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“AtMBD9 Modulates Plant Arabidopsis Development through the Dual Epigenetic Pathways of DNA Methylation and Histone Acetylation”

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ABSTRACT:

Mutations within the Arabidopsis METHYL-CPG BINDING DOMAIN 9 gene (AtMBD9) cause pleiotropic phenotypes including early flowering and multiple lateral branches. Early flowering was previously attributed to the repression of Flowering Loci C (FLC) due to a reduction in histone acetylation. However, the reasons for other phenotypic variations remained obscure. Recent studies suggest an important functional correlation between DNA methylation and histone modifications. By investigating this relationship, we have found that the global genomic DNA of *atmbd-9* was over-methylated, including the FLC gene region. Recombinant AtMBD9 does not have an *in vitro* detectable DNA demethylation activity, but rather has histone acetylation activity. Ectopic overexpression of AtMBD9 and transient DNA demethylation promotes flowering and causes partial recovery of the normal branching phenotype. Co-immunoprecipitation assays suggest that AtMBD9 interacts *in vivo* with some regions of the FLC gene and binds to histone 4 (H4). Gene expression profile analysis revealed the earlier up-regulation of some flower-specific transcriptional factors and the alteration of potential hormonal and signal transducer axillary branching regulatory genes. In accordance with this result, AtMBD9 itself was found to be localized in the nucleus and expressed in the flower and axillary buds. Together, these results suggest that AtMBD9 controls flowering time and axillary branching by modulating gene expression through DNA methylation and histone acetylation. This reveals another component of the epigenetic mechanism controlling gene expression.