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## Chromatin-level regulation in maize

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Epigenetic regulation of gene expression is determined by chromatin packing. Transcriptionally active genes are associated with open, less compacted chromatin, whereas transcriptionally less active or silent genes are found in tightly packed, inaccessible chromatin. At the DNA level, genes that are silenced by chromatin frequently have high levels of cytosine methylation. Our goal is to understand the mechanisms behind chromatin-level regulation in maize. We are taking a functional genomics approach by making transgenic lines that use RNA interferences (RNAi) to knock down expression of a large number of chromatin genes and assay the phenotypes in the resulting RNAi lines. Among the genes we are studying are chr101 and chr106, which are duplicates with sequence similarity to a gene in Arabidopsis that is involved in chromatin remodeling and DNA methylation. As a step in understanding how chr101 and chr106 function, we have crossed the RNAi lines to a line containing the Pl-Blotched gene. This gene is an allele of the Purple gene, which controls the synthesis of purple anthocyanin pigments in the corn plant. Pl-Blotched leads to a variegated pattern of pigmentation, rather than the normal uniformly purple phenotype. At the molecular level, this variegation is associated with closed chromatin and high levels of DNA methylation. If the chromatin state of Pl-Blotched is regulated by chr101 and / or chr106, then knocking out expression of these genes by RNAi should lead to higher levels of expression of Pl-Blotched. To test this idea, we are comparing anthocyanin levels in Pl-Blotched plants carrying the chr101 and chr106 RNAi transgenes to the pigment levels in non-transgenic siblings.