

THE EFFECTS OF HISTONE ACETYLATION ON THE MAIZE ALLELE *PL1-BLOTCHED*

ABSTRACT

Covalent modifications of DNA and nucleosomal histone proteins associated with eukaryotic chromatin have the potential to alter expression of a gene without change in its DNA sequence. One gene regulated through this so-called epigenetic process is the *Pll-Blotched* gene of maize. *Pll-Blotched* is an allele of the *purple1 (p11)* gene, which encodes a transcription factor that activates synthesis of purple anthocyanin pigments. *Pll-Blotched* is unusual in that it leads to variegated, rather than uniform, pigmentation. At the molecular level, this phenotype is associated with low expression of *p11* mRNA, a novel pattern of DNA methylation and condensed chromatin structure. To ask if acetylation of nucleosomal histone proteins might be involved in regulating the chromatin organization of *Pll-Blotched*, this allele was crossed into 40 lines containing transgenes that target reduction of various histone acetyltransferase and histone deacetylase genes. Some of the lines led to altered *Pll-Blotched* pigmentation. Detailed analysis of molecular changes underlying the altered pigmentation resulted in models that implicate both histone acetyltransferase and histone deacetylase genes in controlling expression of *Pll-Blotched*. These findings lay the foundation for future studies aimed at further understanding the interplay between histone modification and regulation of gene expression.