

## **Growth and Yield Differences in Pure- Versus Mixed-Family Stands: Six-Year Results From Slash and Loblolly Pine Trials**

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Sustainable forest management involves using practices that maintain both biodiversity and productivity, while ensuring that future ecological and economic functions are also fulfilled. To create sustained economic yield over a smaller landbase, forest managers in the South deploy elite fast-growing southern pine genotypes. Intensive silvicultural treatments that include site preparation, competition control, fertilization and thinnings accompany these germplasm deployment decisions. Families that show high growth potential and disease resistance in single-tree plot greenhouse and field trials are selected with the belief that final yields of wood fiber per unit area when deployed in pure stands will be representative.

Pure plantings of elite single families and clones of southern pines are becoming more common, and represent the focus of much current research. For example, questions related to differences in yield potential, genetic x silvicultural treatment (environment) interactions, and the susceptibility of these “new” generation stands to abiotic and biotic damaging agents are relevant and require designed experiments to answer them. Moreover, decisions about which families to plant in pure stands are often made based on single-tree plot mixed-family planting trials, yet there is not sufficient evidence that mixed-progeny trials correlate well with pure-genotype plantations. In order for trees to produce superior yields, they must efficiently exploit the available site resources while not competing adversely with neighboring trees; however, families chosen for pure plantings are usually those that successfully compete in the mixed-progeny trials.

The specific objectives of this project were to investigate the following questions: 1) Do elite families of southern pine yield more when grown in pure or mixed family plantings?, 2) Can estimates of stand level attributes, i.e., diameter at breast height (DBH), basal area (ba), trees per hectare (tph), and diameter distributions in pure family plantings be predicted from single tree mixed family plots?, 3) Does spacing, silvicultural intensity, or genotype influence relationships between pure and mixed plantings?, and 4) How long can stand-level estimates of pure plantings be made from single-tree mixed plots (prior to the onset of inter-genotypic competition)?

### **MATERIALS AND METHODS**

In 2000, the Forest Biology Research Cooperative (FBRC) at the University of Florida installed trials to test the growth and yield effects of mixed versus pure-family plantings. Replicated experimental trials were installed at five sites in the Southeast, controlling for planting densities and levels of silvicultural treatment intensity. Pure- and mixed-stands were planted using six elite families of loblolly and slash pine, resulting in more than 100 plots at each of five locations. Each plot contains 48 measured trees, surrounded by a treated buffer strip.

Differences between pure and mixed-family plots were investigated using several measures of tree yield as response variables. These trials were installed as a replicated randomized complete block design, with treatments applied in a manner that approximated a split-plot. Thus, analyses

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were conducted in a mixed models framework with random effects for blocks and their interactions. Error covariance structures were explicitly defined to account for correlation among trees in each plot, and a repeated measures structure for annual measurements by tree was included where appropriate. The change in response variable was modeled as a function of deployment and its interactions with density, silviculture, family, and site; however, interactions were limited to second- and third-order effects so that biological interpretation was possible.

Response variables included annual tree dbh (cm), as well as measures of stand occupation, such as ba ( $\text{m}^2/\text{ha}$ ), tph (tree/ha), and mortality (%), stand structural diversity as described by the distribution of tree dbh by plot, and disease and damage (%). Basal area per acre was calculated as tree basal area divided by its growing space. Growing space per tree was estimated using an average value over the plot, as plot area divided by the number of live trees in the plot. To facilitate comparisons by family, tph was calculated as the number of live trees per plot divided by the proportion of the plot area initially planted in that family. Because plot-level data for mixed plots included <10 trees in each family, dbh distributions by family could not be analyzed without some pooling of observations. Thus, trees in the same treatment (family within spacing and silviculture) were adjusted to eliminate block effect, and then pooled.

