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Genetic Improvement Effects on Growth and Yield of Loblolly Pine Plantations

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ABSTRACT. A series of hypotheses concerning stand dynamics and growth patterns in loblolly pine plantations of improved stock relative to plantations of unimproved stock were developed and tested. Results of these tests indicated that at the seed source and family levels: (1) the shape of the height-age curve is influenced by the site, but the level of the height-age curve is influenced by the seed source or family; (2) at the seed source and family levels, the shape of the height-diameter relationship at a given age is influenced by the site and by the initial density; and (3) the level of the height-diameter relationship is affected by the seed source or family and is directly related to the dominant height of the seed source or family at that age. Indications are that by choosing the height curve carefully, differences in development among seed sources and families on a given site can be modeled by altering the level of the height-age curve.

Data from temporary plots in stands planted operationally with genetically improved stock were used to test for differences in stem quality and volume relationships as compared to comparable plots from unimproved plantations. Stem quality in the improved stands was not substantially different than in unimproved stands in the same region and of the same age range. There was no difference in stem taper or individual tree volume between improved and unimproved stock.

Yield equations, based on the independent variables age, average height of dominants and codominants, and surviving number of trees, were fitted to these same plot data from operationally planted improved and unimproved stands. There were no significant differences in the yield equations, indicating that a single yield equation should suffice when the independent variables are correctly specified. FOR. SCI. 33(3):707–724.

ADDITIONAL KEY WORDS. *Pinus taeda*, modeling, tree improvement.

FOR THE LAST 10 TO 15 YEARS, there has been a steady increase in the proportion of genetically improved loblolly pine (*Pinus taeda* L.) seedlings planted, and it is expected that this general trend will continue.[1] Accurate volume and value forecasts are requisite to forest management and long-range planning. As more acres are planted with genetically improved stock and the resulting stands mature, it becomes increasingly important to model the development of these stands so that accurate yield forecasts and sound management decisions can be made.

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A large amount of work has addressed the question of what sources or families should be planted on a given site. Projected percentage increases in volume production for stands of improved stock have been put forth. Several studies have explored the ramifications of changing existing growth and yield models to reflect hypothetical changes in stand growth due to improved stock (Tisdale 1973, Mitchell 1975, Nance and Bey 1979, Thurmes 1980, Nance 1982). These studies did not use data from actual improved stands for testing the validity of the modifications made in the models. Nance and Wells (1981a) compared plot volumes in the Southwide Pine Seed Source Study with volumes generated from a growth and yield model, finding that growth and mortality were correlated with site index except in those instances where severe catastrophic mortality had occurred and that actual plot volumes were less than those predicted from the model for most plots due to catastrophic mortality on many of the plots. An assessment of the effect of seed source on the variation of site index for loblolly pine was presented by Nance and Wells (1981b). Spirek et al. (1981) used the Weibull distribution to model the distributions of diameters and heights in slash pine (*P. elliotti* Engelm.) progeny tests. However, we still do not have a complete understanding of the dynamics of stands of improved stock or of what modifications, if any, are needed in current growth and yield models to reflect the growth and development of stands of improved stock. This study was conducted to: (1) investigate the dynamics of genetically improved stands by using available data to test hypotheses concerning growth of improved stands, and (2) explore ways to model, or to incorporate into existing models, the impact of genetic improvement on the growth and yield of loblolly pine plantations.

In modeling the growth and yield of forest stands, we seek to mathematically describe and interpret the biological relationships that underlie stand development. Key components in the understanding of stand dynamics are: (1) the development of dominant height over time (the height-age relationship); (2) the development of the height and diameter distributions through time; (3) the relationship of the mean height by diameter class across the range of diameters at a given age, (the height-diameter relationship); and (4) the mortality-time relationship. A logical place to begin is by testing for differences in these relationships among different genetic material. Quantifying the similarities and differences in the shapes and levels of these relationships for varied genetic material is an initial step in understanding the development of stands of improved stock and will provide requisite information for modeling their growth.

The objective of this study was to state logical hypotheses regarding the dynamics of genetically improved stands, to derive testable statistical hypotheses from these statements, and to test the hypotheses using available data. This report details hypotheses tested, methods of testing, test results, results using data from operational plots, and implications for modeling the growth of stands of genetically improved stock.

DATA

The data available for this study were of diverse types and not, by study design or plot structure, the kind usually used for growth and yield analysis. The limited database dictated that the hypotheses be constructed and tested and that the implications be proposed through the synthesis of fragmented information, rather than the usual model-building techniques.

The database used was comprised of three components: (1) the Loblolly Phase of the Southwide Pine Seed Source Study to age 25; (2) a 15-year-old block-plot open-pollinated progeny test planted near Bogalusa, Louisiana, belonging to Crown Zellerbach Corporation; and (3) data from temporary plots in 34 stands planted operationally with improved stock located in the Coastal Plain of North Carolina, South Carolina, and Georgia, and the North Carolina Piedmont.

The Southwide Pine Seed Source Study was established in 1952–1953 to determine the degree that genetic variation in four southern pine species is associated with geographic variation in climate and physiography. In the loblolly phase, seed from 15 geographic areas was obtained from representative stands and grouped into 2 series. Three sources were common to each series, and 6 sources were unique to each series. At each of 19 locations, the seedlings were planted in a randomized complete block design with 4 blocks. All locations were not planted with both series. Each source plot contained 121 trees on a 6 ft × 6 ft spacing. The inner 49 trees on each plot were measured at 1, 3, 5, 10, 15, 20, and 25 years after planting, although some measurements were made at 16, 22, and 27 years instead of 15, 20, and 25 years. Data through age 25 or 27 were available for 15 planting locations, and data were available through age 20 or 22 for 2 planting locations. Further details are given in Wells and Wakeley (1966) and Wells (1983).

