GENETICS OF PURE AND MIXED FAMILY PLOT YIELDS IN LOBLOLLY PINE

C. Dana Nelson,¹ Kurt H. Johnsen, John Butnor, Larry H. Lott, G. Sam Foster, and Warren L. Nance

¹Southern Institute of Forest Genetics, Southern Research Station, USDA Forest Service, Saucier, MS

Mixed and pure family plots of 10 half-sib families of loblolly pine (*Pinus taeda* L.) were planted in replicated experiments at two spacings on two sites in south Mississippi and Louisiana. Plots sizes were 70 trees (10 x 7 tree blocks) with three complete replications per spacing per site. Tree spacings were 1 x 2 and 2 x 2 meters (~2000 and ~1000 TPA, respectively) and individual tree measurements were made at ages 5, 10 and 15 years. Mixed plots consisted of paired families randomized in 75/25 and 25/75 ratios of trees planted as well as all families in randomized rows and all families in random mixes. By age 10 the wider spacing plots were yielding at or near to the closer spacing plots. Stem volume yield differences among treatments (family composition X plot type) appeared stronger at closer spacing (1 x 2 m) than wider spacing (2 x 2 m), and family composition was the strongest factor, over mixed vs. pure plots and ratios within mixed plots. Mixed family plots yielded higher than pure family plots, although family x mixture ratio and family x spacing were significant sources of variation. Some binary family mixes appeared promising for maximizing plot yield. From a genetic testing standpoint family row plots were more highly correlated with family pure plot yields than were non-contiguous plots.