

Gene Expression in an Association Population of Loblolly Pine

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As part of the Plant Genome project “Association Genetics of Natural Genetic Variation and Complex Traits in Pine” we are analyzing expression of approximately 200 genes involved in xylem development and disease responses in loblolly pine. An association population containing rooted cuttings of genotypes from across the natural range was developed at North Carolina State University. At Texas A&M University, real-time qPCR is being used to assay expression levels in 2 ramets of 426 genotypes. We plan to relate expression levels to the geographic origin of the parents, to look for genes that are coordinately expressed, and to associate variation in expression to the genotype and metabolite data being produced at UC-Davis and to phenotype data being produced at U. Florida and North Carolina State. Expression data for the first 23 genes involved in lignin biosynthesis has been gathered and will be presented. Other xylem-related genes to be analyzed include those involved in cellulose and cell wall biosynthesis, cell wall proteins, and genes involved in signal transduction.