British Journal of Agroecology and Environmental Studies

DOI: 10.61424/bjaes
Journal Homepage: www.bluemarkpublishers.com/index.php/BJAES

BJAES
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| RESEARCH ARTICLE

The Central Role of Epigenetic Regulation in Establishing Stress Memory in Plants

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| ABSTRACT

Plants, as sessile organisms, have evolved sophisticated mechanisms to cope with environmental stresses through a phenomenon known as stress memory. This adaptive strategy enables plants to respond more efficiently to recurring stress events by retaining information from previous exposures. Epigenetic regulation plays a central role in establishing and maintaining stress memory through dynamic modifications of chromatin structure, DNA methylation, and histone modifications. These molecular changes allow plants to "remember" stress experiences without altering their DNA sequence, providing a flexible yet heritable mechanism for stress adaptation. This review examines the fundamental epigenetic mechanisms underlying stress memory formation, including DNA methylation patterns, histone post-translational modifications, chromatin remodelling, and the involvement of non-coding RNAs. We discuss the molecular basis of somatic, intergenerational, and transgenerational stress memory, with particular emphasis on responses to temperature extremes, drought, and pathogen attacks. Furthermore, we explore the temporal dynamics of memory formation and erasure, highlighting the balance between maintaining adaptive responses and avoiding maladaptive persistence of stress-induced changes. Understanding these epigenetic mechanisms has significant implications for crop improvement strategies, particularly in developing climate-resilient varieties capable of withstanding increasingly unpredictable environmental conditions. Recent advances in epigenome editing technologies offer promising avenues for engineering stress-tolerant crops through targeted manipulation of epigenetic marks. This review synthesises current knowledge on epigenetic stress memory and identifies key questions for future research in this rapidly evolving field.

| KEYWORDS

Epigenetic regulation, stress memory, DNA methylation, histone modifications, chromatin remodelling, priming, somatic memory, transgenerational memory, abiotic stress, plant adaptation.

| ARTICLE INFORMATION

ACCEPTED: 18 August 2023 **PUBLISHED:** 28 November 2023 **DOI:** 10.61424/bjaes.v1.i1.680

1. Introduction

Climate change has intensified the frequency and severity of environmental stresses, posing unprecedented challenges to global agriculture and natural ecosystems (Lobell et al., 2011). As sessile organisms, plants cannot escape unfavourable conditions and must instead rely on sophisticated molecular and physiological adaptations to survive and reproduce under stress. Beyond immediate responses to environmental perturbations, plants have evolved the remarkable ability to remember previous stress exposures, enabling more rapid and robust responses to recurring stress events. This phenomenon, termed stress memory or priming, represents a critical adaptive strategy that enhances plant fitness in fluctuating environments (Lämke and Bäurle, 2017).

Stress memory in plants manifests at multiple temporal scales, ranging from short-term somatic memory that lasts hours to days within an individual's lifetime, to long-term transgenerational memory that can persist across multiple generations (Kinoshita and Seki, 2014). Unlike animals with nervous systems, plants achieve memory formation through epigenetic mechanisms heritable changes in gene expression that occur without alterations to the underlying DNA sequence. These epigenetic modifications provide a molecular substrate for encoding stress information and maintaining altered gene expression states long after the initial stress stimulus has dissipated (Chinnusamy and Zhu, 2009).

The molecular basis of stress memory encompasses several interconnected epigenetic mechanisms, including DNA methylation, histone post-translational modifications, chromatin remodelling, and the action of small regulatory RNAs (Friedrich et al., 2021). These modifications work in concert to alter chromatin accessibility, thereby influencing the transcriptional competence of stress-responsive genes. Importantly, some epigenetic marks can be mitotically and even meiotically inherited, providing a mechanism for transmitting stress information to daughter cells and subsequent generations (Saeed et al., 2022).

However, stress memory is not simply a matter of maintaining all stress-induced changes indefinitely. Recent evidence suggests that the predominant response following stress exposure is actually forgetting or resetting to the pre-stress state, with memory formation representing a more selective process (Crisp et al., 2016). This balance between remembering and forgetting is crucial for optimal plant performance, as constitutive activation of stress responses can impose significant fitness costs under favourable conditions. Understanding the molecular switches that govern memory formation versus erasure is therefore essential for comprehending plant stress adaptation strategies.

The study of epigenetic stress memory has important practical implications for agriculture. By elucidating the mechanisms underlying stress priming, researchers can develop strategies to enhance crop resilience through either genetic breeding programmes or direct epigenetic interventions. Recent advances in epigenome editing technologies offer the tantalising possibility of engineering crops with pre-programmed stress memories, potentially providing a competitive advantage in stress-prone environments (Bäurle and Trindade, 2020).

This review provides a comprehensive examination of the central role of epigenetic regulation in establishing stress memory in plants. We begin by outlining the fundamental concepts of plant stress responses and the types of stress memory. Subsequently, we explore the molecular mechanisms underlying epigenetic regulation, including DNA methylation, histone modifications, and chromatin dynamics. We then discuss specific examples of stress memory in response to various environmental challenges, including temperature extremes, drought, and biotic stresses. Finally, we consider the temporal dynamics of memory formation and maintenance, the ecological and evolutionary significance of stress memory, and future directions for research and application in this field.

2. Literature Review

2.1 Conceptual Framework of Stress Memory in Plants

Stress memory in plants represents a sophisticated adaptive mechanism whereby previous exposure to environmental challenges enhances the capacity to respond to subsequent stress events (Lämke and Bäurle, 2017). This phenomenon can be conceptualised as a form of learning at the molecular level, wherein plants encode information about past environmental conditions and utilise this information to optimise future responses. The concept of stress memory builds upon the broader framework of phenotypic plasticity, representing a temporal component of adaptive responses that extends beyond immediate acclimation (Crisp et al., 2016).

