Dynamics and function of DNA methylation in plants

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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 paramutation. 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.

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 regions and result in non-additive increases or decreases in DNA methylation in the F1 progeny compared to the parents. Mutations in Pol IV or Pol V abolish methylome interactions in A. thaliana hybrids, 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 interactions, indicating that TCdM may result from reduced efficiency of pairing between siRNAs or P4 RNAs from one allele and scaffold RNAs on the other allele. 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 interactions. Methylome interactions can also occur in epihybrids, which are produced by crossing two isogenic individuals with different DNA methylomes. 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.
References:


