PREDICTING THE EFFECTS OF GENETIC TREE IMPROVEMENT ON STAND YIELD

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Abstract .--At any given age, height and diameter distributions from loblolly pine seed sources with larger dominant heights have a greater proportion of stems in the larger size classes than do seed sources with smaller dominant heights. For the same number of stems per unit area, both the average stem size and the total volume were positively correlated with site index. Implications are that genetic improvement does not fundamentally alter the pattern of loblolly pine stand development and that both the total volume per area and the average stem size at a given time are predictable from the dominant height at that time.

Additional keywords: Height distributions, diameter distributions, <u>Pinus taeda</u>, stand trajectory.

Programs to improve the growth rate, form, and pest resistance of loblolly pine (<u>Pinus taeda</u> L.) through tree breeding have been underway in excess of 25 years. Until recently, however, relatively little effort has been directed toward understanding the development of stands of selected genotypes. Questions about selected genotypes are most often stated in terms of gain. We are ultimately concerned with the gain in value associated with a given treatment or choice of genetic material.

In simple terms, we can consider value to be some function of total volume, size distribution, and stem quality. For predicting the growth and relative value of any forest stand, three important questions are: 1) What volume is produced by the stand? 2) What is the distribution of that volume in terms of stem height, diameter, and taper)? 3) How can this information be incorporated into models for stand growth and dynamics? This paper reviews some of the information learned about the dynamics of genetically improved loblolly pine stands and discusses the implications for predicting stand growth.

DATA

The data used for much of the work reported here are from two sources: 1) the loblolly phase of the Southwide Pine Seed Source Study

¹Research Forester, Southeastern Forest Experiment Station, USDA Forest Service, Charleston, South Carolina. (SWPSSS) and 2) a 15-year-old block-plot half-sib progeny test planted near Bogalusa, Louisiana, belonging to Cavenham Forest Industries, Inc. A complete description of the Southwide Pine Seed Source Study design was given in Wells and Wakeley (1966).

The block-plot progeny test was replicated four times at a single location. Each replication contained 12 121 tree plots (11 x 11 trees); the inner 49 trees were measurement trees. The spacing was 8 x 8 feet. Each replication contained 11 plots of selected genotypes and 1 plot of local woodsrun origin as a control.

RESULTS AND DISCUSSION

Using data through age 27 for the SWPSSS, Nance and Wells (1981) found that site index differed among seed sources. Using a slightly different model for the height-age relationship than that used by Nance and Wells, Buford and Burkhart (1987) found that the shape of the height-age profile was the same for all seed sources or families at a given location, but that the level of the height-age curve differed by seed source or family. This result was consistent across all sets of data.

At a given location of the SWPSSS, the shape of the height-diameter relationship did not vary by seed source at age 15, but the level of that relationship did vary by source (Buford 1986). In addition, the level of the height-diameter relationship was strongly and positively correlated with the dominant height of the source at that age. Buford and Burkhart (1987) reported the same result for the block-plot progeny test at age 8. Thinnings prevented this relationship from being investigated at older ages in both sets of data.

It has been suggested that while increasing mean tree size, genetic selection might reduce stand value by reducing stand-level variance. That is, although the mean size might be increased, reduced phenotypic variance would translate into fewer large trees (Nance and Bey 1979, Thurmes 1980). Buford and Burkhart (1985) compared the variances of heights and diameters among the families in the block-plot progeny test using Bartlett's test for homogeneity of variances. An observational rank analysis also determined the relative size and rank of the variances of the 12 families. The conclusion was that with equally intense and successful silvicultural treatments, variances of height and diameter in stands originating from selected genotypes are not different or consistently smaller than those in stands originating from nonselected genotypes.

> A single stand volume equation of the following form: $log(Y) = -b_0 + b_1 A^{-1} + b_2 log(H_D) + b_3 N$

where Y equals total volume, A equals plantation age (years), H $_{\rm D}$ equals dominant-codominant height (feet), and N equals surviving trees per acre, was found sufficient to predict the volume in stands of both genetically unimproved and improved loblolly pine (Buford and Burkhart 1987). For the same age and number of surviving stems, increasing the dominant height gave a greater predicted stand volume. At any given age, both height and diameter distributions from seed sources with larger dominant heights had higher proportions of larger stems than those from seed sources with smaller

dominant heights. Observed height and diameter distributions through time illustrated this trend (fig. 1).



Figure 1.--Observed diameter (a,b) and height (c,d) distributions at ages 10, 16, 20, and 25 for two seed sources at the Southeast Louisiana planting of the Southwide Pine Seed Source Study.

Nance and others (1987) proposed that the self-thinning trajectory (or the so-called '-3/2 line') (Yoda and others 1963, White 1981) may vary with genetic material on a given site. The self-thinning trajectory is often presented graphically as the logarithm of the mean stem size vs the logarithm of the number of stems per area at that stem size. An example of this is given in fig. 2b. Age increases as one moves from right to left along the horizontal axes in fig. 2. One hypothesis put forward by Nance and others (1987) was that the level of the stand trajectory on a given site, or the carrying capacity, might vary with the genetic material planted on that site. Using 30-year data from the SWPSSS, Buford² has shown that the trajectories for logarithm of total volume and logarithm of average stem volume relative to the logarithm of the number of surviving stems varied by



Figure 2.--Observed logarithm of total volume per acre (a) and logarithm of average stem volume (b) vs. logarithm of number of stems per acre for selected seed sources at ages 10, 16, 20, 25, 27, and 30 years at the Southeast Louisiana planting of the Southwide Pine Seed Source Study.

²Buford, M. A. 1988. Mean stem size and total volume development of various loblolly pine seed sources planted at one location. (In preparation).

seed source in level but not in shape. In addition, the level was highly correlated with the site index of the seed source (r=0.87 with <0.001 for the total volume trajectory). Total volume per acre and mean stem volume trajectories for selected seed sources at one location are shown in fig. 2. In practical terms, for the same number of stems per acre, say 350 (log=5.85), the NE MS source (lowest) had approximately 2345 (log=7.76) cubic feet per acre while the SE LA source carried approximately 4447 (log=8.40) cubic feet per acre (fig. 2a). The NE MS and SE LA seed sources reached 350 stems per acre at approximately age 20 and age 25 years, respectively.

IMPLICATIONS

The primary implications of these results for predicting the effect of genetic tree improvement on loblolly pine growth are: 1) genetic improvement does not fundamentally alter the pattern of stand development; 2) changes in genetic material on a given site will likely affect the level, but not the shape of basic relationships such as that between height and age; and 3) at a given age, height and diameter distributions from seed sources with larger dominant heights have a greater proportion of stems in the larger size classes than do seed sources with smaller dominant heights. Based on the information reviewed here, the development of genetically improved loblolly pine stands can be predicted with the incorporation of the appropriate height-age relationship into an existing valid, well-behaved growth model.

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