

## LOSS OF DNA METHYLATION AFFECTS THE RECOMBINATION LANDSCAPE IN *ARABIDOPSIS*

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Regulation of meiotic recombination depends on both DNA sequence and chromatin properties. Indeed, it is known that cross-overs (COs) are not evenly distributed along chromosomes and are suppressed in chromosomal regions encompassing compact, hypermethylated centromeric and pericentromeric DNA. Among the epigenetic marks playing an essential role in stabilizing heterochromatin, DNA methylation is the best-characterized one. The objective of this work was to determine whether specific variations in DNA methylation would affect recombination and whether these effects would differ in euchromatic vs. heterochromatic chromosomal regions. To address this question we used hypomethylated mutant of *Arabidopsis thaliana* (*met1*) and analyzed its meiotic recombination in comparison to a wild-type plant. We observed unexpected and counterintuitive effects of DNA methylation losses on CO distribution. Moreover, our data revealed that recombination was further promoted in the hypomethylated chromosome arms while it was inhibited in heterochromatic regions encompassing pericentromeric DNA. Notably, the total number of COs was not affected, implying that loss of DNA methylation led to a global redistribution of COs along chromosomes. To determine whether altered levels of DNA methylation influence recombination directly in *cis* or indirectly in *trans* by changing expression of genes encoding recombination components, we analyzed CO distribution in mapping populations derived from two different epigenetic recombinant inbred lines (epiRILs) characterized by randomly distributed and well-mapped hypomethylated chromosomal segments. The results of these experiments, supported by expression profiling data, suggest that DNA methylation affects meiotic recombination in *cis*. Because DNA methylation exhibits significant variation even within a single species, our results imply that it may influence the evolution of plant genomes through the control of meiotic recombination.