



Editorial

Epigenetic Modifications and Breeding Applications in Horticultural Plants

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1. Introduction

Epigenetics is an expansive and rapidly evolving field, fundamentally concerned with heritable changes in gene expression that do not involve alterations to the underlying DNA sequence. This field encompasses a variety of molecular mechanisms, including DNA methylation, histone modifications, chromatin remodeling, and non-coding RNAs (ncRNAs), each playing a pivotal role in regulating gene expression. The intricate orchestration of these mechanisms ensures the precise control of genetic information, which is pivotal for plant growth, development, and survival [1]. Epigenetic regulation in plants is not merely a supplementary layer of gene control, it is essential for interpreting developmental cues and adapting to environmental changes. Epigenetic modifications have been shown to be key players in plant responses to a myriad of stresses, including drought, salinity, and temperature fluctuations. Furthermore, epigenetics plays a crucial role in developmental processes, such as flowering time regulation [2], seed dormancy, and fruit ripening, serving as a versatile mechanism to fine-tune gene expressions in response to internal and external stimuli. Plant-epigenetic modifications also play vital roles in acclimatization, stress tolerance, adaptation, and evolutionary processes. The agronomically important traits of crop life, such as flowering time, fruit development, risk avoidance from environmental factors, and crop immunity, are attained by epigenetic modifications [3].

Additionally, breeding applications in horticultural plants represent a critical intersection of genetics, technology, and agriculture. Advances in this field are transforming our approach to crop improvement, enabling the development of varieties with enhanced traits such as increased yield, disease resistance, and nutritional quality [4]. By integrating traditional breeding techniques with cutting-edge genomic tools, researchers are unlocking new possibilities for optimizing plant characteristics [5]. These innovations are crucial in addressing global challenges, such as food security, climate change adaptation, and sustainable agriculture, making breeding applications a cornerstone of horticultural research and development. This Special Issue showcases these pivotal advancements, underscoring their profound impact on the future of horticulture.

Through a series of meticulously selected papers, this Special Issue offers a panoramic view of the latest developments in plant epigenetics, showcasing innovative research on epigenomic profiles, regulation of developmental processes, environmental adaptation, and breeding approaches. The collection encompasses a broad spectrum of studies, including



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the impact of cultivation modes on bioactive components in fruits, the intricacies of natural deastringency in persimmons (*Diospyros kaki*), the effects of grafting on epigenetic changes, and the exploration of crucial genes in crops like walnut (*Juglans regia*) and Rosaceae family members. This editorial will guide you through these groundbreaking studies, underscoring their significance and potential to advance our understanding of plant epigenetics and its application in horticulture.

2. Epigenetic Regulations in Horticultural Plants

In the realm of horticulture and agriculture, epigenetics holds immense potential. It offers insights into plant development, stress response, and adaptation, which are crucial for crop improvement and sustainability. DNA methylation, which involves the addition of methyl groups to the DNA, is a critical epigenetic mechanism in plants, playing a pivotal role in regulating gene expression and plant development.

The studies in this Special Issue highlight the remarkable impact of epigenetic mechanisms in horticultural plants. Recent molecular and epigenomic studies have established that epigenetic regulations are crucial for fruit development and ripening. This complex process involves not only plant hormones and transcription factors but also key epigenetic modifications [6]. In the first contribution of this Special Issue, Narváez et al. delved into the epigenetic intricacies of dormancy in sweet cherry (*Prunus avium*) varieties, examining how genome-wide DNA methylation changes contribute to crucial developmental processes like chilling requirements. This research offers invaluable insights into the epigenetic control mechanisms that govern plant development and adaptation to environmental cues. Adding to this rich tapestry of epigenetic understanding, Tian et al. (contribution 2) provided a detailed characterization of *N*⁶-methyladenosine (m⁶A) regulatory genes in *Citrus grandis*. Their work illuminates the role of m⁶A modification in fruit development, contributing significantly to our understanding of post-transcriptional modifications in plants. Similarly, contribution 3 explored the epigenetic consequences of grafting in horticultural plants. Their comprehensive review highlights how grafting, a traditional agricultural practice, can induce significant epigenetic changes that affect gene expression, chromatin structure, and ultimately, the plant phenotype. This study underscores the complexity and importance of epigenetic modifications in agricultural practices. Additionally, Shaikh et al. (contribution 4) further expanded on the theme of epigenetic mechanisms in crop improvement. Their discussion on the potential roles of DNA methylation and demethylation in plant development emphasizes how epigenetic variations can be harnessed to enhance crop traits, which is a vital consideration in modern agricultural strategies.

