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## **Effect of reduced chromatin gene expression on the epigenetically regulated maize gene, PI-Blotched**

Eukaryotes can regulate gene expression using epigenetic mechanisms that involve changes in chromatin packing. Open, loosely packed chromatin is accessible and actively transcribed, whereas closed, tightly packed chromatin is less accessible and associated with gene silencing. Many studies have furnished information about how covalent modifications of the DNA and histone components of chromatin can alter its structure. However, much remains to be learned about regulation of those changes. To address this problem, we are analyzing the expression of an epigenetically-regulated gene, PI-Blotched, that controls the synthesis of purple anthocyanin pigments in maize. The maize anthocyanin pathway offers an excellent system for studying gene control mechanisms, because the genetics is well understood and pigment levels are an accurate reporter for activity of the underlying genes. PI-Blotched has a variegated phenotype that is associated with a unique pattern of DNA methylation and more closed chromatin structure than usual. To understand how these epigenetic features are controlled, we have introduced PI-Blotched into lines with reduced expression of genes involved in DNA methylation, histone acetylation and chromatin remodeling. By measuring and comparing pigment levels in plants with and without the chromatin-gene mutations, we can gain insights about which chromatin genes might be involved in controlling the epigenetic state of PI-Blotched. Our results thus far implicate multiple classes of chromatin genes--including several involved in histone acetylation--as regulators of PI-Blotched expression.