The block-plot progeny test was planted at one location in a randomized complete block design with four blocks. Each block contained twelve 121-tree plots (11 × 11 trees) with the inner 49 trees as measurement trees. Spacing was 8 ft × 8 ft. Each block contained 11 plots of selected open-pollinated genotypes and 1 plot of local woodsrun origin as a control. Measurements were made at ages 1 to 8, 10, and 15. All plots were thinned for spacing and quality after the age 8 measurement.

Data for the operational phase of this study came from 34 plantations on cutover sites planted with genetically improved stock. Temporary plots were established in 33 of the stands during the 1984–1985 dormant season. Information for the remaining stand came from permanent plots established after planting. Information from these stands included diameter at breast height, total height, height to live crown and stem quality for all planted pines; height, diameter and species of all hardwoods and volunteer pines in the main canopy; and number by diameter class of all hardwoods and volunteer pines not in the main canopy. There were 40 plots yielding 54 observations including the remeasurements on the permanent plot. The distributions of age, site index, density, and stand origin for the 39 plots are given in Table 1. Plot size was 0.1 ac for the temporary plots and 0.26 ac for the permanent plots.

Analysis of the Seed Source Study allowed hypotheses to be tested regarding similarity or difference of growth pattern of different seed sources at the same location and at different locations. Analysis of the open-pollinated block-plot progeny test allowed hypotheses to be tested regarding growth patterns of open-pollinated families at the same location. The operational plot data allowed further testing of hypotheses concerning operationally established stands of improved and unimproved stock. Data from unthinned stands of sufficient age to study the mortality-time relationship were not available.

METHODS AND RESULTS

Test Considerations

The probability of a Type I error for all the statistical tests performed in this study was 0.05 unless otherwise stated for a specific test. The power of the

TABLE 1. Distributions of age, predicted site index, and density for the 54 observations (a and b) and stand origin for the 39 stands (c).*

(a)	Age	Site index 40–55	Site index 55–70	Site index >70
	<7 yr	2	2	11
	8–14 yr	1	5	23
	>14 yr	—	3	7

(b)	Density stems/ac	Site index 40–55	Site index 55–70	Site index >70
	<500	1	3	12
	500–700	1	6	27
	>700	1	1	2

(c)	Seed orchard condition	Genetic makeup of stand: Individual clones	Genetic makeup of stand: Seed orchard mix
	Rogued	—	15
	Unrogued	—	24

* Site index predicted from Type B curve in Clutter et al. (1984) using the average height of the dominant-codominant trees.

tests involving the height-age and height-diameter relationships was calculated for $\alpha = 0.05$. It was assumed that differences of 10 feet or more at the oldest age or greatest diameter were of practical significance. Computations followed procedures outlined in Neter and Wasserman (1974); in all cases, the power of the tests equaled or exceeded 0.85.

Height-age Relationship

When modeling stand development, a very important relationship to understand and correctly characterize is the height-age relationship. The analysis of the height-age profiles in the data available was therefore of primary interest.

Nance and Wells (1981b) used the Southwide Pine Seed Source Study and a fairly inflexible height-age model (Smalley and Bower 1971) to study differences in site index among different seed sources. One result of their work was that at any given location of the Seed Source Study, the shape of the height-age curve is the same for all seed sources, but the level of the curve is affected by seed source and block. To determine whether or not these results were an artifact of the model used by Nance and Wells (1981b), the analysis was repeated using the more flexible Richards' function:

$$H = A(1 - \exp(-b \cdot \text{age}))^c + \epsilon \qquad (1)$$

where

H = height at a given age
A = asymptotic or maximum height
b = rate parameter
c = shape parameter
ϵ = random error.

Equation (1) was fitted to the tallest 7 trees at each age (roughly analogous to the tallest 100 trees per acre) for each seed source × block × location combination. Analysis of variance (using the estimates of A, b, and c as response variables), comparison of asymptotic confidence intervals for A, b, and c, and graphical analysis of the resulting curves for each location showed significant seed source and block effects on A, the asymptotic height, but generally no seed source or block effects on b and c, the rate and shape parameters, respectively. These results support the findings of Nance and Wells (1981b) and also indicate that an extremely flexible function is not necessary for this analysis. Therefore, the function chosen to study the height-age pattern was:

$$\log(H) = a + b(A^{-1}) + \epsilon \qquad (2)$$

where

H = height at any given age, A
a = level parameter
b = slope or shape parameter
log = base e logarithm.

Values of R^2 from Equation (2) were consistently greater than 0.94. Although there was some small bias at ages less than three years, examination of residual plots showed no general evidence to indicate that Equation (2) was inappropriate for these data. Equation (2) has been previously used to model height-age relationships in loblolly pine (Burkhart et al. 1972, Coile and Schumacher 1964, Lenhart 1971), has easily interpretable coefficients, and can be fit by linear least squares. The slope parameter in Equation (2), b, is the shape parameter of the fitted relationship when transformed to the arithmetic scale. The intercept parameter in Equation (2), a, is the logarithm of the asymptotic height and governs the level of the fitted curve. The three questions of primary interest in the analysis of the height-age relationships for sources and families were:

1. Is there a common shape of the height-age relationship among the different seed sources or families on a given site?
2. If equality among the shapes, b, at a given location is assumed, are there significant seed source effects on the intercept, or level, a? and
3. If equality among the shapes may not be assumed for a given location, are there significant seed source effects on the shapes, b?

