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ANALYSIS OF THE METHYLATION DYNAMICS AT THE MAIZE FLOWERING TIME LOCUS *Vgt1* IN MAIZE

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The nature of genetic variability for flowering time in maize is mainly quantitative, with only a few mutants described and causing a discrete phenotypic effect. The *Vegetative to generative transition 1 (Vgt1)* locus was positionally cloned on chrom. bin 8.05 after its localization as a major QTL (Salvi et al., 2007, PNAS, 104: 11376-11381). *Vgt1* corresponded to an upstream (70 kb) non-coding regulatory element of *ZmRap2.7*, an Ap2-class transcription factor which was shown to influence flowering time. A transposon (MITE) insertion was identified as a major allelic difference within *Vgt1*. One of the hypotheses is that *Vgt1* might function by modifying *ZmRap2.7* chromatin through an epigenetic mechanism. Therefore, we decided to investigate the methylation state at multiple regions of ca. 250 bp each, within *Vgt1* and the promoter of *ZmRap2.7*. Following digestion with McrBc, an endonuclease that acts upon methylated DNA, real time PCR analyses were performed on genomic DNA from near-isogenic maize lines. Target tissues were leaves and shoot apices at 1st-, 3rd-, 5th- and 7th-leaf stages of development. Preliminary results showed a trend of reduction of methylation from the 1st- through the 7th-leaf stage, with the exception of a short genomic region flanking the MITE insertion, which showed a constant and very dense methylation throughout leaf development and for both alleles.