## **RESULTS AND DISCUSSION**

In modeling DBH and BA per unit area, there was a significant interaction between families and deployment in years 5 and 6, though differentiation by deployment did not occur until year 6 for most families. Differences were consistent by year, but not by family; some families performed better in mixtures than in pure plots and vice versa. The largest and smallest families were the same by deployment (i.e., there was no rank change at the extremes); however, mixed plots had a wider range than pure plots by age 6, with larger differences between the largest and smallest families (Figure 1). This suggests that larger families grew larger at the expense of smaller ones when growing in an intimate mixture. There was no interaction between spacing and deployment at this age, likely due to the onset of crown competition in both spacings.

Parametric analysis of DBH distributions indicated greater negative skewness (i.e. more smaller trees) in pure plots versus mixed plots. This was most pronounced and statistically significant at age 3 but lessened with time perhaps due to mortality occurring in these smaller trees as a result of disease or climatic events such as wind or drought.

When analyzed by year, annual mortality rates for mixed and pure slash pine plantings were significantly different; however, this difference is only biologically significant in some years and sites. For slash pine, there were no significant differences in the number of live trees per acre in mixed versus pure plantings over the time period. However, for loblolly, there were significant interactions with site. In some sites, significant interactions by year indicated that a mortality pulse occurred in the mixed plots at age 4, whereas this pulse occurred in year 5 for mixed plots. This difference is also reflected in the annual estimates of the number of live trees per acre, which shows a sharp drop in mixed plantings earlier than those of pure.

While basal area per acre is marginally higher in the mixed plots, as was demonstrated previously in cottonwood (Foster et al. 1998), tree survival was higher in pure plots. These

differences may be in part explained by differences in disease susceptibility. Trees in mixed plots were far more susceptible to pitch canker, weather damage, and forking, especially in loblolly stands. This is somewhat unexpected, given the widespread evidence that diverse forests are more resistant to insects and pests (Carnus et al. 2006).

## APPLICATIONS

Although these results are preliminary, they have important implications for forest managers, who must make decisions about the composition of intensively managed pine plantations to promote both ecological and economic sustainability. These results could be applied to applications such as clonal screening trials where large numbers of clones are evaluated in mixed single tree plots. These results show that there is no interaction with silvicultural intensity. Competition between trees occurs fairly early in intimate mixtures with the fastest growing genotypes getting larger at the expense of slower growing ones as has been previously reported (DeBell and Harrington 1997). This appears to bias the prediction of rapidly growing genotypes upward in pure plots as early as 5 years at densities between 1330 tph and 2990 tph. Also, predictions from mixed plots can be confounded by mortality due to diseases (such as fusiform rust) which may interact with deployment method

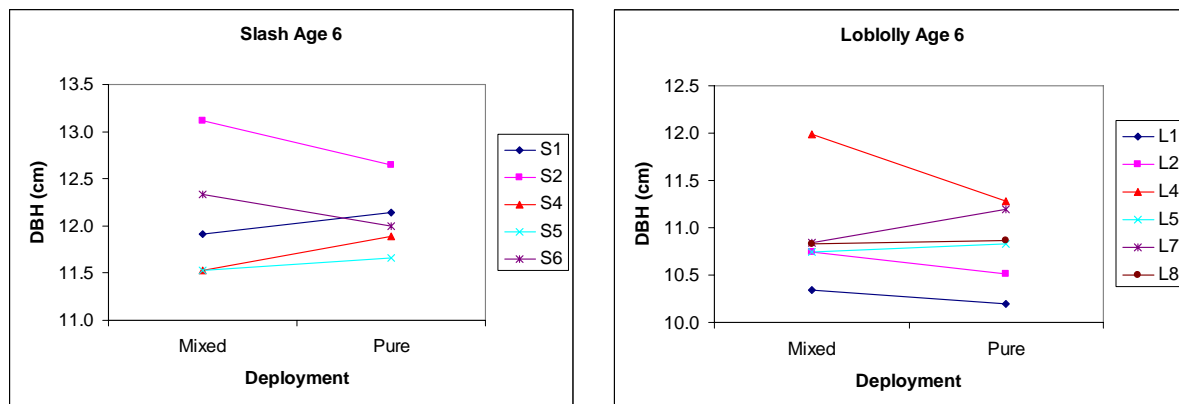


Figure 1. Significant family by deployment by year interaction for loblolly and slash pine.

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