Stress memory can be categorised into distinct types based on temporal persistence and cellular scope (Table 1). Transcriptional memory represents the shortest-lived form, typically persisting for hours to a few days following stress removal and primarily mediated by the stability of stress-induced transcripts and proteins. Somatic stress memory extends from days to weeks within the lifespan of an individual plant, often involving chromatin modifications that can be mitotically inherited. Intergenerational memory spans a single generation, transmitted from parent to offspring through the germline. Finally, transgenerational memory persists across multiple generations in the absence of the inducing stimulus, representing the most stable form of epigenetic inheritance (Kinoshita and Seki, 2014; Saeed et al., 2022).

Table 1: Types of stress memory in plants and their characteristics

Memory Type	Duration	Cellular Scope	Key Mechanisms	Heritability
Transcriptional	Hours to days	Individual cells	mRNA/protein stability, signalling molecules	Non-heritable
Somatic	Days to weeks	Whole plant (mitotic)	Histone modifications, chromatin remodelling	Mitotically heritable
Intergenerational	One generation	Through germline	DNA methylation, histone marks, small RNAs	Single generation
Transgenerational	Multiple generations	Through germline	Stable DNA methylation, RNA-directed changes	Multi-generational
Reset/Forgetting	Variable	Whole plant	Active demethylation, histone modifications, RNA turnover	Context-dependent

2.2 Molecular Mechanisms of Epigenetic Regulation

2.2.1 DNA Methylation

DNA methylation represents one of the most stable epigenetic modifications in plants, primarily occurring at cytosine residues in three sequence contexts: CG, CHG, and CHH (where H represents A, T, or C) (Chinnusamy and Zhu, 2009). Unlike mammals, which exhibit predominantly CG methylation, plants maintain methylation across all three contexts through distinct enzymatic pathways. Methylation at CG sites is maintained by DNA METHYLTRANSFERASE 1 (MET1), CHG methylation by CHROMOMETHYLASE 3 (CMT3), and CHH methylation primarily by DOMAINS REARRANGED METHYLTRANSFERASE 2 (DRM2) through the RNA-directed DNA methylation (RdDM) pathway (Lämke and Bäurle, 2017).

Stress-induced alterations in DNA methylation patterns have been documented across diverse stress conditions, including heat, cold, drought, and pathogen attack. These changes can result in either hypermethylation or hypomethylation at specific loci, depending on the stress type and genomic context (Saeed et al., 2022). For instance, cold stress in Arabidopsis induces genome-wide hypomethylation, particularly at transposable elements, whilst heat stress can trigger localised hypermethylation at stress-responsive genes. The dynamic nature of these methylation changes some transient and others stable determines whether they contribute to short-term acclimation or long-term memory (Adhikari et al., 2022).

2.2.2 Histone Post-Translational Modifications

Histone proteins, which form the core of nucleosomes, undergo extensive post-translational modifications (PTMs) that profoundly influence chromatin structure and gene accessibility. These modifications occur predominantly on the N-terminal tails of histones H3 and H4, although modifications on H2A and H2B also play important roles (Bhadouriya et al., 2021). Key modifications include acetylation, methylation, phosphorylation, ubiquitination, and sumoylation, each catalysed by specific enzymes and associated with distinct transcriptional states (Friedrich et al., 2021).

Histone acetylation, mediated by histone acetyltransferases (HATs), generally correlates with transcriptional activation by neutralising positive charges on lysine residues, thereby loosening DNA-histone interactions and increasing chromatin accessibility. Conversely, histone deacetylases (HDACs) remove acetyl groups, promoting chromatin compaction and gene silencing. In the context of stress memory, histone acetylation patterns at stress-responsive genes often remain elevated following stress removal, contributing to transcriptional priming (Bäurle, 2018).

Histone methylation presents a more complex regulatory landscape, as its effects depend on both the specific residue modified and the degree of methylation. Trimethylation of histone H3 at lysine 4 (H3K4me3) is typically associated with active transcription and represents a hallmark of transcriptional memory genes. This mark is deposited by SET domain-containing methyltransferases and can persist for extended periods after stress exposure, maintaining genes in a primed state (Lämke and Bäurle, 2017). Conversely, H3K27me3, deposited by Polycomb Repressive Complex 2 (PRC2), is associated with gene silencing and plays a crucial role in maintaining the repressed state of developmental regulators and transposable elements during stress (Saeed et al., 2022).

Figure 1: Schematic illustration of major epigenetic mechanisms involved in stress memory, including DNA methylation, histone modifications, chromatin remodelling, and small RNA pathways. The figure shows the interplay between these mechanisms in regulating stress-responsive genes.