Moreover, epigenetic factors have recently emerged as key drivers in understanding the processes involved in floral transitions. These modifications affect key developmental processes, thereby influencing plant morphology, timing of flowering, and fruit development. This new focus on epigenetics provides deeper insights into how plants regulate the critical shift from vegetative to reproductive stages. In a focused study on walnuts, Jin et al. investigated the differential expression of genes and miRNAs in early flowering varieties. Their findings offer new insights into the genetic control of flowering time, which is a critical factor in plant breeding and cultivation (contribution 5). ncRNAs contribute significantly to the epigenetic regulation of gene expression, in addition to their established roles in transcriptional and post-transcriptional processes. They are categorized into two main classes based on their transcript size. Long ncRNAs (lncRNAs), which span more than 200 nucleotides, in contrast with short ncRNAs, which are less than 200 nucleotides in length and include microRNAs (miRNAs) [7]. miRNAs are small noncoding RNAs that are around 18–25 nucleotides long and play complex roles in epigenetic regulation. They modulate protein levels by targeting mRNAs without altering gene sequences and are subject to epigenetic modifications, including DNA methylation, RNA modification, and histone modifications [8]. Additionally, the role of miRNAs in fruit crops, reviewed in contribution 6, reveals the intricate regulatory networks at play in plant biology. The study underscores the importance of miRNAs in controlling various biological and metabolic

functions, especially in response to environmental challenges, highlighting the nuanced interplay between genetic regulation and external factors.

Lastly, the identification of lncRNAs in tomato (*Solanum lycopersicum*) fruits by Wang et al. (contribution 7) opens new avenues in understanding fruit development. By revealing the roles of lncRNAs in tomato fruit expansion and ripening, this study adds a new layer to our understanding of the genetic and epigenetic factors that shape plant growth and development. Collectively, these studies not only advance our knowledge of plant epigenetics but also pave the way for innovative approaches in horticultural science and crop improvement. The implications of this research are far-reaching, offering new possibilities for enhancing crop resilience, yield, and quality through epigenetic understanding and manipulation.

3. Breeding Applications in Horticultural Plants

Horticultural plants, encompassing fruits, vegetables, and ornamentals, play a vital role in enriching our diets, beautifying our living spaces, and aiding environmental conservation. The horticulture sector has seen tremendous advances in recent decades, enabling a year-round availability of high-quality produce [9]. However, it still grapples with challenges like biotic and abiotic stresses, the time-consuming development of elite cultivars, rising labor and production costs, and inefficiencies in production. To address these issues, in-depth biological studies on horticultural plants are crucial. Understanding their adaptation to environmental changes and pathogens is key to developing more resilient plants, either through advanced breeding techniques or new stress tolerance methods. Moreover, unraveling the molecular mechanisms behind critical traits, such as flowering, fruit development, and metabolism, will significantly accelerate the genetic enhancement of these crops. The research in this Special Issue spans a wide array of breeding applications in horticultural plants, offering significant advancements in crop improvement strategies.

Fruit crops, grown in nearly every country and region, are crucial agricultural commodities of significant economic importance. They play a vital role in global food security by offering a variety of foods and nutrients essential for sustaining human life and health [5]. Recent strides in biotechnologies and genomics have opened new avenues for genomic and genetic research on fruit crops, offering unparalleled opportunities for scientific advancement. Tian et al. conducted a comprehensive analysis of JMJ domain-containing proteins in *Citrus grandis* providing a basis for understanding their role in fruit development (contribution 8). Another study by Mo et al. (contribution 9) explored the molecular mechanisms underlying anthocyanin accumulation in mulberry (*Morus* L.) fruits. This study contributes to our understanding of the genetic regulation of important secondary metabolites in fruits.