Equation (2) was expanded to the following to facilitate testing the statistical hypotheses of interest:

$$\log(H) = a_1X_1 + a_2X_2 + \ldots + a_kX_k + b_1Z_1 + b_2Z_2 + \ldots + b_kZ_k + \epsilon \qquad (3)$$

where

$$X_i = \begin{cases} 1 \text{ if seed source or family } i, \\ 0 \text{ otherwise;} \end{cases}$$

$$Z_i = \begin{cases} A^{-1} \text{ if seed source or family } i, \\ 0 \text{ otherwise;} \end{cases}$$

k = number of seed sources or families in a given block or replication at a given location.

For the Seed Source Study, Equation (3) was fitted to the tallest 7 trees at each age (roughly analogous to the 100 tallest tree per acre) for each block × location combination. The first question can be stated symbolically as:

$$H_0: b_1 = b_2 = \ldots = b_k \text{ from Equation (3).}$$

$$H_A: \text{at least one } b_i \text{ different}$$

To test this hypothesis, the following equation was fitted to the data in each of the block × location combinations in the Seed Source Study:

$$\log(H) = a_1X_1 + a_2X_2 + \ldots + a_kX_k + b(A^{-1}) + \epsilon \qquad (4)$$

where X_i is as defined in Equation (3) and b is a common slope. For each block × location combination, the F-ratio,

$$\left(\frac{SSE_4 - SSE_3}{SSE_3}\right)\left(\frac{n_3}{n_4 - n_3}\right),$$

where SSE_i = error sum of squares and n_i = error degrees of freedom, respectively, for Equation (i), was compared to the tabulated $F_{.05}$ with $n_4 - n_3$ and n_3 degrees of freedom. The results are presented in Table 2. The test is robust under departures from the assumptions of independently and normally distributed errors with mean zero and common variance.

Question 2 was addressed by testing the following hypothesis.

$$H_0: a_1 = a_2 = \ldots = a_k \text{ from Equation (4).}$$

The following equation was fitted to the data in each of the block × location combinations:

$$\log(H) = a + b(A^{-1}) + \epsilon \qquad (5)$$

where a and b are common intercept and slope, respectively. For each block × location combination, the F-ratio

$$\left(\frac{SSE_5 - SSE_4}{SSE_4}\right)\left(\frac{n_4}{n_5 - n_4}\right)$$

was compared to the tabulated $F_{.05}$ with $n_5 - n_4$ and n_4 degrees of freedom. The results are presented in Table 2.

For only 1 of the 17 locations was the hypothesis of equality slopes rejected (Table 2). Since this hypothesis was not generally rejected, it was unnecessary to address Question 3. The hypothesis of no seed source effects on the intercept was rejected for 38 of the 60 plots (Table 2). For these data, the general conclusion is that at a given location, the shapes of the height-age relationships are the same among seed sources; but the level of the height-age relationship likely differs by seed source. This same conclusion was reached by Nance and Wells (1981b) using a different type of analysis. The consistency of height rank over time among the seed sources reported by Wells (1983) complements these results.

The same type of analysis was performed on the open-pollinated block-plot progeny test. Equations (3), (4), and (5) were fitted, by block, to the tallest 7 trees at each age per plot (family × block combination). This number is roughly analogous to the 100 tallest trees per acre for each family. The F-ratios for testing the hypothesis of equality of slopes and equality of intercepts for the height-age relationship among the families in a given block are given in Table 3. From Table 3, the hypothesis of equality of slopes of the height-age curves among the families within a block is not rejected for any of the blocks. The general conclusion for these data is that the shapes of the height-age relationships do not differ by open-pollinated family at a given

TABLE 2. Calculated F-ratios for testing hypothesis of equality of slopes and intercepts for the height-age relationship among the seed sources in a given block × location combination of the Southwide Pine Seed Source Study.

Series 1				Series 2			
		F-ratio for				F-ratio for	
Location	Block	slopes	intercepts	Location and series	Block	slopes	intercepts
E MD	1	0.27	2.18*	E NC	1	1.30	2.47*
	2	0.99	2.69*		2	0.29	2.20*
	3	0.16	2.09*		3	0.70	1.52
	4	0.29	3.71*		4	0.37	1.37
E NC	1	0.23	2.67*	W SC	1	0.19	3.03*
	2	0.17	3.16*		2	0.30	2.88*
					3	0.30	3.38*
E NC	1	0.97	3.59*		4	0.32	2.18*
	2	1.35	1.69				
	3	0.88	1.37	C GA	1	1.46	3.36*
	4	1.05	3.67*		2	0.97	4.30*
					3	0.84	2.81*
SW GA	1	0.38	1.56		4	0.77	2.00*
	2	0.54	1.02				
	3	0.32	3.06*	C AL	1	1.02	3.55*
	4	0.50	1.19		2	0.39	1.46
					3	0.86	1.01
C AL	1	1.12	2.59*		4	0.27	1.93
	2	0.56	4.40*				
	3	0.68	4.10*	S MS	1	0.24	2.25*
	4	0.22	1.67		2	0.27	2.36*
S MS	1	1.53	1.14	N MS	1	0.84	2.18*
	2	1.80	2.13*		2	0.57	1.12
					3	0.18	4.96*
W LA	1	6.02*[1]	2.65*		4	0.39	2.24
	2	5.90*	3.22*				
	3	4.26*	3.27*	W LA	1	1.20	3.95*
	4	4.27*	1.76*		2	0.98	3.47*
					3	1.64	4.76*
E TX	1	0.62	3.49*		4	2.65	4.40*
	2	0.14	1.50				
				SW AR	1	0.95	1.45
SW AR	1	0.14	1.71		2	0.49	1.81
	2	0.06	2.10		3	0.64	1.77
	3	0.30	1.04		4	0.64	2.53*
	4	0.20	1.31				

[1] An asterisk implies statistical significance at $\alpha = 0.05$.

location, but that the levels of the height-age relationship do differ by open-pollinated family.

