

Dynamics and function of DNA methylation in plants

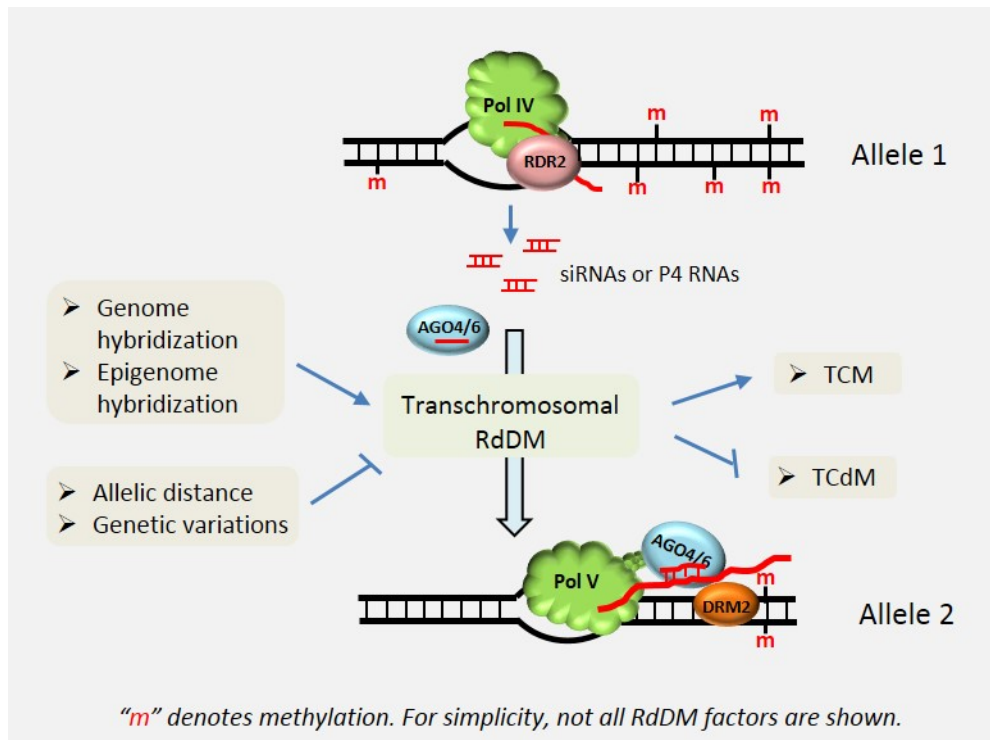
Huiming Zhang, Zhaobo Lang and Jian-Kang Zhu

<https://doi.org/10.1038/s41580-018-0016-z>

Supplementary Box 1. DNA methylation in gene behavior

DNA methylation can promote non-Mendelian allele segregation in progenies. A good example of this is paramutation, which occurs when an epigenetically silenced allele triggers silencing *in trans* of the other allele in the nucleus, thereby making the newly silenced allele — the paramutated allele — an independent and stable source for new paramutation¹. Paramutation is best characterized in maize and is generally attributed to the activity of small RNAs, largely resembling RNA-directed DNA methylation (RdDM) in *Arabidopsis thaliana*².

In genetic hybrids and epigenetic hybrids, siRNAs or RNA polymerase IV (Pol IV)-transcribed RNAs (P4 RNAs) from one allele may act *in trans* to guide DNA methylation on the other allele (see the figure). Transchromosomal DNA methylation (TCM) and transchromosomal DNA demethylation (TCdM) can occur at thousands of genomic regions³ and result in non-additive increases or decreases in DNA methylation in the F1 progeny compared to the parents³⁻⁶. Mutations in Pol IV or Pol V abolish methylome interactions in *A. thaliana* hybrids^{3, 7}, suggesting that methylome interactions are mediated by RdDM. Genetic variations between the parents at TCdM loci appear to be greater than those at loci without DNA methylation interactions³, indicating that TCdM may result from reduced efficiency of pairing between siRNAs or P4 RNAs from one allele and scaffold RNAs on the other allele⁸. The physical distance between two parental alleles in the F1 may also affect the efficacy of transallelic DNA methylation, and thus may contribute to methylome interactions⁸. Methylome interactions can also occur in epihybrids, which are produced by crossing two isogenic individuals with different DNA methylomes⁹. Grafting may also trigger methylome interactions between the scion and the root, because siRNAs are mobile across the graft union and can trigger epigenetic modifications^{10, 11}.



References:

1. Chandler, V.L. Paramutation: From maize to mice. *Cell* **128**, 641-645 (2007).
2. Giacomelli, B.J. & Hollick, J.B. Trans-Homolog interactions facilitating paramutation in maize. *Plant Physiol* **168**, 1226-36 (2015).
3. Zhang, Q. et al. Methylation interactions in Arabidopsis hybrids require RNA-directed DNA methylation and are influenced by genetic variation. *Proc Natl Acad Sci U S A* **113**, E4248-56 (2016).
4. Chodavarapu, R.K. et al. Transcriptome and methylome interactions in rice hybrids. *Proc Natl Acad Sci U S A* **109**, 12040-5 (2012).
5. Shen, H.S. et al. Genome-wide analysis of DNA methylation and gene expression changes in two Arabidopsis ecotypes and their reciprocal hybrids. *Plant Cell* **24**, 875-892 (2012).
6. Greaves, I.K. et al. Trans chromosomal methylation in Arabidopsis hybrids. *Proc Natl Acad Sci U S A* **109**, 3570-3575 (2012).
7. Greaves, I.K. et al. Twenty-four-nucleotide siRNAs produce heritable trans-chromosomal methylation in F1 Arabidopsis hybrids. *Proc Natl Acad Sci U S A* **113**, E6895-E6902 (2016).

8. Zhang, H.M. & Zhu, J.K. New discoveries generate new questions about RNA-directed DNA methylation in Arabidopsis. *National Science Review* **4**, 10-15 (2017).
9. Rigal, M. et al. Epigenome confrontation triggers immediate reprogramming of DNA methylation and transposon silencing in *Arabidopsis thaliana* F1 epihybrids. *Proc Natl Acad Sci U S A* **113**, E2083-E2092 (2016).
10. Molnar, A. et al. Small silencing RNAs in plants are mobile and direct epigenetic modification in recipient cells. *Science* **328**, 872-875 (2010).
11. Lewsey, M.G. et al. Mobile small RNAs regulate genome-wide DNA methylation. *Proc Natl Acad Sci U S A* **113**, E801-E810 (2016).