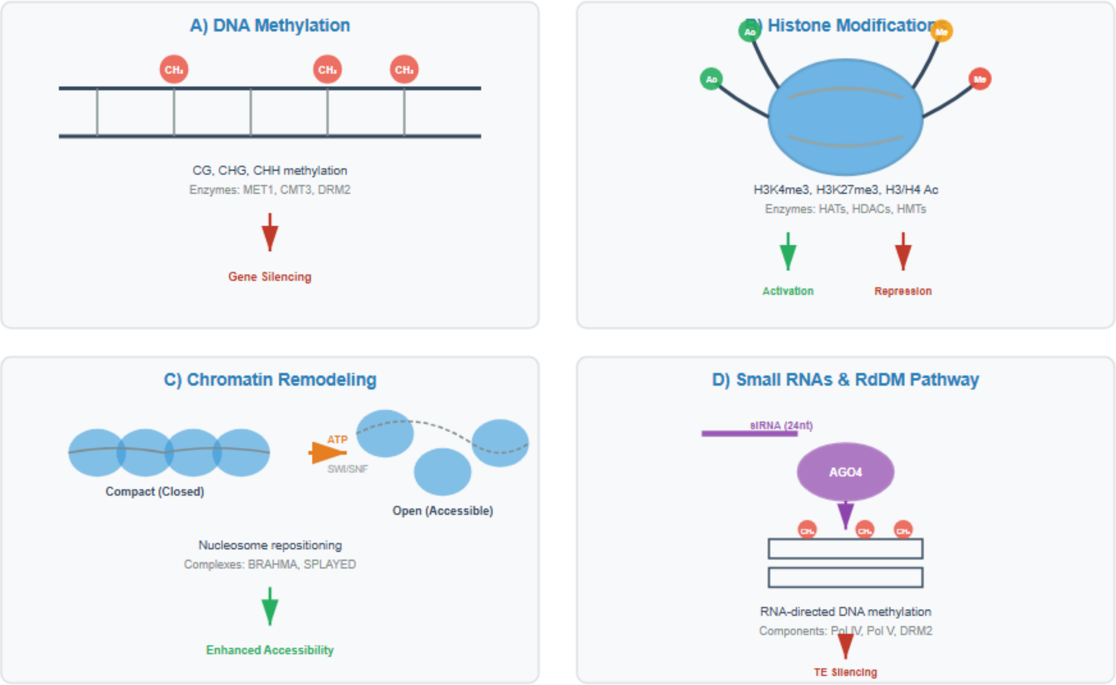


Table 2: Major histone modifications and their roles in stress memory

Modification	Enzymes Involved	Transcriptional Effect	Role in Stress Memory	Stability
H3K4me3	ATX1, SDG2	Activation	Transcriptional memory, priming	Hours to days
H3K4me2	ATX1, ATXR3	Activation	Priming of defence genes	Days
H3K9me2	SUVH4, SUVH5, SUVH6	Repression	TE silencing, heterochromatin	Weeks to stable
H3K27me3	PRC2 (CLF, SWN)	Repression	Developmental memory, FLC silencing	Stable
H3K36me3	SDG8	Activation/elongation	Transcriptional regulation	Moderate
H3 acetylation	HATs (HAC1, GCN5)	Activation	Rapid stress response	Hours
H4 acetylation	HATs	Activation	Chromatin accessibility	Hours to days
H2B ubiquitination	HUB1, HUB2	Activation	H3K4me3 deposition	Transient

2.2.3 Chromatin Remodelling Complexes

Chromatin remodelling complexes utilise ATP hydrolysis to alter nucleosome positioning, composition, and density, thereby modulating DNA accessibility to transcriptional machinery. In plants, several families of chromatin remodellers have been implicated in stress responses and memory formation, including the SWI/SNF family (such as BRAHMA and SPLAYED), the ISWI family, and the CHD family (Bhadouriya et al., 2021).

The SPLAYED (SYD) protein, a SNF2-family chromatin remodeller, plays a particularly important role in stress-responsive gene regulation. SYD is required for the proper induction of numerous stress-responsive genes and contributes to maintaining open chromatin states at these loci following stress exposure. Loss of SYD function results in impaired stress memory and reduced priming capacity, highlighting the essential role of chromatin remodelling in establishing epigenetic memory states (Lämke and Bäurle, 2017).

2.2.4 Small RNAs and RNA-Directed DNA Methylation

Small regulatory RNAs, including microRNAs (miRNAs) and small interfering RNAs (siRNAs), play crucial roles in both immediate stress responses and the establishment of stress memory. These molecules regulate gene expression post-transcriptionally and can direct epigenetic modifications through the RNA-directed DNA methylation (RdDM) pathway (Nuthikattu et al., 2013). In the RdDM pathway, 24-nucleotide siRNAs guide DNA methylation to specific genomic loci through interaction with ARGONAUTE 4 (AGO4) and recruitment of the de novo methyltransferase DRM2 (Chinnusamy and Zhu, 2009).

Stress exposure alters the expression and activity of numerous small RNAs, some of which contribute to memory formation. For instance, changes in siRNA populations targeting transposable elements can lead to heritable alterations in DNA methylation patterns that persist across generations (Bilichak et al., 2015). Additionally, stress-induced changes in miRNA expression can contribute to developmental reprogramming and may facilitate transgenerational adaptation to stress environments (Ding et al., 2022).