The conclusion of this phase of the study is that at a given location, the shape of the height-age profile is the same among seed sources or families, but the level of the height-age curve differs by seed source or family. This result is consistent across the Southwide Pine Seed Source Study, and the block-plot open-pollinated progeny test. Examples of actual height-age curves are given in Figures 1 and 2.

TABLE 3. Calculated F-ratios for testing hypothesis of equality of slopes and equality of intercepts for the fitted height-age curve for the families in a given block of the open-pollinated block-plot progeny test.

Block	F-ratio for slopes	F-ratio for intercepts
1	0.29	2.37*[1]
2	0.70	1.78*
3	1.07	3.106*
4	0.62	2.11*

[1] An asterisk implies statistical significance at $\alpha = 0.05$.

HEIGHT-DIAMETER RELATIONSHIP

Height-diameter relationships are used in many growth and yield models to predict the mean height for a given diameter or diameter class. The diameter and predicted height values are then used in stand volume and value calculations. The wide use of this relationship dictated its investigation. Only data from unthinned studies or unthinned parts of studies were suitable for analysis of the height-diameter relationship as thinning alters stand structure and, with it, the baseline development of the height-diameter relationship. Nine locations of the Seed Source Study unthinned by age 15 were used (Table 4). The block-plot progeny test was thinned after age 8. Given that the dominant heights ranged from 38 to 50 feet at age 8 in these plots, the height-diameter relationship was well developed at age 8, and these data were appropriate for the analysis.

The function used to model the height-diameter relationship in this analysis was:

$$\log(H) = c + m\,(D^{-1}) + \epsilon \tag{6}$$

where

H = mean height for a given diameter, D
c = level or intercept parameter
m = slope or shape parameter
log = base e logarithm.

Equation (6) is commonly used to model height-diameter relationships (Curtis 1967) and has been used for loblolly pine (Burk and Burkhart 1984). The slope parameter in Equation (6), m, is the shape parameter of the relationship in the height-diameter scale. The intercept parameter in Equation (6), c, is the logarithm of the maximum height at that particular age and governs the level of the curve. Equation (6) was fitted to the data described above. Values of R^2 were consistently larger than 0.90, and examination of residual plots showed no trends to indicate that Equation (6) was inappropriate.

The three questions of primary interest in the study of the height-diameter relationships were:

1. Is there a common shape of the height-diameter relationships among the different seed sources or families on a given site?
2. If essential equality of curve shape is assumed among the seed sources or families on a given site, are there significant seed source effects on the intercept, or level, parameter? and

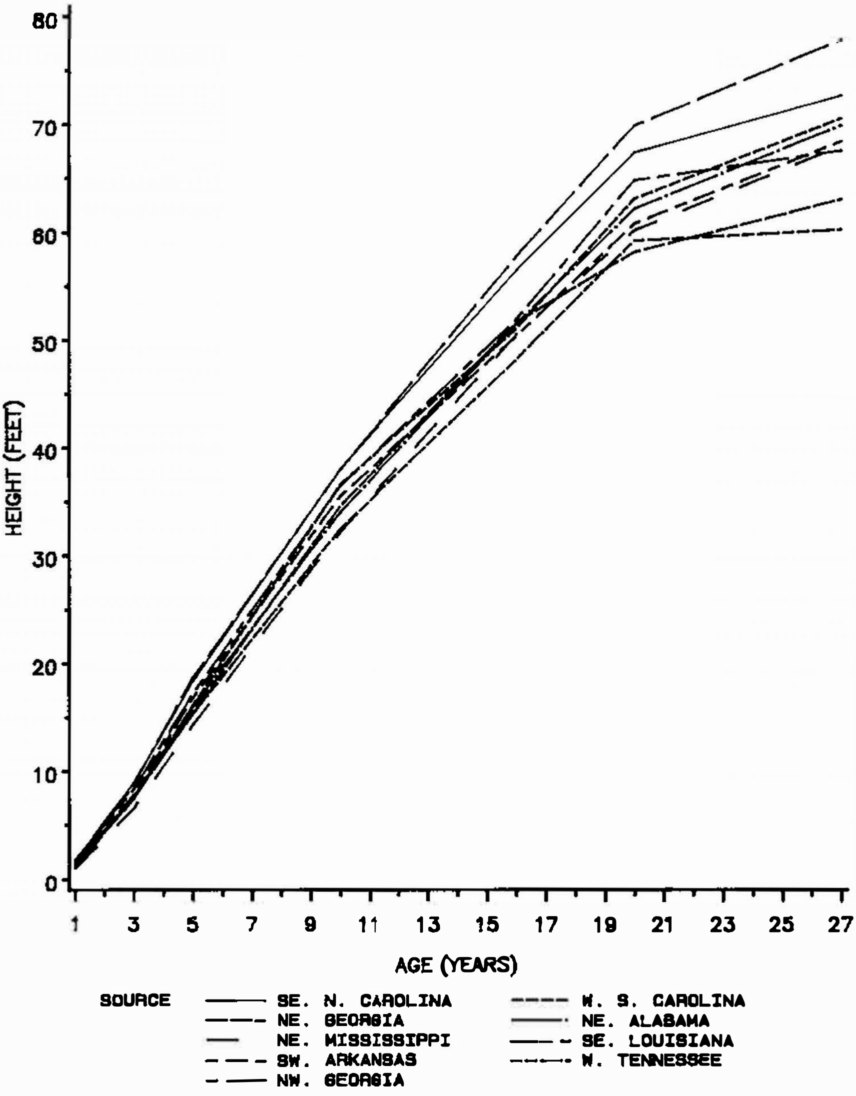

FIGURE 1. Actual height-age relationships for seed sources at southeast Louisiana Series 2 planting of Southwide Pine Seed Source Study.

