ADJUSTING SITE INDEX AND AGE TO ACCOUNT FOR GENETIC EFFECTS IN YIELD EQUATIONS FOR LOBLOLLY PINE

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Abstract—Nine combinations of site index curves and age adjustments methods were evaluated for incorporating genetic effects for open-pollinated loblolly pine (*Pinus taeda* L.) families. An explicit yield system consisting of dominant height, basal area, and merchantable green weight functions was used to compare the accuracy of predictions associated with type of adjustment. Site index was adjusted by including height-age curves developed for the check family, all improved families combined, and for specific families. Age was adjusted by using a variant of the Pienaar and Rheney (1995) function. Age adjustments included none, all improved families combined, and for specific families. The best results were obtained by using height-age curves for all improved families combined and a family-specific age adjustment function. These results suggest that adjusting either site index alone or age alone is not sufficient for predicting the yield of genetically improved loblolly pine families planted in single-family blocks.

INTRODUCTION

Despite the need for forest growth models that include genetic effects in loblolly pine (*Pinus taeda* L.), few such models have been developed. Data from seed source and progeny tests generally are not suitable for model development because the linear arrangement of families in rows does not represent competition in stands. In addition, the type and method of genetic selection has progressed rapidly from seed sources, half-sib open-pollinated families, full-sib controlled mass pollinated families, clones obtained through rooted cuttings, and finally clones obtained by somatic embryogenesis.

Generally, growth models with interrelated components have been used to account for genetic differences. Only one function may need to be modified in order to incorporate genetic differences in growth models with interrelated components, whereas several functions may need to be modified in growth models with unrelated component equations (Burkhart and Matney 1981). As a result, research has focused on incorporating genetic differences into height-age functions (Buford and Burkhart 1987, Cao and Durand 1991a, Knowe and Foster 1989, Knowe and others 1998, Nance and Wells 1981, Sprinz and others 1987) and height-diameter functions (Buford 1986, Buford and Burkhart 1987, Knowe and others 1998) because of their utility in expressing stand structure and dynamics in forest growth models. Models developed for eastern cottonwood (*Populus deltoides* L.) plantations have been developed to account for differences in stand basal area and volume (Cao and Durand 1991b) and diameter distributions (Knowe and others 1994).

Research involving large plots of similar genetic composition suggests that the basic growth relationships are similar among loblolly pine seed sources and families. Nance and Wells (1981) and Buford and Burkhart (1987) detected significant differences in site index but not the shape (slope) of height-age profiles. Buford and Burkhart (1987) and Buford (1986) reported similar results for height-diameter functions. Using more flexible models, differences in height growth patterns have been associated with loblolly pine seed sources (Sprinz and others 1989) and half-sib families (Knowe and Foster 1989).

An age adjustment approach (Pienaar and Rheney 1995) has been used to incorporate the effects of silvicultural treatments including fertilization, competition control, and soil tillage (bedding, disking, and subsoiling). This approach involves adding a treatment response function to a yield model for an untreated stand (eq. 1).

$$Y_T = Y_U + \varpi_1 A \exp\left\{\varpi_3 A\right\} \qquad (1)$$

where Y_T=yield of treated stand, Y_U=yield of untreated stand, and A=plantation age. The peaking function in equation 1 is sufficiently flexible to represent Types A, B, and C treatment responses. An advantage is that currently available models can be used to represent the yield with standard genetics and only the response function needs to be fit to data from non-standard seedlots. This approach is a departure from the traditional method of site index adjustment but may be useful in modeling genetic effects.

The purpose of this study was to examine the effects of different height-site index curves and age adjustments on basal area and merchantable green weight of open-pollinated loblolly pine families. This represents an extension of an earlier study based on a limited set of data (Knowe 2003). Several goodness-of-fit statistics for the models were compared. Height-site index curves were developed for a commercial check, all improved families combined, and for individual families. Observed height at age five was used to estimate site index and subsequently a predicted height at each measurement age. Predicted heights from the appropriate height-site index curve were substituted into basal area and stand merchantable green weight equations. The stand-level basal area and merchantable weight equations included no age adjustment, an age adjustment for all improved families combined, and family-specific age adjustments. Nine combinations of height-site index curves and age adjustments were examined.

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METHODS

Data

Data from three block-plot experiments involving open-pollinated families of loblolly pine were used to develop and compare models of genetic effects. These experiments included an open-pollinated progeny test established in 1969 near Bogalusa, LA, and two family mixing studies established in 1985 near Bogalusa and Saucier, MS (table 1). The open-pollinated progeny test was planted at 8 by 8 feet spacing, thinned at age 8, and measured at ages 10 and 15 years. The family mixing studies were planted at spacings of 6 by 6 feet and 6 by 3 feet and measured through age 10. All studies included the same unimproved Livingston Parish check lot and six improved open-pollinated families from Livingston and Washington Parishes, LA and southern MS. These families represent good, average, and poor performance relative to the Livingston Parish check lot. After combining the block-plot experiments, 659 observations were available for developing and comparing models of genetic effects.

Explicit Yield System for Loblolly Pine

Following the example of Cao and Durand (1991b), an explicit yield system was used to model genetic effects in open-pollinated families of loblolly pine. The yield system consists of a height-age-site index equation, an equation to predict basal area, and an equation to predict merchantable green weight.