3. Stress-Specific Memory Mechanisms

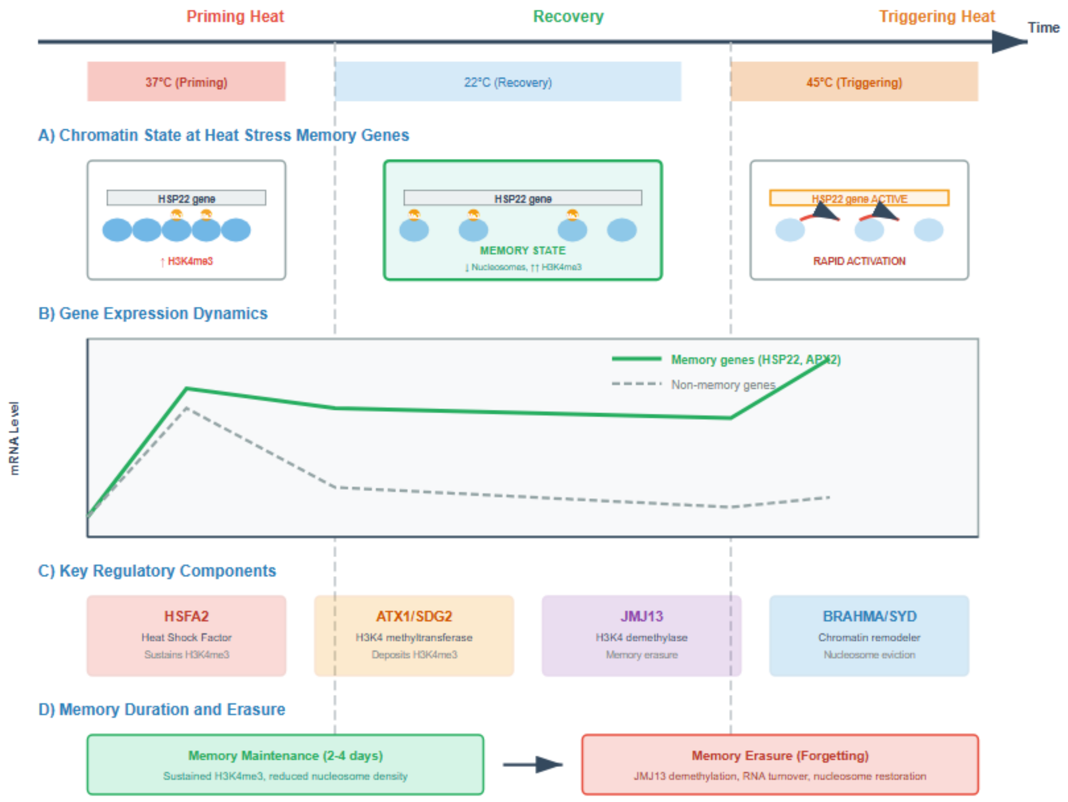
3.1 Heat Stress Memory

Heat stress represents one of the most extensively studied systems for understanding somatic stress memory in plants (Friedrich et al., 2021). Exposure to moderately elevated temperatures can prime plants to survive subsequent, otherwise lethal heat stress a phenomenon termed acquired thermotolerance. This memory persists for several days after the initial heat exposure and is mediated by sustained changes in chromatin state at specific heat stress memory (HSM) genes (Bäurle, 2018).

Key HSM genes include those encoding heat shock proteins (HSPs), such as HSP22 and HSP17.6, as well as the ASCORBATE PEROXIDASE 2 (APX2) gene. Following an initial heat stress, these genes maintain elevated levels of H3K4me3 and reduced nucleosome occupancy at their promoters, facilitating rapid re-activation upon subsequent heat exposure (Lämke and Bäurle, 2017). The transcription factor HEAT SHOCK FACTOR A2 (HSFA2) plays a central role in establishing heat stress memory by promoting sustained histone modifications at HSM gene loci (Hasanuzzaman et al., 2013).

Interestingly, the duration of heat stress memory appears to be actively regulated through multiple mechanisms. The histone demethylase JUMONJI C DOMAIN-CONTAINING PROTEIN 13 (JMJ13) contributes to memory erasure by removing H3K4me3 marks, whilst RNA turnover mechanisms actively degrade stress-induced transcripts during the recovery period (Crisp et al., 2016). This active regulation of memory duration suggests that plants have evolved mechanisms to balance the benefits of priming against the costs of maintaining constitutive stress responses.

Figure 2: Molecular mechanisms of heat stress memory formation.



The diagram illustrates the establishment and maintenance of elevated H3K4me3 levels and reduced nucleosome density at heat stress memory genes following priming stress, enabling rapid transcriptional reactivation during recurring heat stress.

3.2 Cold Stress and Vernalisation Memory

Cold stress memory in plants manifests in two distinct forms: short-term cold acclimation memory and long-term vernalisation memory. Cold acclimation enables plants to survive freezing temperatures through the cold-induced expression of C-REPEAT BINDING FACTOR (CBF) genes and their downstream targets, the COLD-REGULATED (COR) genes (Adhikari et al., 2022). Following cold exposure, some plants maintain enhanced freezing tolerance for days to weeks, representing a form of somatic cold memory mediated by chromatin modifications at CBF and COR loci (Banerjee et al., 2017).

Vernalisation represents a more stable form of cold memory, wherein prolonged winter cold exposure induces flowering competence that persists throughout the entire subsequent growing season. This remarkable epigenetic switch centres on the FLOWERING LOCUS C (FLC) gene, a potent repressor of flowering (Antoniou-Kourounioti et al., 2021). During vernalisation, FLC becomes progressively silenced through the accumulation of repressive histone marks, particularly H3K27me3, deposited by Polycomb Repressive Complex 2. This silencing is maintained throughout mitotic divisions via a self-reinforcing epigenetic loop involving the Polycomb system (Duan et al., 2017).

The molecular mechanism of FLC silencing during vernalisation involves multiple steps. Initially, cold exposure induces the long non-coding RNA COLD ASSISTED INTRONIC NONCODING RNA (COLDAIR), which facilitates PRC2 recruitment to the FLC locus. Subsequently, nucleation of H3K27me3 spreads across the gene body, creating a stable repressive chromatin domain. Additional factors, including VERNALIZATION INSENSITIVE 3 (VIN3) and VERNALIZATION 2 (VRN2), are required for establishing and maintaining this repressed state (Saeed et al., 2022). Importantly, whilst this epigenetic silencing persists mitotically throughout plant development, it is reset in the next generation, allowing each new plant to independently sense and respond to winter cold.

