expanding research to include a wider diversity of tree species will enhance our understanding of the generality and variability of epigenetic responses. From a policy perspective, integrating epigenetic insights into forest management and conservation practices is crucial. Policies should promote the conservation of genetic and epigenetic diversity within tree populations, as this diversity underpins their adaptive capacity. Furthermore, incorporating epigenetic knowledge into breeding programs can aid in the development of tree varieties with enhanced stress tolerance, contributing to sustainable forestry and climate adaptation efforts. By fostering interdisciplinary collaborations and integrating epigenetic research into policy frameworks, we can better support the health and resilience of forest ecosystems in the face of ongoing environmental changes.

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Conflict of Interest Disclosure

The authors affirm that this research was conducted without any commercial or financial relationships that could be construed as a potential conflict of interest.

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