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“The Power of Epigenetics: Exploring the Science Beyond Turning Genes On and Off for Climate Smart Crop Breeding”

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Abstract

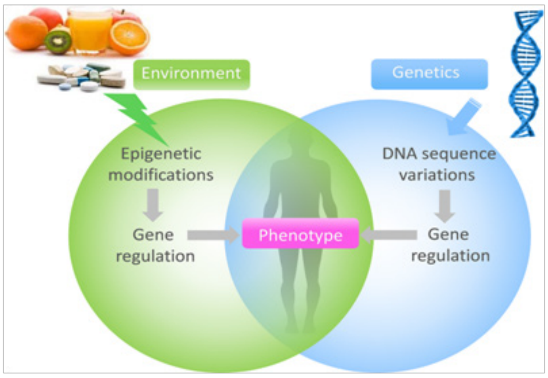
Epigenetics refers to both heritable and non-heritable changes in cell and tissue-specific patterns of gene expression that are not caused by changes in DNA sequences i.e., genetic changes. Epigenetic changes involving DNA methylation, histone modifications, chromatin re-modeling and small RNAs are heritable but don’t follow the inheritance pattern. Plant response to abiotic stresses is complex and involves multiple mechanisms, activated and controlled by massive changes in gene expression and nuclear organization. Abiotic stresses negatively impact plant growth and development, severely affecting crop yield and leading to huge economic losses. Plant cell chromatin exists in dynamic states, enabling precise regulation of gene expression to adapt efficiently to environmental stimuli. Modifications of chromatin states involve a wide range of post-transcriptional histone modifications, histone variants, DNA methylation, and activity of non-coding RNAs, which can epigenetically determine specific transcriptional outputs. As most epigenetic mechanisms are known they may be important for the improvement of crop adaptation and resilience to environmental changes, ultimately leading to the generation of stable climate-smart crops.

Keywords: Epigenetics, DNA methylation, histone modifications, non-coding RNA

Introduction

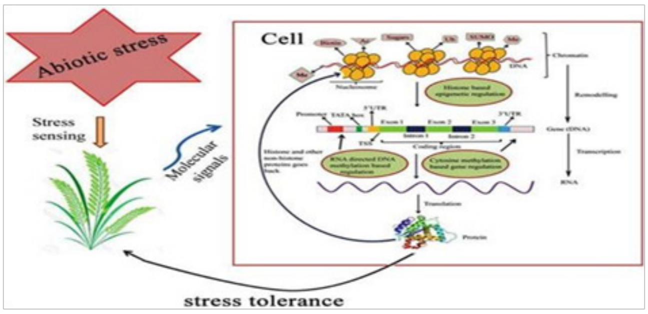
Epigenetics refers to both heritable and non-heritable changes in cell and tissue-specific gene expression patterns that are not caused by changes in DNA sequence i.e., genetic changes.The term epigenetics was coined by C. H. Waddington in 1942.

1. Epigenetic changes are heritable.



2. Epigenetic changes which involves DNA methylation, histone modifications, chromatin remodelling and small RNAs are heritable but don’t follow the pattern of inheritance.
3. Plant response to abiotic stresses is complex and involves multiple mechanisms, activated and controlled by massive changes in gene expression and nuclear organization. Abiotic stresses negatively impact plant growth and development with severe effects on crop yield leading to huge economic losses (Wu et al., 2025).

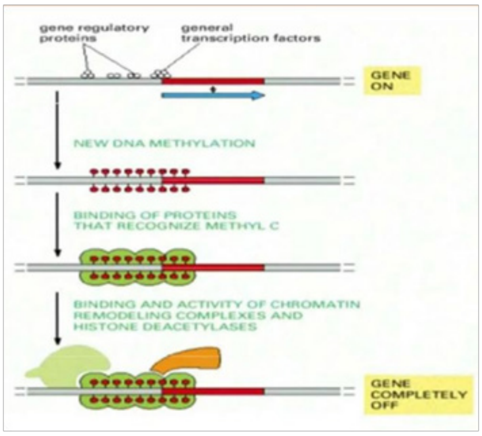
Hence, recent studies focusing on epigenetic mechanisms have primarily focused on crop plants responses to environmental changes, highlighting the critical role of epigenetics in enhancing crop resilience to abiotic stress for better adaptation to environmental changes and breeding of climate-smart crops (Miryeganeh et al., 2025).