Table 3: Examples of epigenetic stress memory in response to different environmental challenges

Stress Type	Model System	Memory Duration	Key Genes/Loci	Epigenetic Marks	Reference
Heat	Arabidopsis	Days	HSP22, APX2, HSP17.6	H3K4me3↑, nucleosome depletion	Lämke & Bäurle, 2017
Cold/Vernalisation	Arabidopsis	Months (mitotic)	FLC	H3K27me3↑, H3K4me3↓	Antoniou-Kourounioti et al., 2021
Drought	Arabidopsis	Days to weeks	RD29B, RAB18	H3K4me3, DNA methylation changes	Ding et al., 2022
Salt	Arabidopsis, Rice	Transgenerational	Various stress-responsive	CHH methylation changes	Bilichak et al., 2015
Pathogen (SAR)	Arabidopsis	Weeks	PR genes, WRKY genes	H3K4me2/me3↑, H3 acetylation	Lämke & Bäurle, 2017
Hyperosmotic	Arabidopsis	One generation	Genome-wide loci	DNA methylation (male-limited)	Crisp et al., 2016

3.3 Drought and Osmotic Stress Memory

Drought represents one of the most significant abiotic stresses affecting global crop productivity (Lobell et al., 2011). Plants exposed to mild drought stress often exhibit enhanced tolerance to subsequent, more severe water deficit a phenomenon attributed to drought stress memory. The molecular basis of drought memory involves coordinated changes in DNA methylation, histone modifications, and the accumulation of protective metabolites and proteins (Ding et al., 2022).

At the transcriptional level, drought-responsive genes such as RD29B, RAB18, and various dehydrins maintain altered expression patterns following stress removal. These changes are associated with sustained histone modifications, particularly H3K4me3 enrichment at gene promoters (Bäurle and Trindade, 2020). Additionally, drought stress induces changes in DNA methylation patterns, with both hypermethylation and hypomethylation observed at different genomic regions. Some of these methylation changes persist following stress relief and may contribute to priming effects observed upon repeated drought exposure.

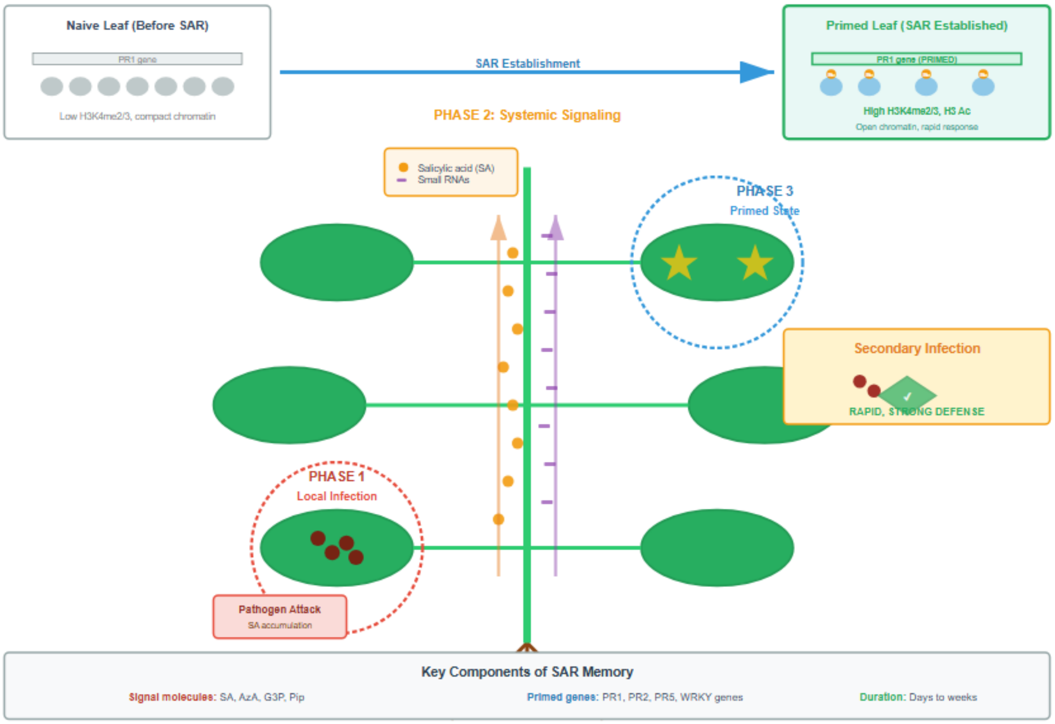
An important regulator of drought stress memory is the retrograde signalling molecule 3'-phosphoadenosine 5'-phosphate (PAP), which accumulates during drought and inhibits RNA degradation. This inhibition may contribute to the maintenance of stress-induced transcripts during recovery, potentially facilitating more rapid re-induction upon subsequent drought stress (Estavillo et al., 2011). The interplay between RNA stability, epigenetic modifications, and metabolic signals highlights the multi-layered nature of drought stress memory.

3.4 Biotic Stress Memory and Systemic Acquired Resistance

Systemic acquired resistance (SAR) represents a well-characterised form of immune memory in plants whereby localised pathogen infection confers enhanced resistance to subsequent infections throughout the plant (Lämke and Bäurle, 2017). This long-lasting immunity, which can persist for weeks to months, depends critically on epigenetic modifications that maintain defence genes in a primed state. Following SAR induction, genes encoding pathogenesis-related (PR) proteins and various WRKY transcription factors exhibit sustained enrichment of activating histone marks, particularly H3K4me2 and H3K4me3, even in the absence of pathogen challenge (Bäurle, 2018).

The establishment of SAR involves the systemic spread of mobile signals, including salicylic acid and potentially small RNAs, from infected tissues to distal parts of the plant. These signals trigger chromatin modifications at defence gene loci in uninfected tissues, establishing a primed state that enables more rapid and robust defence responses upon subsequent pathogen encounter. The maintenance of these chromatin states requires ongoing activity of histone-modifying enzymes and appears to be actively regulated to prevent excessive fitness costs associated with constitutive defence activation (Bhadouriya et al., 2021).

Figure 3: Systemic acquired resistance (SAR) as a model for biotic stress memory.



The figure depicts the induction phase, systemic signalling, and the establishment of chromatin-based priming at defence genes in systemic tissues, leading to enhanced resistance upon secondary infection.