3. If essential equality of curve shapes may not be assumed, are there significant seed source effects on the slope parameter?

Equation (5) was expanded to the following to facilitate testing statistical hypotheses of interest:

$$\log(H) = c_1X_1 + c_2X_2 + \ldots + c_kX_k + m_1Z_1 + m_2Z_2 + \ldots + m_kZ_k + \epsilon \qquad (7)$$

where

$$X_i = \begin{cases} 1 \text{ if seed source of family } i, \\ 0 \text{ otherwise;} \end{cases}$$

$$Z_i = \begin{cases} D^{-1} \text{ if seed source or family } i, \\ 0 \text{ otherwise;} \end{cases}$$

k = number of seed sources or families on a given site.

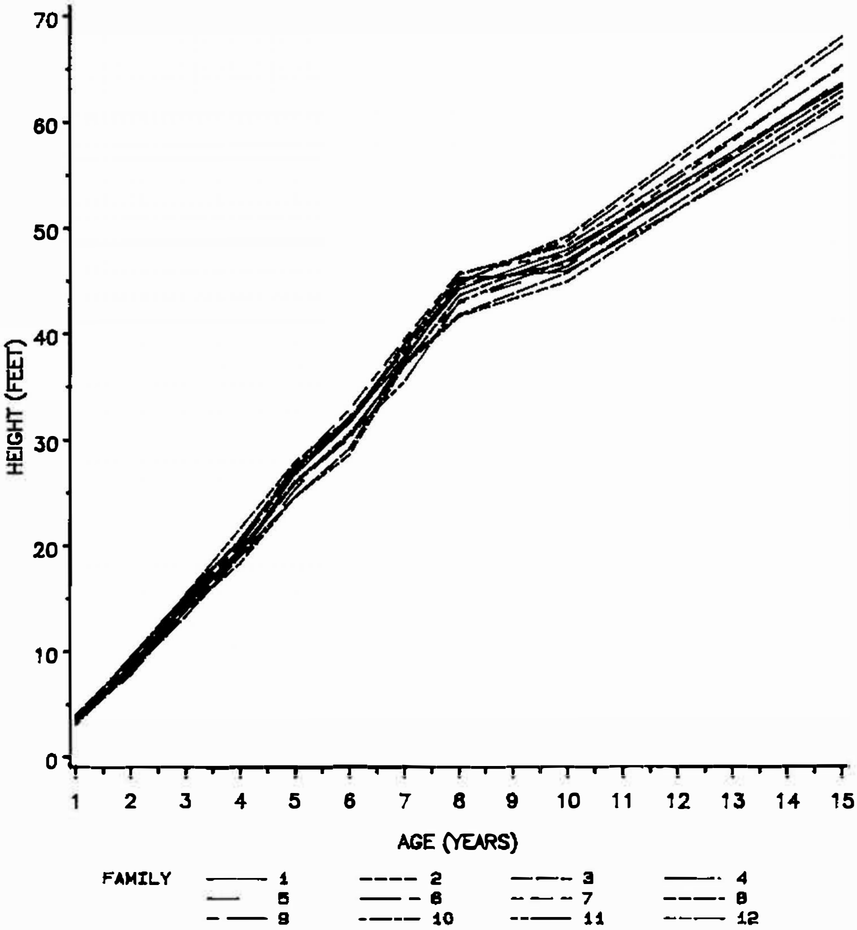

FIGURE 2. Actual height-age relationships for open-pollinated families in block 4 of the block plot progeny test in southeast Louisiana.

Question (1) was investigated by testing the null hypothesis:

$$H_0: m_1 = m_2 = \ldots = m_k.$$

To test this hypothesis, the following equation was fitted to the appropriate data:

$$\log(H) = c_1X_1 + c_2X_2 + \ldots + c_kX_k + m(D^{-1}) + \epsilon \qquad (8)$$

where X_i is as defined above and m is a common slope. The F-ratio,

$$\left(\frac{SSE_8 - SSE_7}{SSE_7}\right)\left(\frac{n_7}{n_8 - n_7}\right),$$

where SSE_i = error sum of squares and n_i = degrees of freedom for error, respectively, for Equation (1), was compared to the tabulated $F_{.05}$ with n_7 and $n_8 - n_7$ degrees of freedom to answer Question (1). Questions (2) and (3) were addressed by performing an analysis of variance (form given in Table 5) on the appropriate coefficients from Equations (7) or (8).

For the Seed Source Study, Equations (7) and (8) were fitted to the

TABLE 4. Location of the nine Southwide Pine Seed Source Study plantations used in the analysis of the height-diameter relationship.

Location	County or parish	State	Series
C AL (2)	Coosa	Alabama	2
E MD (1)	Worcester	Maryland	1
N MS (2)	Winston	Mississippi	2
S MS (1)	Pearl River	Mississippi	1
S MS (2)	Pearl River	Mississippi	2
SE LA (1)	Washington	Louisiana	1
SE LA (2)	Washington	Louisiana	2
SW GA (1)	Dooly	Georgia	1
W SC (2)	Newberry	South Carolina	2

height-diameter data in each of the 32 block × location combinations and the analysis described above was performed. Details of this analysis can be found in Buford (1986). The conclusion for these data is that there is a common curve shape for the height-diameter relationships at age 15 for all the seed sources planted on a given site, but that the level of the curves differs by seed source on a given site and that the level of the height-diameter relationship is strongly related to the dominant height of the seed source (Buford 1986).

