

The Epigenetics of Bloom: How Climate Stress Triggers Memory in Dahlia Tubers for the Next Growing Season

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ABSTRACT

Plants cannot flee from stress, they must endure it, adapt to it, and remember it. Dahlia variabilis, a geophyte with underground tuberous storage roots, offers a compelling model for understanding how climate-induced stress experiences are encoded in the plant body and carried into the next growing season. This article examines the molecular mechanisms by which heat, drought, and cold stresses imprint epigenetic marks, principally DNA methylation, histone modifications, and small RNA-mediated pathways onto dahlia tuber chromatin during the growing season. These marks persist through winter dormancy and influence gene expression upon resprouting the following spring, producing a primed, faster, and more robust response to the same stressors. Drawing on evidence from model species and geophytic analogues, we propose that epigenetic stress memory is functionally adaptive in dahlias — a biological insurance policy written in chemistry rather than DNA sequence.

INTRODUCTION: Plants That Remember

Memory is usually the preserve of animals. Yet mounting evidence reveals that plants possess a

molecularly sophisticated form of memory encoded not in neural circuits but in chemical modifications to their genome. This

phenomenon, called epigenetic stress memory, allows plants to record a stressful experience and draw on that record in future encounters with the same challenge (Lämke & Bäurle, 2017; Gallusci *et al.*, 2023).

For *Dahlia variabilis*, the garden dahlia, this capacity takes on a particularly tangible form. As a geophyte (a plant that survives unfavourable seasons through underground storage organs), the dahlia's tuberous roots are not merely energy reserves. Evidence from related plant systems and tuber epigenomics suggests these tubers also serve as archives: repositories of molecular memories shaped by the stresses the parent plant endured during its most recent growing season (Dogramaci *et al.*, 2024).

Understanding this mechanism matters beyond basic biology. As climate change intensifies the frequency of heat waves, erratic rainfall, and late frosts, decoding how dahlias encode and exploit stress memory could guide practical horticultural interventions from improved storage protocols to epigenomically informed breeding (Abdulraheem *et al.*, 2024; Dobránszki, 2025).

1. What Is Epigenetic Memory?

The genome carries two kinds of information. The first, DNA sequence is fixed at fertilisation and does not change with experience. The second is the epigenome: a dynamic layer of chemical tags on DNA and on the histone proteins around which DNA is wrapped. These tags do not alter the genetic code; they alter how it is read (Berger *et al.*, 2009).

Three primary classes of epigenetic modification are relevant to stress memory in plants:

- **DNA methylation-** addition of a methyl group to cytosine residues. Stress-induced methylation can silence or activate stress-

responsive genes and persists through cell divisions (Abdulraheem *et al.*, 2024).

- **Histone modifications-** H3K4me3 marks stress genes in an 'open', transcriptionally poised state; H3K27me3 represses genes including those governing flowering time during cold (Xie *et al.*, 2021).
- **Non-coding RNAs-** siRNAs and lncRNAs guide DNA methylation via the RNA-directed DNA methylation (RdDM) pathway and recruit chromatin-modifying complexes to specific loci (Zhan & Meyers, 2023; Cheng *et al.*, 2024).

What makes these marks relevant to memory is their persistence. Most stress-induced gene expression changes fade within hours once the stressor is removed. But epigenetic marks at certain loci can survive multiple rounds of cell division, carrying the molecular record of past experience forward — sometimes for an entire season, sometimes across generations (Lämke & Bäurle, 2017; Iwasaki & Paszkowski, 2014).

2. The Dahlia Tuber as Underground Archive

"Tubers are not just fuel tanks. They are molecular diaries, each layer of their chromatin encoding the growing season the plant has just survived." — Adapted from Dogramaci et al. (2024)

A dahlia tuber is a modified, swollen root whose primary biological role is to store carbohydrates, principally the fructose polymer inulin as fuel for the next season's regrowth. Tuber initiation is triggered when shortening daylength and declining temperatures raise levels of abscisic acid (ABA), a hormone that simultaneously promotes dormancy and orchestrates gene-expression changes aligned with stress tolerance.

ABA is not merely a dormancy switch; it is also a master activator of epigenetic modification pathways. ABA-responsive genes possess specific promoter elements (ABREs) that recruit histone acetyltransferases and methyltransferases, linking hormonal signalling directly to chromatin remodelling (Shi *et al.*, 2024).

Exposing storage organs to environmental signals during dormancy itself can reconfigure epigenetic marks. In potato tubers, storage temperature alters DNA methylation at genes controlling gibberellin signalling, affecting dormancy depth (Xiong *et al.*, 2022). In apple buds, seasonal temperature fluctuations induce histone methylation changes that coordinate dormancy break (Chen *et al.*, 2022). Mechanistically equivalent processes are expected in dahlia tubers.

