

# HIGHLIGHTING THE AFTERMATH OF THE EPIGENETIC MODULATIONS IN THE PLANT CELLS

Tavisha Singh

Punjab Agricultural University, Ferozpur Road, Ludhiana, Punjab 141027, India

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## **Corresponding author:**

Singh, T.

tavisha-bot@pau.edu

## ABSTRACT

Epigenetic modifications regulate heritable gene expression without altering any changes in the genomic DNA sequences and are being accounted for in plants which frequently correspond with contributing to flexible survival strategies of sessile plants against any biotic or abiotic stress. Notably, epigenetic changes include alteration of DNA base, histones and small non-coding RNAs. Histones are subjected to post-translational modifications which affect transcription, replication, chromosome condensation/segregation, as well as DNA repair. Methylation of a promoter may repress gene transcription, while methylation of the coding region of a gene may cause post-transcriptional gene silencing. Furthermore, epigenetic changes may likewise be acquired over the generations as epialleles, which are considered as a cause of variation in heredity for crop improvement. The parts of epigenetic changes in plants are getting progressively apparent, eventually proposing that epigenetic components have a major role in conferring the stress resistance, acclimatization, transformation and advancement measures significantly. Eventually, such findings are shedding light to understand the new avenue of research on the mechanisms regulating epigenetic modifications in plants, and their conceivable use in crop improvement.

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# INTRODUCTION

The measure of the function of the DNA is actually carried out by the genes encoded in it termed as genome. Overall instructions in the cell are carried out by the genes that command the cell how to perpetrate and eventually define its fate. Nonetheless, when the genes are defined to be in a compacted version, the outcome of such changes makes the gene expression unreadable. This knocks the door to a new field of genetics called epigenetics. Where, 'Epi' refers to 'on top of' and 'genetics' means 'genes', which addresses a set of information that lay down on top of the DNA and associated protein complexes called histones. Moreover, such epigenetic traces on the genetic makeup operate through small chemical marks which lay down on the DNA and instruct in a way whether to remain in compact or decompact form. Basically, such instructions govern the overall status of the cell to read the modified genes encoded in the DNA and some epigenetic marks can help chromatin to become condense as a result obscure the expression of genes preventing from being readable by the cell machinery (Bird. 2002). As a consequence, they turn off the expressions of genes. Whereas, other epigenetic marks have a role in loosening of the chromatin texture and when they carry out such a task, the gene eventually turns on and its expression is regulated by various factors profiles. These mentioned types of epigenetic marks have profound influence in the biological system. Consider, for instance, what is it that makes a nerve cell look different from a muscle cell? Instead, these cells have exactly the identical genetic material (Blignaut. 2012). Therefore, the answer lies in the fact that their differential gene expressions due to different epigenetic instructions help them to instruct in a way whether which genes to switch on and which ones to switch off. Possibly, the different expressions of genes at play make cells distinct among each other (Fedoriw et al. 2012).

Moreover, environmental status inside the cell and prevailing environment situations outside the developing embryo limits the expressions of epigenetic mechanisms by restructuring it. Here the curiosity begins with a query as to what would be the hidden mechanism that governs the different gene expressions resulting in such a diverse form to exist. Interestingly, the explanation relies on the fact that such diversification is due to changes in chromatin structure which specifically includes the modification of histones (methylation and acetylation), chromatin remodelling, DNA methylation and noncoding RNA (ncRNA) in controlling the expression rather than altering any base sequence in the genome. Such changes brought altered consequences in gene expression just described, are events associated with epigenetics. Epigenetics has a role in the phenotypic variation and evolution and the term cited for such changes in DNA makeup was applied to various genetic phenomena that could not be easily explained by traditional principles of genetics. These epigenetic events have a diverse role in controlling the gene regulation processes from embryo development in plants. Earlier, it was believed that noncoding RNAs (ncRNAs) are hallmark of imprinted regions and such regions (base sequences) are recognize on DNA which do not encode any protein as we know the biological function of a gene is to produce specific proteins for a particular trait to be expressed phenotypically. However, mechanisms based on RNA of epigenetic regulation are not well decipherable as compared to phenomena based on methylation of DNA and protein complexes arranged in an octamer called histones. A majority of ncRNAs shed their crucial roles in altering the sequence, structure, or expression of mRNAs and thereby modifying the overall protein expression from these genes. They regulate the gene expression at specific stages and sub-stages of central dogma viz., transcription, RNA processing, translation and

