GLOSSARY OF EPIGENETICS

Term	Description	Ref
Bisulfite sequencing	Technique used to determine the pattern of allelic DNA methylation (5mC) at specific genomic regions.	8
Chromatin	Complex of DNA and proteins that makes up chromosomes in the nucleus of eukaryotic cells.	
Chromosome condensation	The process by which chromatin is compacted into chromosomes during cell division.	
Chromosome conformation	The three-dimensional structure of a chromosome within the nucleus.	
Chromatin immunoprecipitation (ChIP)	A laboratory technique used to isolate specific regions of chromatin for analysis.	
Chromatin marks	Covalent modifications of the chromatin that include the methylation of the fifth carbon of cytosine (5mC) on the DNA molecules and histone post-translational modifications (PTMs). Histone PTMs include methylation, acetylation, ubiquitination, phosphorylation, sumoylation, and poly (ADP) ribosylation. Genes, transposable elements, heterochromatin, and so on are marked by a particular combination of epigenetic marks that define their epigenetic state. When inherited, stable chromatin marks are referred to as ‘epigenetic marks’.	1
Chromatin remodelling	The modification of chromatin structure through changes in the accessibility of condensed genomic DNA to the proteins that regulate transcription, allowing for dynamic regulation of gene expression in response to different signals	22
Differentially methylated position (DMP)	Sites with statistically significant differences in average methylation levels between groups.	
Differentially methylated region (DMR)	A genomic region that has different DNA methylation patterns among multiple samples	21
DNA demethylation	The removal of a methyl group from position 5 of a cytosine base (5mC). DNA demethylation may occur through either a ‘passive’ mechanism that relies on replication-dependent dilution or an ‘active’ process driven by enzymatic replacement independently of DNA replication. As DNA methylation is associated with transcriptional silencing, DNA demethylation can generate a transcriptionally competent state.	8
DNA methylation	A covalent modification of the nucleotide cytosine, which is heritable during cell division and is associated generally with gene silencing.	11
Endogenous small RNAs	Small RNAs that are encoded in the genome or are amplified based on genomically encoded small RNAs. Small RNAs are abundant and are predicted to regulate the expression of thousands of coding and non-coding transcripts.	16

Epialleles	Alleles that are genetically identical (no sequence difference) but present distinct epigenetic profiles due to differences in chromatin marks, such as DNA methylation, that may be associated with changes in gene expression depending on the location of the modification.	1
Epichemicals (Small molecule epigenetic modulators)	Compounds (frequently small molecules) that affect the activity of epigenetic regulators and provoke global (genome wide) changes in epigenetic marks	30-32
Epigenetic	Mitotically and/or meiotically heritable changes in gene function that cannot be explained by changes in DNA sequence	34
Epigenetic inheritance	Inheritance of a phenotype in a manner that is independent of the DNA sequence and that remains self-perpetuating in the absence of the initial stimulus that caused the phenotype in the parental cell or organism.	10
Epiegenetic marker	A chemical modification of DNA or histones that serves as a "mark" for the regulation of gene expression.	
Epigenetic modifiers	Genes whose products modify the epigenome directly through DNA methylation, post-translational modifications of chromatin, or higher-order chromatin structure.	12
Epigenetic modulators	Factors that influence the activity or localization of epigenetic modifiers, representing a bridge between the environment and the epigenome.	12
Epigenetic recombinant inbred lines (EpiRILs)	A population of genetically identical plants that present mosaic epigenomes. They are classically obtained by crossing parents with hypomethylated genomes (mutants in genes necessary to maintain DNA methylation) with isogenic wild-type parents. Plants of the F1 progeny are genetically identical, but have hybrid epigenomes. After outsegregation of the mutation in the F2 generation, plants are selfed across seven to eight generations, which results in a population with wild-type genotypes but mosaic epigenomes.	2
Epigenetic reprogramming	Genome-wide reorganisation of epigenetic modifications that overcomes stable epigenetic barriers and enables acquisition of genomic potential. During the mammalian life cycle, epigenetic reprogramming occurs in PGCs and in early zygotic development. In crop and forest plants, epigenetic reprogramming occurs during induction of somatic embryogenesis.	8, 27-29
Epigenetic stochasticity	A mechanism for increased variability of epigenetic marks at a given location due to random, unpredictable fluctuations of epigenetic modifications	13
Epigenetic editing	refers to a targeted change of a specific epigenetic mark (i.e., methylated cytosine or histone tail methylation, acetylation, etc.) at a predefined genomic site, mostly in order to modulate transcription	34
Epigenetics	Changes in gene expression or cellular phenotype that are transmitted during mitosis and/or meiosis or that are stably maintained in cells in the absence of any triggering signal and are not due to a change in the underlying DNA sequence.	1
Epigenetic memory	(somatic memory and inter/transgenerational memory), which allows cells to maintain their identity during plant development and “remember” favourable alterations leading to a selective advantage (i.e in adverse environments)	34