The same type of analysis was performed on the open-pollinated block-plot progeny test data at age 8. Equations (7) and (8) were fitted to the height-diameter pairs for each plot (family × block combination). The calculated F-ratios for testing equality of slopes of the height-diameter curves among the families within a block are given in Table 6. The hypothesis is not rejected for any of the four blocks. The F-ratio calculated from the analysis of variance of the intercept terms from Equation (8) is 9.01 with 11 and 33 degrees of freedom and is significant at $\alpha = 0.05$. Simple correlations between the dominant height at age 8 of a given family and the appropriate intercept term from Equation (8) were greater than 0.92 for all four of the blocks. While this is an expected result due to the form chosen for the height-diameter equation [Equation (6)], the empirical result facilitates understanding the association of the intercept, or level, and dominant height. The conclusion from this portion of the analysis is that height-diameter relationships are the same shape cross open-pollinated families at age 8, but that the level of the curves differs by family with the level of the height-diameter relationship strongly related to the dominant height of the family at age 8.

The conclusion of this phase of the study is that at a given location, the shape of the height-diameter relationship at any age is the same among seed sources or families, but the level of the height-diameter curve at that age differs by seed source or family. In addition, the level of the height-diameter

TABLE 5. Form of analysis of variance for seed source or family effects on the parameters of the height-diameter relationship at a given location.

Source of variation	Degrees of freedom	Mean square	F-ratio
Block (or rep)	$b - 1$		
Seed Source (or family)	$s - 1$	MSS	$F_s = MSS/MSE$
Error	$(b - 1)(s - 1)$	MSE	

TABLE 6. Calculated F-ratios for testing equality of slopes of the height-diameter curves among the open-pollinated families within a block for the block-plot progeny test.

Block	F-ratio
1	1.38
2	1.69
3	1.99
4	1.27

curve is directly and strongly related to the dominant height of that seed source or family at that age. These results are consistent for the Southwide Pine Seed Source Study, and the block-plot open-pollinated progeny test. An example of a set of fitted curves for one site of the Seed Source Study at age 15 is given in Figure 3, showing a common shape and differing levels among the curves. In this instance, the actual range of diameters was 2.2 to 11.0 in. and the actual range of heights was 16 to 65 ft.

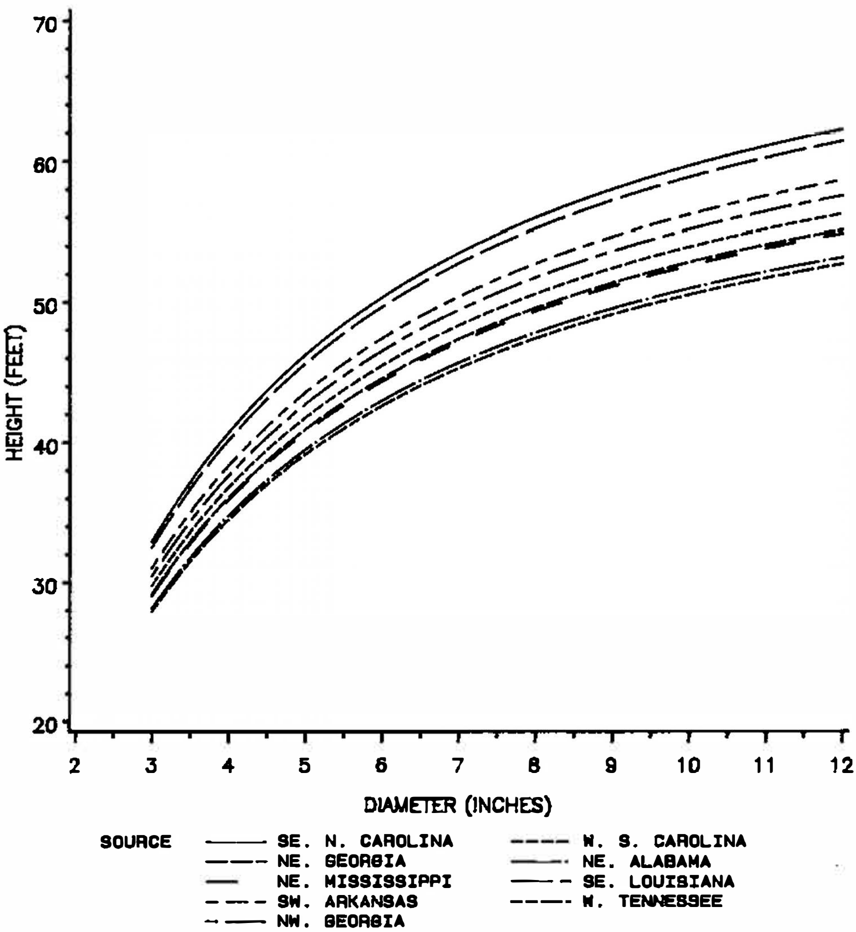

FIGURE 3. Fitted height-diameter curves for seed sources at southeast Louisiana Series 2 planting of Southwide Pine Seed Source Study.