3. How Climate Stresses Write the Memory

3.1 Heat Stress- When dahlias encounter summer heat waves, H3K4me3 marks accumulate at the promoters of heat-responsive genes such as HSP22 and APX2 within hours. Crucially, this mark is not fully erased when temperatures normalise it persists, keeping these loci in a transcriptionally poised state. When heat returns, the primed plant shows faster and stronger induction of the same genes (Brzezinka *et al.*, 2019; Singh *et al.*, 2021).

3.2 Drought Stress- Drought triggers well-characterised DNA methylation changes. The methyltransferase DRM2, acting via the RdDM pathway, lays down stress-specific methylation patterns influenced by stress type, genotype, and tissue (Abdulraheem *et al.*, 2024). In drought-tolerant tomato and rice varieties, methylation changes at stress-gene promoters persist after rewatering, enabling faster stomatal closure upon a second drought event (Kumar *et al.*, 2024). Analogous marks written in dahlia tubers during summer

drought may recapitulate protective responses in the following season.

3.3 Cold and Vernalization- Cold is the most extensively characterised epigenetic signal in plants, primarily through the vernalization pathway: extended winter cold epigenetically silences the floral repressor FLC via H3K27me3 deposition by Polycomb Repressive Complex 2 (PRC2), guided by cold-induced lncRNAs (Heo & Sung, 2011; Gao & He, 2024). The result is a durable epigenetic memory of winter that persists into spring. Although dahlias are not strict vernalization responders, early autumn cold signals tuber dormancy and the cold period experienced during winter storage has documented effects on sprouting vigour the following spring, consistent with cold-induced histone modification of tuber chromatin.

4. The Epigenetic Seasonal Cycle

The dahlia's annual cycle can be reframed as an epigenetic information cycle, in which the growing season writes molecular memories into tuber chromatin and the dormant season preserves them for the next plant.

Figure 1. Epigenetic Seasonal Cycle in *Dahlia variabilis*

SUMMER Growing Season	AUTUMN Dormancy Onset	WINTER Tuber Storage	SPRING Primed Regrowth
Heat/drought/UV Epigenetic marks written	ABA rises; methylation patterns locked in tuber	Histone codes & ncRNAs preserve stress memory	Marks guide faster, stronger stress response

ABA = abscisic acid. Epigenetic marks written during the growing season are preserved through winter dormancy and inform gene expression in the following spring.

This cycle has important practical consequences. A tuber produced by a plant that endured severe heat carries a different



epigenome than one from a cooler season. The first tuber's offspring are molecularly primed, better prepared to mount a rapid heat-stress response and potentially to flower more successfully under the same conditions that challenged their parent.

This is not genetic adaptation: the DNA sequence is unchanged. It is somatic memory transmitted through the vegetative propagation cycle (Lämke & Bäurle, 2017). Because dahlias propagate primarily through tuber division and cuttings, this somatic memory can propagate stably across many seasons, conferring a genuine adaptive advantage.

"Unlike genetic mutation, epigenetic stress memory is potentially reversible and cyclical — the plant can reset its memory as conditions change, yet retain the capacity to re-learn." — Gallusci et al., 2023

5. Implications for Growers and Breeders

These insights carry direct practical significance:

- Storage temperature matters epigenetically. Cooling tubers slowly and storing at consistently cool (non-freezing) temperatures preserves beneficial epigenetic marks while avoiding methylation disruption from freeze-thaw cycling (Dogramaci *et al.*, 2024).
- Stress priming before storage may be beneficial. Brief, sub-lethal heat or mild drought exposure before lifting tubers could intentionally prime the epigenome, enhancing the following season's stress tolerance, a concept demonstrated in crops and being explored in ornamentals (Hilker & Schmülling, 2019).
- Epigenomic selection is a future breeding frontier. As whole-epigenome sequencing becomes affordable, breeders may select cultivars for favourable methylome

profiles, conferred resilience to the climate stresses projected for their growing region (Dobránszki, 2025).

CONCLUSION

The dahlia tuber is far more than a carbohydrate storage organ. Emerging evidence positions it as a repository of epigenetic memories — molecular records of the climate stresses the parent plant endured, preserved through winter dormancy and deployed to prepare the next season's growth. DNA methylation, histone modifications, and non-coding RNA pathways constitute a biochemical writing system capable of encoding, maintaining, and erasing these memories in response to changing environments.

As climate change reshapes the stress landscapes dahlias face, understanding and eventually harnessing this epigenetic memory system offers one of the most promising avenues for developing ornamental cultivars that are not only beautiful, but resilient.

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