IDENTIFYING GENETIC VARIATION IN SITE ADAPTABILITY IN LOBLOLLY PINE

Laura Townsend[1] and Ross Whetten

[1]Tree Improvement Program, NC State University Dept. of Forestry and Natural Resources, Raleigh, NC

Pine plantations are an important economic commodity, and loblolly pine is the leading southern pine species produced in the U.S. The projected increase in severe weather events due to climate change has potential to harm plantation stands and impact the forest industry. Loblolly pine has a very diverse gene pool and is adapted to various environments, and is thus a good candidate to breed for adaption to climate change. An ideal way to accomplish this is to identify associations of individual genetic marker loci with growth or quality characteristics using climate factors as covariates. To accomplish this, a cost effective, easily implemented, and high-throughput genotyping method is needed. To identify the appropriate genetic markers, a set of phloem tissue samples will be collected in 2 different sites from the plantation selection seed source study (PSSSS). The PSSSS consists of 140 pollen mix families planted in 20 test locations representing the entirety of the loblolly pine range. Phenotypic data from measurements at ages 4 and 8 years are available to be used in genetic marker analysis. The DNA from the phloem samples will be extracted using cost effective buffers adapted from the Canadian Center for DNA Coding protocol. Genotyping-by-sequencing (GBS) will be employed using methylation-sensitive enzymes to enrich gene regions. A preliminary experiment was conducted to test the recovery of marker fragment sequences from DNA of a single loblolly pine parent tree and a set of 90 haploid megagametophytes from seeds of that parent. About 15% of single-end sequence tags show the expected 1:1 ratio of presence and absence in the haploid DNA samples and map to a single contig in the v 0.6 draft assembly of the pine genome sequence. These promising results will be extended with further processing of samples and improved software analysis.