4. Temporal Dynamics Of Stress Memory Formation And Maintenance

4.1 The Balance Between Memory and Forgetting

A critical aspect of stress memory that has garnered increasing attention is the phenomenon of memory erasure or forgetting (Crisp et al., 2016). Whilst the concept of stress memory emphasises the retention of stress-induced changes, accumulating evidence suggests that active resetting to pre-stress states represents the predominant response following most stress events. This balance between remembering and forgetting is essential for optimising plant performance across fluctuating environments (Friedrich et al., 2021).

The decision between memory formation and erasure appears to be influenced by multiple factors, including the severity and duration of stress exposure, the developmental stage of the plant, and the ecological context. Mild, transient stresses may trigger primarily short-lived transcriptional responses that are rapidly reversed upon stress removal, whilst severe or prolonged stresses are more likely to induce stable epigenetic changes that persist as memory (Bäurle and Trindade, 2020). This differential response likely reflects an adaptive strategy wherein plants invest in costly memory formation only when the probability of recurring stress justifies the associated fitness costs.

At the molecular level, memory erasure involves active processes including histone demethylation, DNA demethylation, and RNA turnover. Histone demethylases such as JMJ family proteins remove activating marks like H3K4me3, whilst DNA glycosylases (DEMETER, REPRESSOR OF SILENCING 1) actively remove DNA methylation marks (Han et al., 2016). RNA degradation pathways, particularly those involving RNA decay machinery, contribute to forgetting by eliminating stress-induced transcripts during recovery periods. The enzyme SAL1 phosphatase regulates levels of PAP, thereby modulating RNA stability and influencing the duration of transcriptional memory (Estavillo et al., 2011).

Table 4: Factors influencing stress memory duration and stability

Factor	Effect on Memory	Mechanism	Timescale
Stress severity	Stronger stress → longer memory	Increased chromatin modification depth	Days to weeks
Stress duration	Longer exposure → more stable marks	Progressive accumulation of modifications	Weeks to transgenerational
Developmental stage	Affects heritability	Germline vs somatic modification	Varies
RNA turnover rate	Faster decay → shorter memory	Active degradation of stress transcripts	Hours to days
Histone demethylase activity	Higher activity → faster forgetting	Removal of H3K4me3, H3K36me3	Days
DNA demethylation	Active demethylation → memory loss	DME, ROS1 activity	Weeks to stable
Environmental context	Recurring stress → stronger memory	Reinforcement of modifications	Variable

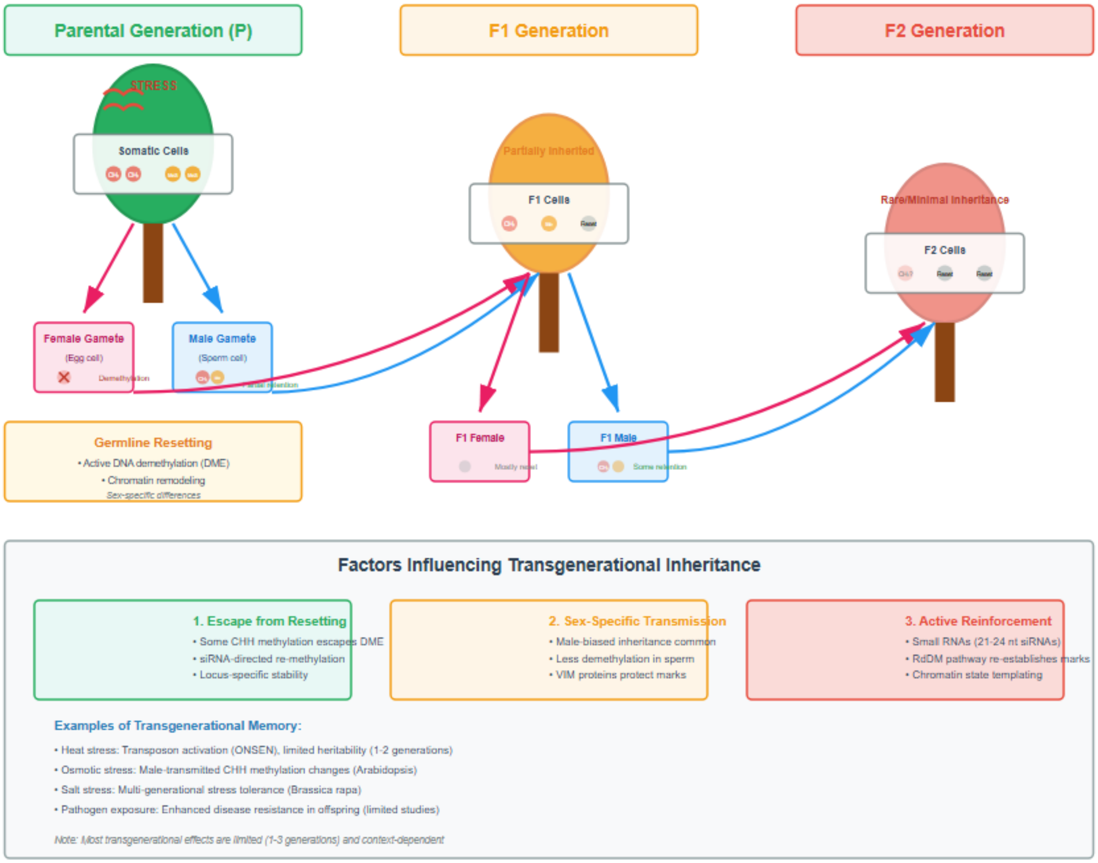
4.2 Transgenerational Inheritance of Stress Memory

Whilst somatic stress memory provides within-generation benefits, the transmission of stress-induced epigenetic changes across generations represents a potentially more profound adaptation mechanism (Kinoshita and Seki, 2014). Transgenerational epigenetic inheritance has been documented in response to various stresses, including heat, drought, salt, and pathogen attack, although the stability and adaptive significance of these inherited changes remain subjects of active investigation (Bilichak et al., 2015).

