LIRIODENDRON EST-SSR MARKER DEVELOPMENT AND GENETIC CONSTITUTION OF A LIRIODENDRON BREEDING ORCHARD

Xinfu Zhang[1], Alanna Carlson, Margaret Staton, Scott E. Schlarbaum, Jeanne Romero-Severson, John E. Carlson, Haiying Liang

[1]Department of Genetics and Biochemistry, Clemson University, Clemson SC

Liriodendron tulipifera L., commonly known as yellow-poplar, is a member of the Magnoliaceae family. It is a fast-growing hardwood tree species with great ecological and economic value. Liriodendron occupies an important phylogenetic position as a basal angiosperm and has been used in studies of the the evolution of flowering plants. Genomic resources, such as EST databases and BAC libraries, have been developed for this species. In this project, we mined available EST databases for putative polymorphic sequence repeat (SSR) markers with the goal of developing 190 informative EST SSRs. These markers will be used to construct the first framework genetic linkage map of *L. tulipifera* with 380 full-sib seedlings. Such a linkage map is essential for future molecular breeding and quantitative trait locus (QTL) mapping, and as a framework for sequencing the Liriodendron genome in the future. Forty high-quality, single-locus markers have been selected to evaluate the genetic constitution of a *L. tulipifera* breeding orchard in Knoxville, TN. The orchard, established in 1966 as part of a tree breeding program in the University of Tennessee, contains approximately 100 grafted clones, representing 34 genotypes. These 34 genotypes will provide a first look at the genetic diversity and allele richness among selections of this unique native species.