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PTMs (post-translational modifications) in eukaryotes. Also, they are involved in guiding synthesis of genome as well as rearrangement. Most ncRNAs are marked as RNA-protein complexes, including ribosomes, guide RNA (gRNA) that base pairs with target mRNA and guides a site-specific cleavage, ligation or modification reaction, snRNPs (small nuclear ribonucleoproteins), snoRNAs (small nucleolar ribonucleoproteins) serves as guide RNA that are essential for processing or modification of pre-rRNA which includes methylation or pseudouridylation, telomerase RNA, siRNAs (small interfering RNA) as well as miRNAs (microRNA) both have role in gene knockdown approach in which gene expression is downregulated in terms of either being completely silenced or low level of expression is modulated unlike in knockout approaches where gene is deliberately removed, thus leading to altered gene expression and lncRNAs (long noncoding RNA) does not encode any protein. It is often capped and polyadenylated present either in nucleus, cytoplasm or both (Zhang and Zhu 2012).

## EPIGENETIC CONTROL

Plants are experts in epigenetic modulations. DNA methylation happens in CG, CHG, and CHH grouping settings in plant genomes, in designs that mirror a harmony between compound exercises that introduce, keep up with, or eliminate methylation. As in different eukaryotes, histone-changing compounds impact epigenetic states in plants and these chemicals are encoded by nearly huge quality families, considered enhanced just as covering capacities. RNA-interceded quality quieting is cultivated utilizing different unmistakable pathways to battle infections, tame transposons, coordinate turn of events, and assist with getting sorted out the genome (Hudson et al. 2010). The interaction between DNA methylation, histone alteration, and noncoding RNAs gives plants

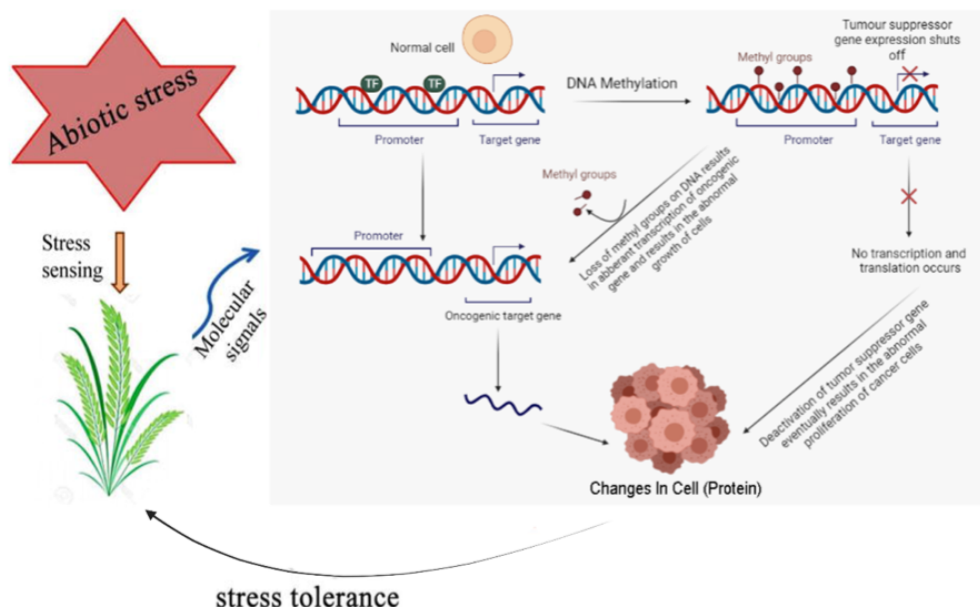
a multifaceted and powerful epigenetic hardware. The unmistakable quality of epigenetic guideline in plants mirrors their method of advancement, way of life, and transformative history. In contrast to development in warm blooded animals, in which organ and tissue arrangement is to a great extent indicated during early stage improvement, plants develop by consistently delivering new organs from self-supporting immature microorganism populaces known as meristems. Thus, postembryonic improvement in plants is a nonstop cycle formed by ecological impacts bringing about a serious level of phenotypic plasticity (an ability to alter physiology or morphology in response to environmental cues). Since plants can't get away from their environmental factors, they are compelled to adapt to inconsistent and regularly negative developmental conditions. Epigenetic administrative instruments can work with metastable changes in quality movement and calibrate quality articulation designs, hence empowering plants to endure and replicate effectively in eccentric conditions. Polyploidization, an increment in the quantity of sets of chromosomes, is normal in plants, intensifying quality families and encouraging the practical specialization of copied qualities, incorporating those associated with epigenetic mechanisms (Jeltsch, 2011). Understanding the epigenetic administrative hardware of plants has come, in huge part, from hereditary screens, most outstandingly in *Arabidopsis thaliana*, an individual from the mustard family that is profoundly manageable to hereditary examinations and was the main plant species to have its genome sequenced. Harvest plants, especially maize, have additionally contributed generously to the revelation of epigenetic wonders and epigenetic administrative components. The investigation of plant epigenetics and epigenomics has a long and rich history and, in cooperative energy with equal examinations in creature and parasitic frame-