Stem Quality

Data taken in the operational plantations included detailed stem quality information. The Loblolly Pine Growth and Yield Research Cooperative at Virginia Tech possesses a region-wide data set from loblolly pine on cutover site-prepared lands that contains the same type of detailed stem quality information. The portion of the Coop regon-wide data set between ages 8 and 17 and covering the Coastal Plain of North Carolina, South Carolina and Georgia, and the Piedmont of North Carolina and South Carolina was used when comparing stem quality of unimproved versus improved stock plantations. The permanent plot observations from the improved stand data were not used in this phase of the study because comparable stem quality information was not available.

The distribution of defect by percent of trees in each defect class for unimproved and improved is given in Table 7. For the first 8 classes in Table 7

TABLE 7. Distribution of defect by percent of trees in each class for unimproved and improved stock.

	Percentage unimproved trees in class	Percentage improved trees in class
No defect	46.667	49.167
Disease	12.384	17.500
Bole sweep	19.468	5.49
Bole sweep, disease	4.679	1.324
Butt sweep	2.119	1.716
Butt sweep, disease	0.491	0.539
Short crook	5.317	13.088
Short crook, disease	1.481	3.529
Broken top	1.824	0.588
Broken top, disease	0.785	0.196
Broken top, bole sweep	0.777	0.049
Broken top, bole sweep, disease	0.262	0.147
Broken top, butt sweep	0.057	—
Broken top, butt sweep, disease	0.016	—
Broken top, short crook	0.344	0.049
Broken top, short crook, disease	0.123	0.049
Fork	1.481	2.990
Fork, disease	0.695	2.059
Fork, bole sweep	0.499	0.294
Fork, bole sweep, disease	0.090	0.490
Fork, butt sweep	0.049	—
Fork, butt sweep, disease	0.008	—
Fork, short crook	0.123	0.539
Fork, short crook, disease	0.065	0.490
Fork, broken top	0.098	—
Fork, broken top, disease	0.016	0.098
Fork, broken top, bole sweep	0.025	—
Fork, broken top, bole sweep, disease	0.025	0.049
Fork, broken top, butt sweep	0.016	—
Fork, broken top, butt sweep, disease	—	—
Fork, broken top, short crook	0.008	—
Fork, broken top, short crook, disease	0.008	—
	100.0	100.0
	12225 trees	2040 trees

(no defect; disease; bole sweep; bole sweep and disease; butt sweep; butt sweep and disease; short crook; and short crook and disease) a t-test of equality of proportion of unimproved and improved trees in each defect class was carried out. Other classes did not have enough observations to support testing. The test results are given in Table 8. Improved stands have a small, but significantly ($\alpha = 0.05$) higher proportion of stems in the defect classes of disease and short crook. Unimproved stands have a significantly higher proportion ($\alpha = 0.05$) of stems in the defect classes of bole sweep and bole sweep and disease. Proportion of stems with no defect is not significantly different between stands of unimproved and improved stock. While proportions differ statistically between improved and unimproved stands in four of the eight classes, stem quality does not appear to be substantially different between improved and unimproved trees in these samples. The eight defect classes tested, including no defect, account for 91 and 92% of the stems in unimproved and improved stands, respectively.

Stem Taper and Volume

Of interest are comparisons of stem taper and individual tree volume from stands of unimproved stock and stands of improved stock. The data used in this portion of the study are the same as that used in the investigation of stem quality. Gray's (1956) taper equation was used to examine the taper of trees from stands of improved stock relative to trees from stands of unimproved stock. The form of the equation is:

$$D_k^2 = a + bh_k + \epsilon \tag{9}$$

where

D_k = diameter at some height, h_k

a,b = coefficients to be estimated.

The coefficient, b, is essentially a parameter indicating the rate of change of D^2 up the bole. The following equation was fitted to the data from improved and unimproved stands:

$$D_k^2 = a_1X_1 + a_2X_2 + b_1Z_1 + b_2Z_2 + \epsilon \tag{10}$$

where

TABLE 8. Test for equality of class proportion between unimproved and improved trees in eight defect classes.

Defect class	Calculated t-value[1]
No defect	−1.24
Disease	−4.41*[2]
Bole sweep	11.68*
Bole sweep, disease	2.40*
Butt sweep	0.25
Butt sweep, disease	−0.03
Short crook	−5.81*
Short crook, disease	−1.42

[1] $t = \dfrac{\hat{P}_{\text{unimproved}} - \hat{P}_{\text{improved}}}{\sqrt{s^2_{\text{pooled}}}}$

[2] An asterisk indicates statistically significant difference at $\alpha = 0.05$.

$$X_1 = \begin{cases} 1 \text{ if improved stock,} \\ 0 \text{ otherwise;} \end{cases}$$
$$X_2 = \begin{cases} 1 \text{ if unimproved stock,} \\ 0 \text{ otherwise;} \end{cases}$$
$$Z_1 = \begin{cases} h_k \text{ if improved stock} \\ 0 \text{ otherwise;} \end{cases}$$
$$Z_2 = \begin{cases} h_k \text{ if unimproved stock,} \\ 0 \text{ otherwise.} \end{cases}$$

The null hypothesis for a statistical test of the equality of the rate of change of D^2 with respect to height up the bole for stems of improved stock vs. stems of unimproved stock can be stated symbolically as:

$$H_0\text{: } b_1 = b_2 \text{ from Equation (10).}$$

To test this hypothesis, the following equation was fitted to the data:

$$D^2 = a_1X_1 + a_2X_2 + bh + \epsilon \qquad (11)$$

where X_i is as defined in Equation (10) and b is a common slope. The F-ratio,

$$\left(\frac{SSE_{11} - SSE_{10}}{SSE_{11}}\right)\left(\frac{n_{10}}{n_{11} - n_{10}}\right),$$

where SSE_i = error sum of squares and n_i = error degrees of freedom, respectively, for Equation (i), was calculated and compared to the tabulated $F_{0.5}$ with $n_{11} - n_{10}$ and n_{10} degrees of freedom. The calculated F was 0.703, which was not significant at the 0.05 level. These results indicate that the rate of change of D^2 with respect to height, that is, the taper, is not different in the trees from the improved and unimproved plantations tested.