Epigenome	Genome-wide distribution of 5mC and of histones PTMs. Epigenome description may also include the genome-wide distribution of small RNAs that are guiding de novo DNA methylation, of nucleosome occupancy and of the histone variants. Methylome refers specifically to the distribution of 5mC over the entire genome.	1
Epigenome-wide association studies (EWAS)	Studies of the relationship between epigenetic variants (differentially methylated regions or differentially methylated positions) in the population and stress phenotypes.	13
Epigenomics	The genome-wide study of modifications to DNA and associated proteins such as a variety of modified and variant histones, nucleosome positioning, transcription factors as well as RNAs.	18
Epigenotype	The stable pattern of epigenetic marks that is outside the actual DNA sequence. Variation among epigenotypes might also be called 'heritable epigenetic variation' or 'transgenerational epigenetic variation'.	19
Epimutation	Epigenetic modification that results in heritable or stable changes in gene expression (activation of a silent gene or silencing of an active gene) but is not associated with modifications to the underlying DNA sequence.	1
epiRIL population	Recombinant inbred lines (RIL) that have wild-type genotypes, but contain mosaic epigenomes based on the parental lines used to establish the population.	18
Epistasis	A form of gene interaction, whereby one gene interferes with the phenotypic expression of another non-allelic gene or genes. Gene X is said to be epistatic to gene Y if an allele of gene X alters the encoded effects of gene Y. In the case of epistasis, the combined phenotypic effect of two or more genes is either less than (negative epistasis) or greater than (positive epistasis) the sum of effects of individual genes.	3
Formaldehyde-Assisted Isolation of Regulatory Elements (FAIRE)	A technique used to isolate all open regions of the chromatin.	26
Genetic methylation unit (GeMe)	A cluster of differentially methylated positions (DMPs) and the single-nucleotide polymorphisms (SNPs) regulating their methylation in the same chromosomal region; GeMes include methylation quantitative trait loci (MeQTLs) and also noncontiguous regions separating the DMPs and their controlling SNPs, even outside the same linkage disequilibrium block.	13
Genomic imprinting	Parent-of-origin–specific epigenetic marks generally associated with comparative silencing of the allele transmitted to the offspring.	13
Genomic imprints	Genomic sequences that exhibit differences in CpG methylation according to the parent of origin. These differentially methylated regions (DMRs) can influence the allele-specific expression of one or more genes.	9
Heritable epigenetic changes	Changes that occur in biological molecules and/or their arrangements that are transmitted across generations without altering the genome sequence. Past definitions have been similarly broad or narrower with a focus on particular chemical modifications (e.g., DNA methylation) or changes in regulators (e.g., small RNAs). The concepts outlined here apply to both types of definitions.	9
Histone chaperone	Proteins or protein complexes that specifically bind histones, thwarting non-specific interactions, and that promote their deposition or removal from DNA in an ATP-independent manner.	11