The final fruit size is determined by cell division and expansion, which are regulated by plant hormones, which in turn are regulated by genes. Karim et al. investigated the role of cell division and expansion in determining the final size of apples. Their findings contribute to our knowledge of the biological processes that influence fruit size, a critical trait in apple breeding (contribution 10). Yang et al. delved into the unique natural deastringency trait of the Chinese pollination-constant non-astringent (C-PCNA) persimmon. This work contributes to the understanding of the genetic and molecular mechanisms underlying fruit astringency, a critical quality attribute in persimmons, and the potential for genetic improvement in breeding programs (contribution 11). Additionally, in another study, Yang et al. assessed various quality indicators in persimmon cultivars, providing comprehensive profiles that are critical for marketing and breeding. This study represents an important step in the genetic improvement of persimmons (contribution 12). Moreover, contribution 13 identified and characterized the *FLOWERING LOCUS C* gene in precocious walnuts, offering significant insights into the regulation of floral transition and breeding strategies for early flowering in walnut cultivars.

Horticultural crops are susceptible to numerous biotic stressors such as fungi, oomycetes, bacteria, viruses, and root-knot nematodes, which hinder their growth, development, yield, and quality while also affecting their adaptability and geographic distribution [10]. Significant

efforts have been directed towards developing disease-resistant horticultural cultivars. A study by Wu et al. (contribution 14) identified the *BAK1* gene in 'Citron C-05' (*Citrus medica*), a citrus cultivar, revealing its role in disease resistance. This research enhances our understanding of plant–microbe interactions and could inform breeding strategies for disease resistance in citrus crops (contribution 14). Additionally, Cao et al. conducted a genome-wide identification of *NLR* genes in Rosaceae plants, providing a reference for understanding the evolution of these genes and their roles in resistance against Valsa canker, a major threat to Rosaceae crops (contribution 15).

The changing global climate and human activities have significantly affected the production and productivity of horticultural crops, with abiotic stress conditions leading to environmental challenges. The most common abiotic stresses are represented by cold, heat, drought, flooding, salinity, nutrient deficiency, and high and low light intensities, including ultraviolet radiation [11]. Understanding how abiotic and biotic stresses impact horticultural crops, and the mechanisms to mitigate these stresses, is key to enhancing crop productivity and quality. Hayat et al. (contribution 16) studied the transcriptional changes associated with cold tolerance in Japanese apricot (*Prunus mume*), highlighting the genetic elements vital for developing improved varieties and contributing to the breeding of cold-resistant varieties. Expanding the scope of stress response in plants, contribution 17 explored the *AP2/ERF* gene family in oily persimmon (*Diospyros oleifera*) and their roles in response to polyamines for adventitious root formation in cultivated persimmon, enhancing our understanding of gene families critical to plant growth and stress responses. Additionally, Mo et al. provided a detailed description of the morphological and phenological stages of different mulberry species. This study is significant for understanding the growth patterns of mulberries in diverse climates, which is essential for breeding and cultivation practices (contribution 18). Moreover, Han et al. analyzed the gene expression and enzyme activity in the nitrogen metabolism pathways of different potato (*Solanum tuberosum*) genotypes. This study provides a theoretical basis for optimizing nitrogen application in potato cultivation, enhancing crop yield and quality (contribution 19).

Finally, Zhang et al. (contribution 20) explored how different cultivation modes affect the bioactive components and antioxidant activities of mulberry fruits. The study reveals significant differences in the phenological stages, yield, and quality of bioactive components under greenhouse and field cultivation, highlighting the potential of environmental manipulation in enhancing the nutritional value of mulberries. Jin et al. studied the gene regulatory networks associated with pellicle development in walnuts. Their research sheds light on the phenolic biosynthetic pathways, which is crucial for understanding astringency and bitterness in walnut consumption (contribution 21). These studies collectively demonstrate the dynamic interplay between genetic understanding and practical breeding applications, offering innovative approaches for the development of superior horticultural-varieties.

4. Conclusions

In this Special Issue, we journeyed through a diverse landscape of research in plant epigenetics and horticultural science. From the subtle interplay of environmental factors and genetic regulation in mulberries to the complexities of disease resistance in citrus and the intricacies of flowering time in walnuts, each study contributes a unique piece to the vast puzzle of plant biology. The epigenetic studies emphasize the fluid and responsive nature of genetic expression, shaped by both internal and external cues. Conversely, breeding-focused research illuminates the tangible outcomes of harnessing genetic knowledge, paving the way for improved crop varieties. Together, these studies underscore the synergy between fundamental epigenetic understanding and practical breeding applications, highlighting a future where such integrated approaches can revolutionize horticultural practices and crop improvement strategies. As we continue to unravel the mysteries of plant biology, the insights gained here will undoubtedly serve as beacons, guiding future research and innovation in the field.

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