Differences in individual tree total volume between stems from stands of improved and unimproved stock. The following equation was fitted to the data from improved and unimproved plantations described above:

$$V = a_1X_1 + a_2X_2 + b_1Z_1 + b_2Z_2 + \epsilon \qquad (12)$$

where

$$X_1 = \begin{cases} 1 \text{ if improved stock,} \\ 0 \text{ otherwise;} \end{cases}$$
$$X_2 = \begin{cases} 1 \text{ if unimproved stock,} \\ 0 \text{ otherwise;} \end{cases}$$
$$Z_1 = \begin{cases} D^2H \text{ if improved stock,} \\ 0 \text{ otherwise;} \end{cases}$$
$$Z^2 = \begin{cases} D^2H \text{ if unimproved stock,} \\ 0 \text{ otherwise;} \end{cases}$$

V = Total volume outside bark;
D = Diameter at breast height;
H = Total height

The hypothesis of interest is whether these regressions are the same, that is, can the same individual tree volume equation be used for unimproved and improved stock? To test this hypothesis, the following equation was fitted to the data:

$$V = a + b\,D^2H + \epsilon. \qquad (13)$$

The F-ratio,

$$\left(\frac{SSE_{13} - SSE_{12}}{SSE_{13}}\right)\left(\frac{n_{12}}{n_{13} - n_{12}}\right),$$

where SSE_i = error sum of squares and n_i = error degrees of freedom, respectively, for Equation (i) was calculated. The same type of analysis was conducted for volume inside bark. The F-ratios (2.97 for inside bark; 2.99 for outside bark) indicate that the hypothesis of equal individual tree volume equations can be accepted at $\alpha = 0.05$.

Conclusions from this portion of the study are: (1) stem taper is not different in trees of improved and unimproved stock; and (2) the same stem volume may be expected from stems of the same diameter and height whether of improved or unimproved stock. These results corroborate those of Tankersley et al. (1983), who found that separate stem volume equations were not needed for improved and unimproved slash pine trees.

YIELD

Given that stem quality and volume do not appear to be practically different between the samples from the operationally planted stands with improved and unimproved stock, volume per acre for each plot was computed using a common tree volume equation. These yield values were then used to test the hypothesis that there is no difference between the yield equations for the improved and unimproved cases. The yield equation employed was that of Burkhart et al. (1985):

$$\ln(Y) = b_0 + b_1 (1/A) + b_2 \ln H_d + b_3 N + \epsilon \qquad (14)$$

where

Y = total cubic-foot volume (outside bark) per acre
A = plantation age, years
H_d = average height of dominant and codominant trees in feet
N = number of trees surviving at time of plot establishment

Dummy variables were defined, and methods analogous to those used to test for differences in the volume equations were employed. Testing the null hypothesis of equality of all parameters resulted in a F-ratio of 1.712 (4 and 53 degrees of freedom), which is not significant at the 0.05 level. Thus, it was concluded that a common yield equation, in which plantation age, height of dominants and codominants, and number of surviving trees are known, is sufficient for improved and unimproved stands. Unfortunately, adequate data for testing survival relationships were not available. But these results do indicate that a single growth and yield function should be adequate for improved and unimproved stands given that the values of the independent variables are correctly specified.

CONCLUSIONS

The major conclusions to be drawn from the work presented here are: (1) at the seed source and family levels, the shape of the height-diameter relationship at a given age is influenced by the site and initial density; (2) the level of the height-diameter relationship is affected by the seed source or family and is directly related to the dominant height of the seed source or family at that age; and (3) at the seed source and family levels the shape of the height-age curve is related to the site, but the level of the height-age curve is influenced by the seed source or family. A very important result of this work is the consistency of the results concerning the height-diameter and height-age relationships in the Southwide Pine Seed Source Study and the block-planted open-pollinated progeny test.

The sampled stands of unimproved stock had essentially the same proportion of stems showing no defect as did the sampled stands of improved stock. Stands of improved stock had a higher proportion of trees with some disease while stands of unimproved stock had a higher proportion of trees with some level of stem sweep or crook. Eight classes of defect (no defect; disease; bole sweep; bole sweep and disease; butt sweep; butt sweep and disease; short crook; and short crook and disease) accounted for 91 and 92% of the stems in the unimproved and improved stands, respectively. Defects were due primarily to poor planting practices, pine tipmoth, and fusiform rust.

Stem taper is not different in trees of improved and unimproved stock. The same total stem volume, on both an inside and outside bark basis, may be expected from stems of the same diameter and height whether of improved or unimproved stock.

Given that stem volume relationships are the same for improved and unimproved trees, and that height of dominant and codominant trees and number of surviving trees are known at the age of prediction, a single stand yield equation should suffice for improved and unimproved stands. The primary relationship that appears to be altered through genetic selection is the height-age (site index) curve. It is extremely important that appropriate site index values and height-age curves be specified when predictions for genetically improved stands are made. These results indicate that, if site index is appropriately specified and the appropriate height-age curve is used, existing growth and yield prediction methodology should give satisfactory results until more refined estimates, based on extensive data from improved stands, are developed. The hypotheses and results from this study should be tested through time and as data from studies designed to address these questions becomes available.

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