

Epigenetic Resilience: The Role of DNA Methylation in Crop Climate Adaptation

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Plants cannot run away when temperatures spike, soils turn salty, or droughts strike (Akhter et al., 2021). Instead, they adjust how their genes are read using epigenetics—heritable, reversible switches in gene activity that alter expression without modifying the underlying DNA sequence (Akhter et al., 2021; Liu and He, 2020). Central to this hidden molecular toolbox is DNA methylation, a chemical marking system that fine-tunes how crops survive environmental extremes (Liu and He, 2020).

The Molecular Switchboard

DNA methylation predominantly occurs by the addition of a methyl group to cytosine bases, forming 5-methylcytosine (5mC), or to adenine bases, forming N6-methyladenine (6mA) (Liu and He, 2020). In plants, cytosine methylation takes place in three distinct sequence contexts: symmetric (CG and CHG) and asymmetric (CHH, where H represents A, T, or C) (Akhter et al., 2021; Liu and He, 2020).

Plants dynamically orchestrate these marks through a three-part molecular cycle:

- **Establishment:** De novo methylation is triggered via the **RNA-directed DNA methylation (RdDM)** pathway, guided by small interfering RNAs (siRNAs) and catalyzed by DOMAINS REARRANGED METHYLTRANSFERASE 2 (DRM2) (Akhter et al., 2021; Liu and He, 2020).
- **Maintenance:** Established marks are maintained across cell divisions by METHYLTRANSFERASE 1 (MET1) at CG dinucleotides, CHROMOMETHYLASE 3 (CMT3) in self-reinforcing loops with H3K9 methylation at CHG sites, and DRM2 together with CMT2 at CHH positions (Liu and He, 2020).
- **Erasing:** Marks are removed passively through dilution during DNA replication, or actively removed via bifunctional DNA glycosylases (such as ROS1, DME, DML2, and DML3) through the base excision repair (BER) pathway (Liu and He, 2020).

Frontline Defense Against Abiotic Stress

When plants face hostile abiotic pressures, methylation patterns shift to activate or suppress crucial stress-responsive genes:

- **Heat Stress:** Repression of *OsCMT3* in rice upregulates *OsFIE1*, while 6mA levels modulate molecular chaperones like *OsHSCA1* and *OsHSP70* to establish basal and acquired thermotolerance (Liu and He, 2020).
- **Cold Stress:** Freezing signals induce DNA demethylation at the promoters of cold regulators such as *ICE1* and *CBF2* in crops like rice and rubber tree (*Hevea brasiliensis*), stimulating cold-responsive (*COR*) genes (Liu and He, 2020).
- **Salt Stress:** Salinity promotes promoter hypomethylation of transcription factors like *GmMYB84* in soybean (activating the potassium transporter *GmAKT1*) and *OsMYB91* in rice, restoring ion and metabolic homeostasis (Liu and He, 2020).

- **Drought:** Repeated water deficits prompt widespread methylation remodeling across maize (*Zea mays*), rice (*Oryza sativa*), and black cottonwood (*Populus trichocarpa*), priming plants for enhanced water retention (Akhter et al., 2021).

Stress Memory: How Plants Remember

Plants retain memories of past stress encounters to prime themselves for future hazards (Akhter et al., 2021; Liu and He, 2020).

- **Somatic Memory:** Mitotically stable chromatin and methylation changes linger in tissues for days or throughout the plant's lifetime, accelerating defense induction upon re-exposure (Liu and He, 2020).
- **Transgenerational Memory:** Because plant DNA methylation marks avoid total erasure during reproduction, stress signatures can be passed on to immediate offspring (intergenerational) or persist across two or more stress-free generations (transgenerational) (Liu and He, 2020).

Case Spotlight: Heat Stress and Barley Germination

A targeted investigation by Sakai et al. (2022) revealed how heat stress experienced during the grain-filling stage reshapes seed germination in barley (*Hordeum vulgare* L.) via targeted methylation switches. Seeds exposed to high temperatures (25 °C vs. 15 °C control) achieved 100% germination within 24 hours of imbibition, compared to only 62% at 60 hours in control grains (Sakai et al., 2022).

Using MeDIP-qPCR, Sakai et al. (2022) demonstrated that heat induced precise epigenetic modifications across key phytohormone and metabolic genes:

- **Hypermethylation** occurred at the promoters of ABA biosynthesis genes (*HvNCED1* and *HvNCED2*), repressing germination-inhibiting ABA (Sakai et al., 2022).
- **Hypomethylation** was detected at the promoters of ABA catabolism genes (*HvABA8'OH1* and *HvABA8'OH3*), boosting transcript levels and accelerating ABA degradation (Sakai et al., 2022).
- **Hypomethylation** at the GA biosynthesis gene promoter (*HvGA3ox2*) and the NADPH oxidase promoter (*HvRbohF2*) stimulated gibberellin (GA₁) accumulation and reactive oxygen species (ROS) signaling, directly driving rapid germination (Sakai et al., 2022).

Conclusions and Future Horizons

DNA methylation serves as a vital epigenetic regulator of plant gene expression, helping stabilize the genome during periods of environmental hardship while maintaining the plastic capacity to adapt to recurring stresses (Akhter et al., 2021). Extensive research across diverse crop species demonstrates that stress-induced DNA methylation and demethylation—whether operating genome-wide or at locus-specific promoters—directly steer the transcription of survival genes (Akhter et al., 2021; Liu and He, 2020; Sakai et al., 2022). Looking ahead, clarifying these mechanistic pathways will prove pivotal for developing climate-resilient crops capable of withstanding global warming, prolonged drought, and soil degradation (Akhter et al., 2021; Liu and He, 2020). Future strategies will increasingly focus on pairing traditional breeding and transcription factor engineering with targeted epigenetic modulation—fine-tuning promoter specificity, enhancer activity, and RNA polymerase processivity to sustainably safeguard global food security (Akhter et al., 2021; Liu and He, 2020).

References

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