INTROGRESSION OF LOBLOLLY PINE ALLELES INTO SLASH PINE; QTL ANALYSIS FOR CROWN, GROWTH, AND GROWTH EFFICIENCY IN A PSEUDO-BACKCROSS ((SLASH X LOBLOLLY) X SLASH) FAMILY

Gary F. Peter,[1] Patricio R. Munoz, Dudley A. Huber, and Tim A. Martin

[1]School of Forest Resources & Conservation, University of Florida, Gainesville, FL

Although slash and loblolly pine are closely related species, they have distinct differences in site preference, crown architecture and stem growth. The objectives of this research are to determine the effect of introgressed loblolly pine alleles into slash pine and to identify quantitative trait loci (QTLs) from the loblolly pine donor to select the best individuals for future introgression into slash pine breeding populations. A single field test was planted with one pseudo-backcross between an F1 hybrid of (*Pinus elliottii* x *Pinus taeda)* x *Pinus elliottii* (BC1) and families of the species progenitors.

Phenotypic analyses of third-year size showed differences in growth efficiency in the BC1 compared with the pure species. The different growth strategies of the two pure species gave BC1 progeny an advantage in crown architecture, yielding greater stem volume per unit crown size with fewer primary and secondary branches and less taper than loblolly pine.

The BC1 population, 490 individuals, was genotyped for 4300 single nucleotide polymorphisms identified in loblolly pine. Eight hundred and two informative markers were used to construct a map containing the 12 linkage groups. QTLs were discovered for growth, crown architecture, survival and growth efficiency, which explain a significant proportion of the variation.