The transmission of epigenetic information through the germline faces significant challenges, as plant reproductive development involves extensive chromatin remodelling and DNA demethylation. In Arabidopsis, the vegetative cell nucleus of the male gametophyte undergoes active DNA demethylation mediated by the DEMETER glycosylase, which may serve to reset transposon silencing and prevent the accumulation of deleterious methylation changes. However, this resetting is incomplete, allowing some stress-induced methylation changes to escape and be transmitted to offspring (Saeed et al., 2022).

Recent studies have revealed that transgenerational stress memory is often restricted to specific genomic regions and may be limited to the male germline. For instance, hyperosmotic stress induces DNA methylation changes that are transmitted through the sperm but not through the egg, suggesting sex-specific epigenetic inheritance mechanisms (Crisp et al., 2016). The adaptive significance of transgenerational stress memory remains debated, with some arguing that it provides offspring with a 'head start' in environments similar to those experienced by parents, whilst others suggest that the limited stability and scope of most transgenerational effects indicates primarily maladaptive or neutral inheritance.

Figure 4: Pathways of transgenerational epigenetic inheritance in plants.



Factors Influencing Transgenerational Inheritance

1. Escape from Resetting
- Some CHH methylation escapes DME
- siRNA-directed re-methylation
- Locus-specific stability

2. Sex-Specific Transmission
- Male-biased inheritance common
- Less demethylation in sperm
- VIM proteins protect marks

3. Active Reinforcement
- Small RNAs (21-24 nt siRNAs)
- RdDM pathway re-establishes marks
- Chromatin state templating

Examples of Transgenerational Memory:
- Heat stress: Transposon activation (ONSEN), limited heritability (1-2 generations)
- Osmotic stress: Male-transmitted CHH methylation changes (Arabidopsis)
- Salt stress: Multi-generational stress tolerance (Brassica rapa)
- Pathogen exposure: Enhanced disease resistance in offspring (limited studies)

Note: Most transgenerational effects are limited (1-3 generations) and context-dependent

The diagram illustrates stress-induced epigenetic changes in somatic tissues, their potential transmission through male and female germlines, resetting processes during reproduction, and the establishment of memory in the next generation.

5. Applications and Future Perspectives

5.1 Agricultural Applications of Stress Memory

Understanding the molecular mechanisms of stress memory has profound implications for developing climate-resilient crops (Bäurle and Trindade, 2020). Several strategies can be envisioned for exploiting stress memory in agriculture. First, seed priming treatments controlled pre-sowing stress exposures can induce protective epigenetic changes that enhance seedling establishment and stress tolerance in the field. This approach has shown promise in improving germination rates and early vigour under suboptimal conditions (Adhikari et al., 2022).

Second, breeding programmes can select for genotypes with enhanced memory capacity or prolonged memory duration. Natural variation in stress memory has been documented across plant accessions, suggesting a genetic basis for memory formation that could be exploited through conventional breeding or marker-assisted selection (Saeed et al., 2022). Third, recent advances in epigenome editing technologies, such as CRISPR-dCas9 fused to epigenetic modifiers, offer the possibility of engineering specific epigenetic states at stress-responsive genes, potentially creating crops with pre-installed stress memories (Distéfano et al., 2021).

Table 5: Potential applications of epigenetic stress memory in crop improvement

Strategy	Approach	Advantages	Challenges
Seed priming	Pre-treatment with stress or chemicals	Simple, cost-effective, immediate benefits	Variable effectiveness, memory duration limited
Breeding for memory capacity	Select natural variation in memory genes	Stable, heritable improvements	Requires extensive phenotyping, slow process
Epigenome editing	CRISPR-based epigenetic modification	Targeted, precise, potentially reversible	Technical complexity, regulatory concerns
Grafting approaches	Transfer memory via grafting	Combine rootstock memory with scion traits	Limited to compatible species
Beneficial microbiome	Microbial-induced memory	Sustainable, multiple stress protection	Stability, environmental dependence
Chemical epimodulators	Application of HDAC/DNMT inhibitors	Flexible, adjustable timing	Potential off-target effects, specificity issues

