Ed Grow, Biology and Music

Year in School: Senior
Hometown: Rolla, MO
Faculty Mentor: Dr. Karen Cone, Biological Sciences
Funding Source: MU Monsanto Undergraduate Research Fellowship

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

Edward Grow & Karen Cone

Suppressor of Plant Blotching 1, or *Spb1*, is a proposed epigenetic modifier of *Pl-Blotched*, an epi-allele that activates the synthesis of purple anthocyanin pigments in maize. Normally, *Pl-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 *Pl-Blotched* mRNA , altered DNA methylation of the *Pl-Blotched* gene, and changes in histone modification of *Pl-Blotched* chromatin. To further understand how *Spb1* modifies *Pl-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 *Pl-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 *Pl-Blotched* expression levels. Preliminary results conducted on a replicate F2 pop indicate the same major chromosome 7 QTL previously identified. 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 *Pl-Blotched*.

This project was completed to fulfill a Capstone requirement.