Histone modification	A change in the chemical composition of histones.	
Histone variant	Core canonical and linker histones are encoded by a number of different histone genes, resulting in a number of non-synonymous substitutions and divergent domains. This variation adds complexity to the epigenetic landscape.	10
Hypermethylation	An increase in normal methylation levels	24
Hypomethylation	A decrease in normal methylation levels	24
Intergenerational versus transgenerational	Transgenerational epigenetic inheritance involves changes that persist to affect progeny that were not exposed to the original trigger. When progeny are directly exposed to the environmental effect, the effect is not 'transgenerational' but 'intergenerational'.	16
Long noncoding RNAs (lncRNAs)	A class of regulatory RNAs longer than 200 nucleotides that are epigenetic regulators of gene expression through their ability to bind chromatin-modifying complexes and guide them to target loci.	19
Long terminal repeat (LTR)	Terminal repeat regions harboring regulatory motifs, present at the 5′ and 3′ ends of retroelements flanking the polyprotein domain. The two LTRs of a TE are identical at insertion time. Accumulation of mutations in the LTRs over time is used to estimate the insertion time of TEs.	19
Methylation quantitative trait loci (meQTLs)	Single-nucleotide polymorphisms (SNPs) associated with differentially methylated positions (DMPs), constituting a link between genomewide and epigenome-wide association studies.	13
Methylation Sensitive Amplification Polymorphism (MSAP)	Methylation Sensitive Amplification Polymorphism (MSAP) is a modification of the Amplified Fragment Length Polymorphism technique. It utilizes cleavage with the methylation-sensitive restriction enzymes HpaII or MspI, followed by adapter ligation, amplification, and further gel analysis. The cleavage capacities of HpaII and MspI are strongly affected by the methylation state of the external and internal cytosine residues within the recognized 5′ -CCGG-3′ sequences. Thus, the methylation state can be determined for specific bands based on the ability of each enzyme to cleave the restriction site.	35
MethylC-Seq	A genome-wide technique to survey base resolution maps of DNA methylation using high-throughput sequencing.	18
Miniature inverted-repeat transposable elements (MITEs)	non-autonomous DNA elements that are less than ~600 bp, derived by deletion of the internal coding region and characterized by their terminal inverted repeat (TIR) structure. They are present in high copy numbers with significantly uniform copies closely associated with genes.	19
miRNAs	Families of short regulatory RNAs, 21–24 nucleotides in length that are master regulators of developmental pathways and the stress response; miRNA precursors are processed by DCL1 and associated with mRNA cleavage resulting in post-transcriptional gene silencing (PTGS).	19
Non-Mendelian inheritance	The phenomenon of transgenerational transmittance of traits not explained by classical Mendelian genetic principles. For instance, the epigenome, which represents the component of the genome beyond DNA sequence variation and has many layers, such as DNA methylation, histone methylation, histone acetylation, and small regulatory RNAs.	20
Nucleosome	The fundamental unit of chromatin, which is composed of DNA wrapped around a set of eight histones.	
Paramutation	Gene silencing phenomenon, whereby one allele can induce heritable changes in another allele at the same locus.	9

Polycomb Group Proteins	A group of proteins involved in the regulation and transcriptional silencing of key developmental genes, including the Homeotic (or Hox) gene loci. Human PcG proteins assemble into Polycomb Repressive Complexes (PRCs), of which PRC2 catalyzes the methylation of H3K27 and PRC1 guides the ubiquitin ligation of H2AK119.	11
Primary and secondary small RNAs	Primary small RNAs (either endogenous or an exogenous) can be gnomically encoded or derive from exogenously supplied dsRNA (which can be provided, for example, by feeding the worms with bacteria that express dsRNA). Primary small RNAs can recruit RdRPs to complementary targets, and thus trigger amplification of additional 'secondary' small RNAs. Secondary (or 'amplified') small RNAs are typically 22 nt in length and possess guanosine as their first nucleotide (22G).	17
Priming	Sensitization of plant responses following exposure to a stimulus; allows a plant to respond in a more rapid and effective way to a later stimulus (the same or equivalent) compared with a nonprimed plant.	2
Priming	a first encounter with the stress can trigger the establishment of a molecular memory that primes or acclimates the plant and/or its offspring, which will be better prepared to respond in the eventual case of a second stress	34
RNA-dependent RNA Polymerases (RdRPs)	Proteins that synthesize amplified small RNAs (e.g. siRNAs) producing dsRNA using a single stranded RNA as template.	
RNA-directed DNA methylation (RdDM)	A mechanism that is involved in silencing through a feedback loop consisting of small RNAs guiding DNA methylation and histone modifications.	18
Single Methylation Polymorphism (SMP)	methylation value at a cytosine position	34
S-adenosylmethionine (SAM)	The active sulfonium form of methionine that serves as the principal donor of methyl groups for methylation reactions.	23
Second trigger	An additional RNAi-inducing dsRNA trigger which differs in its sequence from the first trigger (that triggered RNAi in a previous generation). Thus, the second trigger is administered to progeny that inherit from their parents a different heritable RNAi response (targeted against a different gene). Second triggers enhance the silencing effect and prolong the duration of the ancestral RNAi responses.	17
Small RNAs (smRNAs)	21–24 nucleotides (nt) RNA species that can guide machinery to silence loci post-transcriptionally (21 nt smRNAs) and/or transcriptionally (24 nt smRNAs).	18
Transcription factor	Protein that binds to specific cis-regulatory DNA sequences, called response elements, to control the transcription of genes.	25
Transgenerational epigenetic inheritance (TEI)	Modifications of gene expression patterns that are transmitted from one generation to the next via germ lines; they are not due to changes in the DNA sequence but to changes in the epigenetic state of the genes.	2
Transgenerational induction	Change in offspring phenotype that is cued by an environmental signal in the parental generation, and is expressed independently of changes in the offspring genotype. It can occur via epigenetic inheritance or due to maternal effects.	19
Transposon/transposable element (TE)	DNA sequences that can 'jump' from one location in the genome to another. They include retrotransposons that are mobile following a 'copy and paste' mechanism and require an RNA intermediate, and DNA transposons that move using a 'cut and paste' mechanism.	2

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