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# Understanding how the genome shapes the epigenome in plants

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## Abstract

Due to their ability to increase their copy number in a genome, Transposable Elements (TEs) constitute more than half of the nuclear DNA content in most flowering plants. To minimize their mutagenic potential, plants have evolved multiple, interacting epigenetic controls to limit TE proliferation. Among these, DNA methylation plays a critical role in preventing TE mobility. While this epigenetic process is well controlled, chromatin boundaries around TEs are not always exact, thus sometimes leading to "spreading" of DNA methylation in flanking regions, possibly modifying gene regulation. Hence, beyond shaping genome structure, there is growing evidence that both TE sequence and chromatin state contribute to gene regulation. In this framework, our work focuses on understanding the interaction between genomes and epigenomes in plants with large genomes and high TE content, such as maize. Previous studies in such species have mainly been limited to the analysis of a single reference genotype, correlating TE annotation and chromatin profiles. We use DNA resequencing and bisulfite-seq data to characterize TE presence/absence and Differentially Methylated Regions (DMRs). This coanalysis of comparative genomics and comparative epigenomics between maize genotypes allows us to test for the stability of TE/methylation associations. We also investigate the impact of these variants on gene expression and the impact of abiotic constraints on their stability.

**Keywords:** Transposable element, DNA methylation, structural variation, plant

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