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DEVELOPMENT

Epigenome dynamics from seed to seedling

“
extensive
remodelling of
the seed DNA
methylome”

Epigenetic silencing of transposable elements (TEs) is vital for the maintenance of genome integrity, but the extent to which this silencing is reprogrammed in plants and the underlying mechanisms have remained elusive. Three studies in *Genome Biology* now reveal the dynamic changes that the *Arabidopsis thaliana* epigenome undergoes during seed development (embryogenesis) and the seed-to-seedling transition (germination).

In plants, DNA methylation is known to occur at cytosine residues in three sequence contexts: CG, CHG and CHH (where H represents A, C or T). CG methylation at gene bodies marks constitutively expressed loci, whereas non-CG methylation is predominantly restricted to genomic regions under active silencing — for example, by RNA-directed DNA methylation (RdDM) — such as TEs and other repetitive DNA.

Kawakatsu *et al.*, Bouyer *et al.* and Narsai *et al.* carried out whole-genome bisulfite sequencing and then compared *A. thaliana* methylomes at different stages of development, from early to late embryonic stages of dry seeds to germinating seeds and including post-germinative seedlings.

Kawakatsu *et al.* observed that global CG and CHG methylation were mainly stable throughout seed development, whereas CHH

methylation levels increased markedly from early to late embryonic stages, before being progressively lost during germination. These results mirror those of Bouyer *et al.*, who found that genome-wide DNA methylation was highest in mature embryos compared with early embryos and seedlings, mainly owing to the very high level of methylation at CHH sites in mature embryos. In agreement with these findings, extensive DNA demethylation during the transition from seed to seedling was reported by Narsai *et al.*, who observed that hypomethylation occurred concomitantly with broad changes in the populations of mRNAs and small interfering RNAs (siRNAs) during germination.

Both Kawakatsu *et al.* and Bouyer *et al.* found that CHH methylation changes occurred within TEs and that the DNA methyltransferase CHROMOMETHYLASE 2 (CMT2), as well as RdDM, which is mediated by DOMAINS REARRANGED METHYLTRANSFERASE 2 (DRM2), are required for DNA methylation during seed development. CMT2-mediated pathways seemed to be active at early developmental stages, whereas RdDM appeared to target TEs in the mature embryo.

Bouyer *et al.* analysed methylome data for the embryo-nurturing

tissue endosperm and observed that sequences that are hypermethylated at CHH in mature embryos are actually hypomethylated earlier during seed development in the endosperm. Moreover, the abundance of seed-derived siRNAs was highest for the same genomic regions, leading the authors to propose that “endosperm-derived siRNAs progressively instruct CHH methylation in the embryo”. Disruption of the seed-to-seedling transition led to the persistence of high levels of CHH methylation after germination, specifically in sequences that were targeted by RdDM, reflecting the inability to terminate an embryonic transcriptional programme.

By comparing methylation levels within TEs of germinating wild-type seeds and seedlings with mutants lacking three DNA demethylases, Kawakatsu *et al.* could further show that global demethylation during germination does not depend on DNA demethylases but instead occurs passively by methylation dilution promoted by cell division. This conclusion was also arrived at by Narsai and colleagues.

The studies reveal novel insights into the extensive remodelling of the seed DNA methylome as it transitions from a dormant state to a metabolically active, growing seedling. The mechanistic understanding gained may eventually contribute to the promotion of efforts for the optimization of plant traits.

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ORIGINAL ARTICLES Kawakatsu, T. *et al.*

Dynamic DNA methylation reconfiguration during seed development and germination. *Genome Biol.* <http://dx.doi.org/10.1186/s13059-017-1251-x> (2017) | Bouyer, D. *et al.* DNA methylation dynamics during early plant life. *Genome Biol.* <http://dx.doi.org/10.1186/s13059-017-1313-0> (2017) | Narsai, R. *et al.* Extensive transcriptomic and epigenomic remodeling occurs during *Arabidopsis thaliana* germination. *Genome Biol.* <http://dx.doi.org/10.1186/s13059-017-1302-3> (2017)

FURTHER READING Kawashima, T. & Berger, F. Epigenetic reprogramming in plant sexual reproduction. *Nat. Rev. Genet.* **15**, 613–624 (2014)