

Understanding Epigenetic Modifications in Fruit Crops Under Stress Condition

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Abstract:

Fruit crops, being highly sensitive to environmental fluctuations, are particularly vulnerable to stress factors such as drought, extreme temperatures, salinity, and pathogen attacks. While genetic adaptations play a role in plant resilience, epigenetic modifications have emerged as key regulators of stress responses. Unlike permanent genetic mutations, epigenetic changes are reversible, heritable, and responsive to environmental stimuli, making them an important mechanism for plant adaptation. This article explores the epigenetic mechanisms in fruit crops under stress, including DNA methylation, histone modifications, and non-coding RNAs, and their role in stress adaptation. We also discuss stress memory, biotechnological applications, and challenges associated with epigenetic studies in fruit crops.

Introduction:

Environmental stress factors significantly impact the growth, development, and productivity of fruit crops. Unlike annual crops, fruit crops experience multiple seasons of growth, making them particularly susceptible to long-term environmental variations. To cope with these challenges, plants employ both genetic and epigenetic strategies.

Epigenetics refers to heritable changes in gene expression that do not involve alterations in the DNA sequence. These modifications act as a molecular switch, regulating how and when specific genes are expressed under stress conditions. Importantly, stress-induced epigenetic modifications can be transmitted across generations, enabling offspring to exhibit improved resilience to stress.

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With advances in next-generation sequencing (NGS) and epigenome mapping, researchers are now uncovering the molecular basis of epigenetic regulation in fruit crops such as tomato (*Solanum lycopersicum*), grapevine (*Vitis vinifera*), apple (*Malus domestica*), banana (*Musa spp.*), and citrus (*Citrus spp.*). Understanding these modifications can provide novel strategies for breeding stress-tolerant fruit crops without genetic modifications, offering a sustainable approach to agriculture.

Mechanisms of Epigenetic Regulation in Fruit Crops

DNA Methylation: A Key Regulatory Mechanism

DNA methylation is one of the most well-studied epigenetic modifications. It involves the addition of a methyl group (-CH₃) to cytosine bases, typically at CG, CHG, and CHH sequences (where H represents A, T, or C). This modification regulates gene expression by silencing or activating specific genes.

DNA Methylation Under Stress

- ✓ Under drought stress, DNA hypomethylation (demethylation) activates genes responsible for osmotic balance, root growth, and ABA (abscisic acid) signalling.
- ✓ Under salinity stress, hypermethylation (increased methylation levels) in stress-

sensitive genes prevents their activation, reducing cellular damage.

- ✓ In grapevine, heat stress induces methylation changes in photosynthesis-related genes, altering their expression to maintain energy production under high temperatures (Xu et al., 2024).

Histone Modifications: Re-modelling the Chromatin Landscape

Histones are protein complexes that package DNA into chromatin. The structure of chromatin plays a crucial role in regulating gene accessibility and transcription. Histone modifications such as acetylation, methylation, phosphorylation, and ubiquitination control whether genes are actively transcribed or silenced.

Types of Histone Modifications in Fruit Crops

- ✓ **Histone Acetylation (H3K9ac, H4K16ac):** Acetylation loosens chromatin structure, allowing transcription factors to bind and activate genes under stress.
- ✓ **Histone Methylation (H3K9me, H3K27me):** Methylation can either activate or repress genes, depending on the site and number of methyl groups added.

Histone Modifications in Fruit Stress Responses

- ✓ In tomatoes, cold stress leads to histone H3K4me₃ modifications, which regulate

antioxidant defense genes, enhancing chilling tolerance (Kang & Lee, 2024).

- ✓ In apples, histone modifications influence ethylene production, controlling fruit ripening under drought stress conditions.
- ✓ In bananas, salt stress alters H3K9 methylation, modulating genes involved in ion transport and osmotic regulation.

Non-Coding RNAs (ncRNAs): Regulators of Gene Expression

Non-coding RNAs, including microRNAs (miRNAs) and long non-coding RNAs (lncRNAs), act as regulatory molecules that fine-tune gene expression during stress responses.

miRNAs in Stress Adaptation

miR393 is upregulated in strawberries under drought conditions, regulating auxin signaling pathways to enhance drought tolerance (Loreto & Atzori, 2024).

- ✓ miR156 plays a role in salinity tolerance in citrus, modulating genes involved in ion homeostasis.

Long non-coding RNAs (lncRNAs) and Stress Response

- ✓ lncRNAs regulate chromatin re-modelling and gene activation under abiotic stress.
- ✓ In grapevine, drought stress alters lncRNA expression, affecting stomatal closure and water retention mechanisms.

Epigenetic Memory: Inheritance of Stress Adaptation

Epigenetic modifications allow fruit crops to remember past stress events and prepare for future occurrences, a phenomenon known as stress memory. This memory can be short-term (within one generation) or transgenerational (inherited by offspring).

- ✓ In apple trees, exposure to drought stress results in DNA methylation changes that persist for multiple growing seasons, leading to improved stress tolerance.
- ✓ In citrus species, repeated pathogen infections induce epigenetic modifications that prime plants for stronger immune responses in subsequent generations (Guo & Wang, 2024).

Understanding stress memory in fruit crops opens new possibilities for breeding naturally stress-resistant varieties without genetic modification.

Biotechnological Applications of Epigenetics in Fruit Crops

Epigenetic modifications provide an opportunity to enhance stress tolerance without altering the genetic code. Some potential applications include:

1. Epigenome Editing: CRISPR-based tools can be designed to modify DNA methylation and histone modifications at specific stress-related genes.
2. Epigenetic Priming: Mild exposure to stress can induce beneficial epigenetic

changes, helping plants cope with future stress conditions.

3. **Marker-Assisted Selection (MAS):** Identifying epigenetic markers associated with stress tolerance can accelerate breeding programs for climate-resilient fruit crops.

Challenges and Future Directions

Despite the promising role of epigenetics in stress adaptation, several challenges remain:

- ✓ **Reversibility of Epigenetic Changes:** Some modifications are unstable and may not be inherited across generations.
- ✓ **Complex Interactions:** Multiple epigenetic mechanisms interact, making it difficult to determine their exact roles.
- ✓ **Environmental Influence:** Different environmental factors may trigger variable epigenetic responses in the same species.

Future research should focus on developing stable epigenetic markers for breeding, exploring the synergistic effects of multiple epigenetic modifications, and utilizing CRISPR-based epigenome editing for precise gene regulation.

Conclusion

Epigenetic modifications play a crucial role in fruit crop adaptation to environmental stress by dynamically regulating gene expression. Advances in DNA methylation profiling, histone modification mapping, and

RNA sequencing have provided new insights into stress tolerance mechanisms. Harnessing epigenetics for sustainable agriculture can lead to the development of stress-resilient fruit crops without genetic modifications, offering a promising solution for future food security.

References

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