M-162

Utilizing multiple approaches to increase transposition of *mPing* in soybean

Lauren Lail,* Center for Applied Genetic Technologies, University of Georgia, Georgia, USA

Ed McAssey, Center for Applied Genetic Technologies, University of Georgia, Georgia, USA

Wayne Parrott, Institute for Plant Breeding, Genetics, and Genomics, University of Georgia, Georgia, USA

Domesticated soybean, *Glycine max*, has over 30,000 genes, many with unknown function. One tool used for gene discovery is the use of transposable elements. *mPing*, a non-autonomous transposable element derived from rice, has been shown to insert near genes at a high frequency. However, the level of germinal transposition for *mPing* averages at just 1 insertion per generation. To further enhance transposition frequency, *mPing* vectors are being redesigned to contain non-pest, meristem promoters as well as using tissue culture to induce transposition. We are using soybean, pea, and Arabidopsis promoters and terminators with germinal expression patterns to drive the gene expression of *Transposase* and *ORF1*, genes necessary for transposition. These types of promoters and terminators have been used to construct a traditional insertional vector as well as a gene silencing vector that uses trans-acting small interfering RNA sequences. Both of these constructs have been biolistically transformed into soybean, are in selection, and await PCR verification. Additional clean vectors are also currently underway. For the second method, lines previously transformed with *mPing*, *Transposase*, and *ORF1* have been introduced back into tissue culture to induce increased transposition, as has been seen in the literature. PCR testing of previously mapped insertions allows for initial insight into the success of tissue culture-induced transposition within these progeny. To test the level of transposition, transposon displays will be used to detect increases in *mPing* copy number. Lines with increased copy number will be further characterized by sequencing to show the locations of new insertions that will then be shared publicly.