works, is contributing fundamentally to our essential comprehension of epigenetic mechanisms in plants. (Kumar. 2016).

## EPIGENETIC RESPONSE TO STRESS

Plants have developed refined hereditary and epigenetic administrative frameworks to react rapidly to horrible natural conditions like warmth, cold, dry season, and microorganism contaminants. Specifically, heat enormously influences plant development and advancement, resistance and circadian mood, and represents a genuine danger to the worldwide food supply. As per temperatures uncovering, warmth can be normally delegated warm encompassing temperature (around 22–27°C), high temperature (27–30°C) and incredibly high temperature (37–42°C, otherwise called heat pressure) for the model plant *Arabidopsis thaliana* (Liu and He, 2014). The hereditary systems of plant reactions to heat have been thoroughly examined, princi-

pally zeroing in on raised surrounding temperature-intervened morphological acclimation and speed increase of blossoming, tweak of circadian clock and plant insusceptibility by high temperatures, and thermotolerance to warm pressure (Luján-Soto and Dinkova. 2021). As of late, incredible advancement has been accomplished on epigenetic guideline of warmth reactions, including DNA methylation, histone adjustments, histone variations, ATP-subordinate chromatin renovating, histone chaperones, little RNAs, long non-coding RNAs and other vague epigenetic components (Pilu. 2011). These epigenetic adjustments manage the declaration of warmth, responsive qualities and capacity to forestall heat-related harms. This survey centers around ongoing advances with respect to the hereditary and epigenetic control of warmth reactions in plants, and focuses closer on the job of the major epigenetic components in plant heat reactions (Figure 1).



**Figure 1.** Role of hypermethylation and hypomethylation. Normal cells undergo two scenarios related to epigenetic mechanisms viz., hypermethylation state in which addition of methyl groups halts the expression of gene and in the case of hypomethylation condition the methyl groups are removed resulting in transcription of undesired genes. Both such conditions result in the changes of normal cells

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## CONCLUSION

There are developing confirmations that epigenetic systems add to pressure reactions and memory in plants. Along these lines, it is apt to theorize that a large number of the reported trans generational pressure reactions could be attributed to epigenetic instruments. It has been shown that plants have an intricate reconstructing framework for epigenetic marks during sexual reproduction. It is conceivable that epigenetic apparatus are more powerful parts in crop plants, which have moderately higher populations of monotonous components in quality rich euchromatic areas. Indeed, DNA methyltransferases and DNA demethylase changes in rice showed more extreme deformities contrasted and the comparing freaks in Arabidopsis. Gene control for pressure open minded transgenic plant advancement by means of DNA methylation at first requires a legitimate determination of the quality. Therefore, fake siRNA from the designated piece of the quality can be presented in the plants for pressure resilience. As host methylation hardware likewise assumes a significant part to coordinate the DNA methylation, over-articulation or hushing of methyl transferase qualities and other key elements (for example siRNA biogenesis) can be consolidated; albeit these suppositions need approval. To comprehend the transformative elements and reactions to natural variations, numerical models have as of late been proposed which consolidate data on the likelihood of transmission of hereditary aggregates, the quantity of epigenetic reset openings among generations, and suppositions on the ecological acceptance of epigenetically directed traits. These models may work with distinguishing proof of the heritable epigenetic fluctuation and contagiousness for future atomic investigations.

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