

Microsatellite DNA Variation within the University/Industry Tree Improvement Cooperatives' Loblolly Pine Founder Population

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Allelic variation for 13 microsatellite loci was evaluated within the Founder Population of loblolly pine (*Pinus taeda* L.) provided by the three Southern U.S. University/Industry Tree Improvement Cooperatives. Our current sample of the population includes nearly 700 trees selected from natural stands in 290 counties across 13 states. Based on mapping results (data not presented), the 13 microsatellites sampled 10 independent (unlinked) regions of the loblolly pine genome. Average expected and observed heterozygosities among the marker loci ranged from 0.25 to 0.95. Most of the loci were quite informative with heterozygosity rates in the 0.70 to 0.90 range. Analyses of the overall structure of the Founder Population clearly showed the widely known west-east subdivision formed at the Mississippi River. In addition we found evidence for a northwest-southeast subdivision of the population east of the river. The line of this subdivision ran from north Mississippi through central Florida. Two independent analytical approaches revealed this three-way population differentiation for most of the markers. No evidence was found for subdivision west of the Mississippi River, even though samples were included from the Lost Pines area of Texas. Future plans include at least doubling the number of microsatellite loci analyzed to improve the resolution of the population structure analyses and increasing the sample size especially in the more lightly sampled areas of southeast Alabama and southwest Georgia. A detailed understanding of population structure is necessary for developing genetic conservation plans and analyzing association genetic studies aimed at mapping quantitative trait loci (QTL) at the population level.

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