Genetic Diversity and Hybridization in Natural Stands of Shortleaf Pine (*Pinus echinata* Mill.) and Loblolly Pine (*Pinus taeda* L.)

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Ninety-three shortleaf pine and 112 loblolly pine trees from 22 seed sources were sampled from Southwide Southern Pine Seed Source Study (SSPSSS) plantings in Oklahoma, Arkansas and Mississippi. These sample trees were grown from shortleaf pine and loblolly pine seed formed in 1951 and 1952, prior to extensive forest management throughout their geographic range. Amplification fragment length polymorphism (AFLP) markers were developed and used to estimate genetic diversity and hybridization in these pine species.

The 22 seed sources were grouped into 16 populations for the genetic diversity study. Grouping was made according to seed source geographic and physiographic region. Forty-eight primer pairs were screened, of which 17 produced 794 AFLPs in shortleaf pine and 21 produced 647 AFLPs in loblolly pine. Analysis of these AFLP data shows high genetic diversity in both shortleaf pine and loblolly pine, and most of the genetic diversity is within populations. The high values of unbiased measures of genetic identity and low values of genetic distance for all pair wise comparisons indicted that the populations have similar genetic structure. The estimated high inter-population gene flow may explain the high similarity among the populations. High gene flow exists between eastern and western populations. For both species there was no correlation between geographic distance and genetic distance.

For the hybridization study, the 48 primer pairs screened revealed 17 primer pairs which produced 96 AFLPs polymorphic across loblolly pine and shortleaf pine. Two hybrids in the loblolly pine samples and two hybrids in the shortleaf pine samples were found using the IDH (isocitrate dehydrogenase) marker. Two more hybrids in the shortleaf pine samples were found combining the 96 AFLPs with IDH markers using software NewHybrids version 1.1 beta. This study suggested that later generation hybrids could be found using molecular markers and confirmed that IDH is a useful marker to detect F1 hybrids between the two species. Hybridization frequency varied geographically, ranging from 25% in Missouri to 0% in other sources in this study. Also, the hybridization level was higher in populations west of the Mississippi River than east of the river. The results suggest that the potential for the existence of hybrids or the creation of hybrids should be considered in forest management decisions.