5.2 Outstanding Questions and Future Directions

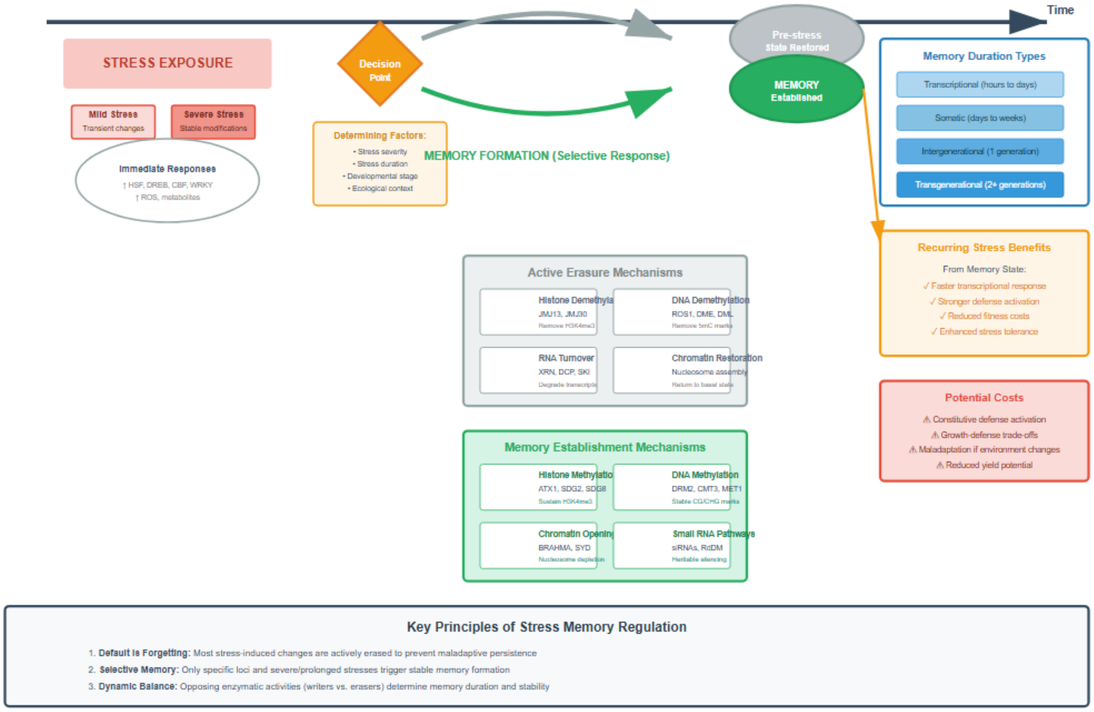
Despite significant progress in understanding epigenetic stress memory, numerous fundamental questions remain unresolved (Friedrich et al., 2021). A central challenge is determining the precise molecular criteria that distinguish memory-forming stress events from those that are rapidly forgotten. What quantitative thresholds in stress intensity or duration trigger the switch from transient acclimation to stable memory formation? How do plants integrate information from multiple simultaneous or sequential stresses to establish appropriate memory states?

The mechanisms regulating memory duration represent another critical knowledge gap. For somatic memory lasting days to weeks, what determines the half-life of specific histone modifications at individual genes? Why do some genes maintain primed states whilst others rapidly reset? Understanding these temporal dynamics will require high-resolution time-course studies combined with mathematical modelling to capture the kinetics of chromatin modification establishment and erasure (Crisp et al., 2016).

For transgenerational memory, key questions concern the specificity and adaptive value of inherited changes. Are there specific classes of genes or genomic regions more likely to transmit stress-induced epigenetic changes across generations? Under what ecological conditions does transgenerational memory provide fitness benefits versus costs? Addressing these questions will require long-term multi-generational studies in natural or semi-natural environments, moving beyond controlled laboratory conditions (Lämke and Bäurle, 2017).

Finally, translating our mechanistic understanding into practical applications demands further research on crop species. Most stress memory research has focused on Arabidopsis, and it remains unclear how broadly these mechanisms apply across plant diversity. Comparative studies examining stress memory in cereals, legumes, and other major crops will be essential for developing effective agricultural interventions. Additionally, understanding how different stresses interact whether they show cross-tolerance or specific priming will be crucial for breeding crops adapted to the complex, multi-factorial stress environments characteristic of climate change scenarios (Saeed et al., 2022).

Figure 5: Integrative model of epigenetic stress memory formation, maintenance, and erasure.



1. **Default is Forgetting:** Most stress-induced changes are actively erased to prevent maladaptive persistence
2. **Selective Memory:** Only specific loci and severe/prolonged stresses trigger stable memory formation
3. **Dynamic Balance:** Opposing enzymatic activities (writers vs. erasers) determine memory duration and stability

The diagram presents a comprehensive framework showing the decision points between memory formation and forgetting, the molecular mechanisms involved at each stage, and the factors influencing memory stability and heritability across cellular and organismal timescales.

6. Conclusion

Epigenetic regulation occupies a central position in the establishment and maintenance of stress memory in plants, providing a sophisticated molecular mechanism for encoding environmental information without altering DNA sequences. Through the coordinated action of DNA methylation, histone modifications, chromatin remodelling, and small RNAs, plants can retain information about previous stress exposures and utilise this information to mount more effective responses to recurring challenges. This adaptive plasticity represents a critical component of plant survival strategies in fluctuating and increasingly unpredictable environments.

Research over the past two decades has revealed that stress memory operates across multiple temporal scales, from hours-long transcriptional memory to multi-generational epigenetic inheritance. Each timescale involves distinct molecular mechanisms and serves different adaptive functions. Short-term somatic memory enables individual plants to respond efficiently to transiently recurring stresses within their lifetime, whilst longer-term transgenerational memory may provide offspring with adaptive advantages in environments similar to those experienced by their parents.

Importantly, stress memory is not a passive consequence of stress exposure but rather an actively regulated process. Plants have evolved mechanisms to balance memory formation with forgetting, ensuring that beneficial adaptations are retained whilst avoiding the fitness costs associated with constitutive stress responses. The molecular switches governing this balance involving histone demethylases, DNA glycosylases, and RNA degradation machinery represent key regulatory nodes that determine whether stress-induced changes persist as memory or are actively erased during recovery.

The practical implications of understanding stress memory are substantial, particularly for agriculture facing the challenges of climate change. Strategies ranging from seed priming to epigenome editing offer promising avenues for enhancing crop stress tolerance. However, realising the full potential of these approaches requires addressing fundamental questions about the mechanisms, duration, and adaptive significance of stress memory across diverse plant species and environmental contexts.

As we advance our understanding of epigenetic stress memory, integration of multiple research approaches will be essential. Combining molecular genetics, genomics, bioinformatics, ecological studies, and mathematical modelling will enable us to develop comprehensive, predictive models of memory formation and maintenance. Such models will not only deepen our fundamental understanding of plant adaptation but also guide the development of next-generation strategies for breeding climate-resilient crops capable of thriving in an uncertain environmental future.

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