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Epigenetic Modifications in Plants under Abiotic Stress : From Chromatin Dynamics to Phenotypic Plasticity

Sangeetha B. G[1]*, T. Makeshkumar[1], E. R. Harish[1], C. Pradeepika[2], R. Arutselvan[3]

[1]Division of Crop protection, ICAR-Central Tuber Crops Research Institute, Sreekariyam 695017, Thiruvananthapuram, Kerala, India
[2]Section of Crop Utilization, ICAR-Central Tuber Crops Research Institute, Sreekariyam 695017, Thiruvananthapuram, Kerala, India
[3]Regional Centre, ICAR-Central Tuber Crops Research Institute, Bhubaneswar, Odisha, India

sangeethageethu214@gmail.com

Plants are always subject to both biotic and abiotic stress in order to adapt themselves for modifications happen at molecular level within plant cell. Epigenetic is defined as the study of mitotically and/or meiotically heritable changes in gene function that cannot be explained by changes in DNA sequence. These changes affect the phenotypic plasticity which in turn helps the plants to survive in adverse conditions. These changes are not related to the DNA sequences but to chemical modifications inherited from one generation to the next. There are three main types of epigenetic marks in plants namely histone modification, DNA methylation, and small RNAs. These modifications will always improve the adaptability of plants towards various stresses. There are three distinct types of epigenetic memory in plants classified into cellular, transcriptional, and transgenerational. The heritable transcriptional states that arise from developmental signals refer to cellular memory whereas the heritable changes that improve the response to environmental stress refer to transcriptional memory. Gene expression that is heritable through meiosis which enables the plant to tolerate different stress is referred as transgenerational memory.

DNA methylation in plants

DNA methylation occurs adding a methyl group at the fifth carbon position of a cytosine ring, by cytosine methyltransferases in sequence specific mode. The methyl group will provide platform for the attachment of protein complexes that modify the histone scaffolds which alters the gene expression. In plants methylation happens in CG, CHH and CHG (where H is A, C, or T) (Law and Jacobsen, 2010). Methylation in genomic DNA to an increased level in plants results in down regulation of the genes which in turn helps the plants to survive for a long period by conserving energy in various stress conditions. At the same time reduction of methylation in genes related to resistance leads to chromatin activation and expression of novel genes for long term.

Histone modifications in plants

The eukaryotic nuclei are structured in the form of nucleosome wrapped by histone proteins. Nucleosomes are mainly composed of histone octamers that comprise two copies each of H2A, H2B, H3, and H4. A total of 147 base pair of DNA sequence is wrapped around the histone core. The N termini of histone proteins called N terminal tails undergo various chemical modifications and generally these histones usually regulate the post-translational modifications (PTMs) in plants. The major histone modifications include acetylation, methylation, biotinylation, suphonylation, ubiquitination and phosphorylation. Acetylation and phosphorylation are mostly associated with induced gene expression while suphonylation and biotinylation are associated with repression of gene expression. These modifications interrupt the DNA accessibility and also affect the transport of specific proteins involved in DNA transcription, replication and repair.

miRNA directed DNA methylation

In epigenetic regulations various classes of noncoding RNAs viz small RNAs and long noncoding RNAs are also involved. These RNAs modify the chromatin structure and repress the transcription by forming RNA scaffolds using histones and DNA methyl transferases. In plants RNAi is sequence specific gene regulation mechanism mediated by miRNA, siRNA and lncRNA (long non coding RNA).

Various epigenetic changes in crops against abiotic stress

The major abiotic factors that cause epigenetic modulation are stress induced due to salinity drought, heat and cold. Salt stress will lead to alterations in gene expressions by increase in DNA methylation and decreased methylation observed salt-sensitive plants. The methyltransferases (MTases) genes were upregulated in *Pyrus betulaefolia* (a wild pear) due to salt stress (et al., 2023). The DNA methyaltion was increased in alfalfa (*Medicago sativa*)due to salt stress (Yang et al., 2024). Temperature is one of the most important environmental signals that regulate plant development and growth. Extreme high temperatures can disrupt cellular homeostasis, which leads to inhibition of plant growth and development. It also induces drastic changes in chromatin architecture of plants. The epigenetic regulation allows plants to adapt to heat stress without change in DNA sequences. This regulation involves DNA methylation, histone modifications, RNA modifications and other epigenetic regulation which contribute to gene expression in response to heat stress. Heat stress in plants cause higher methylation in sensitive genotypes compared to resistant genotypes with more demethylation events and affect cytosine methylation across various genes (Hilker et al., 2016). Alteration in expression of stress related genes and DNA methyaltion was observed during somatic embryogenesis due to high temperature in *Pinus halepensis* (Guan et al., 2013). DNA methylation and demethylation mechanisms were observed in *Arabdiopsis* due to high temperature (Guihur et al., 2022). Heat induced transcription factors HsfA1s (heat shock transcription factors) always play important role for both drought and heat stress responses. Mutations in three HsfA1a, HsfA1b, and HsfA1d genes significantly lead to loss of heat shock response in plants (Wang et al., 2009, Xue et al., 2021, Yamaguchi and Ito 2021). The transcription factors activate Heat Shock Proteins (HSPs) and ROS-scavenging enzymes, which protect against HS-induced protein unfolding and oxidative stress. The expression of histone deacetylases (HDACs) was upregulated in *Zea mays* during cold stress which leads to the deacetylation at lysine residues of histone subunits H3 and H4 (Hu et al., 2011). Low temperature usually deteriorate the physiology of plants which cause chilling injury, apoptosis, chlorosis, damage to the membranes and eventually leads to wilting of plants. Precocious flowering during autumn or winter is a floral regulatory process which prevent precocious flowering during autumn or winter. It is a memory response correlated with epigenetic regulation.

Conclusion

Epigenetics is important regulatory mechanism in plants influenced by environmental stimulus. The changes are inherited over generations which contribute significant role in providing stress tolerance to plants. Modern high-throughput techniques help us to identify epigenetic changes and knowledge on the effect of epigenetic changes in gene regulation. Manipulation of DNA at specific loci helps to regulate gene expression and neighbouring chromatin which leads to modification of cell physiology and biochemistry. One of the unexplored ways to improve stress tolerance is to enhance stress memory in plants by the modification of epigenome using biotechnological approaches. Hence epigenetic variation remains as an alternate solution for developing abiotic stress tolerant crop varieties.

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