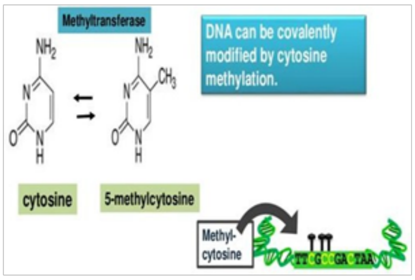


Epigeneticmodifications:

1.DNAmethylation

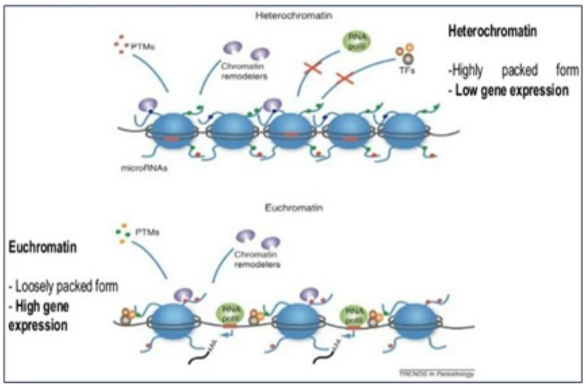
DNAmethylationisa crucialepigeneticmechanismthat regulates gene expression in eukaryotic cells. This serves as a stable and heritable epigenetic signaling tool that typically silences genes activity. This predominantly occurs innon-codingregionsand interspersed repetitiveelements but is notably absent from the CpG islands of actively transcribed genes. The addition of methyl groups to DNA is a tightly regulated process, orchestrated by a family of enzymes known as DNA methyltransferases (DNMTs).Threeprimary DNMT1,DNMT3aand DNMT3bareessential forestablishmentand maintenance of DNA methylation patterns.This epigenetic modifications plays a vital role in transcriptional silencing, genome stability, genome imprinting, X inactivation andtissue specific gene expression (Abdulraheem et al., 2024).

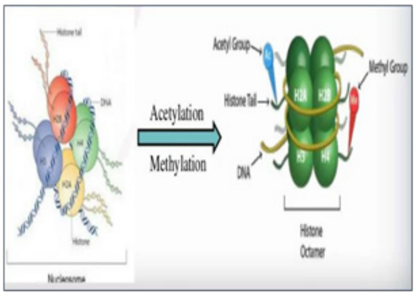




2.Histone modifications

Histone modificationsinvolvechemical changes occurring on the N-terminal tails of nucleosomal histones. Thesemodificationsinfluencechromatinstructure, transitioning it betweenopen(active)and closed (repressive) states, thereby modulating transcriptional activity. Notably, the N-terminal tails of histones are highly accessible due to their protrusion from the nucleosome and their lack of defined structure (Chhatwal et al., 2024).PTMs primarily function by creating binding sites for specific regulatory factorsorby alteringexistinginteractions to

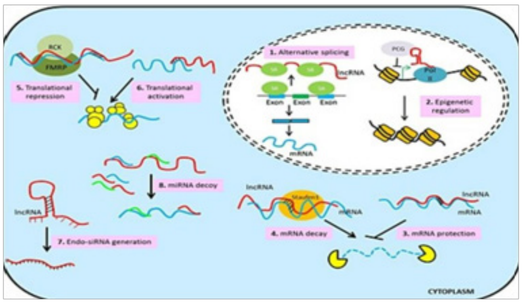




disrupt prior molecular associations.To facilitate transcriptional activity, chromatin must first adopt a relaxed conformation, enabling cellular machinery to access DNA effectively.

3. Non-codingRNA:

Anon-coding RNA(ncRNA) is a functional RNA molecule transcribed fromDNA that does not undergo translation into protein but plays a pivotal role in regulating gene expression.Epigenetic-relatedncRNAs, such as microRNAs(miRNAs),small interfering RNA (siRNAs),PIWI-interacting RNAs (piRNAs)and long non-coding RNAs (lncRNAs) are particularly important.ThesencRNAsregulategeneexpressionatthetranscriptional and post-transcriptional level, which influence a wide range of cellular processes and epigenetic modifications.



Plantpriming:adaptationtoclimaticchange

Creatingclimate-smartcropsrequiresknowledgeofhowepigeneticchangesaretransmitted across generations.Itis widely accepted that the epigenetic modifications includes priming or memory which involves in improving capacity to withstand future stresses (Zhang et al., 2024). However, priming can affect plant growth and development.In Arabidopsis, it has been shown that plant progeny preserve an adaptive epigenetic memory of temperature conditions of their ancestors.

Roleofepigeneticsingeneexpressionunderabioticstress

Tocopewithclimatechangesandunpredictableenvironmentalconditions,plantshave developed genetic and epigenetic mechanisms that enable them to withstand abiotic stresses.

Crop	Abiotic stress	Epigenetic Mechanisms
Maize	Drought, Cold	Enrichment in H3K9ac and decrease in DNA methylation and H3K9me
Rice	Drought, Salinity	Hypomethylation, demethylation at promoter region of *Os-MYB91* gene and rapid histone modifications at *OsMYB9* locus
Wheat	Heat	Increased histone demethylation of the various genes
Barley	Drought	Hc-SiRNA mediated hyper methylation at CYTOKI-NIN-OXIDASE 2.1 promoter
Soyabean	Drought	miR1514a modulation of a NAC transcription factor transcript
Rapeseed	Heat and Salinity	Increased DNA demethylation

Applicationsinclimatesmartcropbreeding

* Useof natural or induced epigenetic variations in creation of climate-smart crops requires stable and heritable variations.

* The environmental buffering effects of epigenetic mechanisms should be exploited to achieve yield stability in climate.

* DNAmethylation gives rise to more permanent mutant alleles to create genetic diversity.

* Hence, epigenetic mechanisms have an important role in increasing crop resilience to specific in climate-smart crop breeding.

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