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Fine-structure QTL mapping of suppressor of plant blotching1 in maize

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Suppressor of Plant Blotching 1, or Spb1, is a proposed epigenetic modifier of PI-Blotched, an epi-allele that activates the synthesis of purple anthocyanin pigments in maize. Normally, PI-Blotched causes a distinct variegated pattern of pigmentation, but in the presence of Spb1, much more pigment is produced. Previous studies showed that the increased pigmentation of Spb1 plants correlated with increased expression of PI-Blotched mRNA, altered DNA methylation of the PI-Blotched gene, and changes in histone modification of PI-Blotched chromatin. To further understand how Spb1 modifies PI-Blotched, we set out to map the genetic location of Spb1. Because preliminary mapping experiments indicated that Spb1 is due to more than one gene, we have taken a quantitative trait loci (QTL) mapping approach. QTL mapping is a process by which loci underlying a quantitative trait (such as Spb1's effect on PI-Blotched pigmentation) can be identified. Capitalizing on the diversity of the maize genome, we selected 155 SSR markers that showed polymorphisms in our 232-individual F2 mapping population and used them for genotyping. We measured phenotypes by extracting and measuring anthocyanin pigments using a spectrophotometric assay. We used QTL cartographer software to determine statistically significant relationships between the phenotypic and genotypic data. We identified five QTL that affect PI-Blotched expression levels. The resolution of our current analysis is approximately 1-3 cM—an area that could contain thousands of genes. Therefore we have begun fine-structure QTL mapping employing a more markers in our QTL regions to analyze a 1,500-individual F2 population to achieve greater resolution for pin-pointing the position of the Spb1 loci. Our eventual goal is to clone the Spb1 genes using a map-based cloning strategy. Then we will be able to study in detail how Spb1 regulates the epigenetic state of PI-Blotched.