**Strategies for Identification of QTLs Controlling Early Height Growth in Longleaf Pine**

L. Wu[1], M. Stine[2], C. D. Nelson[3]

[1]Graduate Assistant, [2]Associate Professor, School of Renewable Natural Resources, Agricultural Center, Louisiana State University, Baton Rouge, LA, USA [3]Research Geneticist & Project Leader, Southern Institute of Forest Genetics, USDA Forest Service, Southern Research Station, Saucier, MS, USA

Simple Sequence Repeat (SSR) markers are being used to map the genome and quantitative trait loci controlling the early height growth (EHG) in a backcross family (longleaf pine x slash pine) x longleaf pine. A total of 208 locus specific SSR markers have been screened against 6 longleaf pine recurrent parents and a sample of 7 slash pine parents. The SSR markers include 80 *PtTX* loci which were developed in Claire William's lab at Texas A&M, 56 *sifg* loci were developed by Craig Echt and Dana Nelson (Southern Institute of Forest Genetics) in collaboration with Daniel Peterson and Surya Saha (Mississippi State University), 6 *RPtest* loci were developed by C. Echt and 66 ***ript*** loci were developed by C. Echt and D. Nelson. Among the 13 parents, 132 markers (63.5%) show polymorphisms including 51 *PtTX* loci (63.8%), 26 *sifg* loci (46.4%), 5 *RPtest* loci (83%) and 50 *ript* loci (75.8%).

Based on the genetic variance in early height data, available sample size, and the number of SSR marker polymorphisms, 6 half-sib families with a common paternal parent (Derr488) were selected from 27 backcross families as the final mapping population. For these 6 half-sib mapping families, there are 97, 95, 89, 89, 99, 102 informative markers, respectively. Within each of the 6 families, the tallest and shortest 8 percent of seedlings (200 seedlings total) were selected for QTL detection (phase I). Then random selections of 8 percent of the seedlings from the rest of the population (100 seedlings) and 10 seedlings from both tails (120 seedlings total) of the within family distributions will be used for unbiased QTL verification and mapping (phase II). For data analysis, the residual which includes within-family genetic effect and specific-site environmental effect will be used as the phenotypic trait value. Progress on the project and results obtained will be presented and discussed.