An algebraic difference formulation used by Knowe and Foster (1989) was selected for the height-age-site index equation (equation 2).

$$H_2 = H_1\left\{\left[1-\exp(-\theta_1 A_2)\right]/\left[1-\exp(-\theta_1 A_1)\right]\right\}^{\theta_2} \qquad (2)$$

where A_1=current plantation age (years), A_2=projected plantation age (years), H_1=current dominant height (feet), and H_2=projected dominant height (feet). Dominant height is defined as the average height of the tallest 100 trees/acre. Desirable features of this equation are any base age for site index may be selected and each curve has an implied asymptote. Replacing H_2 with site index (SI) and A_2 with base age (25) produces an equation for predicting either dominant height or site index,

$$SI = H\left\{\left[1-\exp(-\theta_1 25)\right]/\left[1-\exp(-\theta_1 A)\right]\right\}^{\theta_2} \qquad (3)$$

$$SI = H\left\{\left[1-\exp(-\theta_1 25)\right]/\left[1-\exp(-\theta_1 A)\right]\right\}^{\theta_2} \qquad (4)$$

where A=plantation age (years), H=current dominant height (feet), and SI=site index (base age 25). Height and age pairs were arranged in non-overlapping growth series, resulting in 560 observations for developing height-age-site index curves.

Three sets of height-age-site index curves were developed: a Check SI set consisting of one equation for the unimproved check; an Overall SI set consisting of one equation for all improved families combined and one equation for the unimproved check; and a Family SI set consisting of six equations for individual improved families and one equation for the unimproved check. On each plot, observed height at age five was substituted into the appropriate set of equations to estimate site index, which in turn was used to predict heights at each measurement age.

Basal area was computed from the surviving trees on each plot at each measurement age and expressed on a per-acre basis. The following basal area prediction equation was selected to represent the unimproved check lot in this study.

$$SI = H\left\{\left[1-\exp(-\theta_1 25)\right]/\left[1-\exp(-\theta_1 A)\right]\right\}^{\theta_2} \qquad (5)$$

where BA=basal area (cubic feet per acre), N=number of surviving trees per acre, A_T=plantation age (years) at time of thinning, N_T=number of trees per acre removed by thinning, N_B=number of trees per acre before thinning, and other terms as previously defined. The model accounts for differences in intensity and timing of thinning. In addition, genetic effects on the height-age-site index curves can be evaluated because dominant height is included in the equation. The basal area prediction equation was fit to data from the unimproved check lot and combined with a variant of the Pienaar and Rheney (1995) age adjustment.

$$BA_{adj} = BA + \varpi_1 A^{\varpi_2}\exp\left\{\varpi_3 A\right\} \qquad (6)$$

where BA_{adj}=basal area with an overall or family-specific age adjustment, BA=basal area in equation 5, and other terms as previously defined. As with height-age-site index, three sets of age adjustments were considered in the basal area prediction equation: No adjustment, which consists of the basal area model fit to only the data for the unimproved check; Overall adjustment, which consists of one adjustment for all improved families combined; and Family adjustments, which consist of fitting six different values of ϖ_1 in equation 6 for specific improved families.

Outside-bark merchantable green weight was computed at each measurement age for trees with d.b.h. greater than 4.5 inches on each plot using the Baldwin and Feduccia (1987) variable top diameter equation. Pulpwood was computed to a 3-inch top diameter (outside bark) for trees with d.b.h. between 4.6 and 8.5 inches, inclusive. Green weight of chip-n-saw material was computed to a 6-inch top for trees with d.b.h. between 8.6 and 11.5 inches, inclusive. Sawtimber was computed to an 8-inch top for trees with d.b.h. greater than or equal to 11.6 inches; only the Bogalusa O.P. test had trees that were large enough to be considered sawtimber.

Merchantable green weight of all products on each measurement plot was combined and expressed as tons per acre. The following merchantable green weight prediction equation was selected to represent the unimproved check lot.

$$V = \beta_0 N^{\beta_{11}+\beta_{12}/A} H^{\beta_{21}+\beta_{22}/A}\exp\left\{A^{\beta_3} + \beta_4 \frac{A_T}{A}\frac{N_T}{N_B}\right\} \qquad (7)$$

V=merchantable green weight (tons, o.b.), and other terms as previously defined. As with the basal area prediction equation, the merchantable green weight model accounts for differences in intensity and timing of thinning and genetic effects on the height-age-site index curves can be incorporated. The merchantable green weight prediction equation in equation 7 was fit to data from the unimproved

Table 1—Summary of loblolly pine open-pollinated tests used to develop and compare models of genetic effects

Test location	Planting year	Planting spacing (feet)	Trees/ac (measurement plot trees)	Measurement ages and comments
Bogalusa O.P. test (5 replications)	1969	8x8	680 (49 trees)	Ages 1-8, 10, and 15; Thinned at 8
Bogalusa mixing (3 replications)	1985	6x6 and 6x3	1210 (40 trees)	Ages 2, 4, 5, 7, and 10
Harrison Exp. Forest mixing (2-3 replications)	1985	6x6 and 6x3	2420 (40 trees)	Ages 2, 4, 5, 7, and 10

check lot and combined with a variant of the Pienaar and Rheney (1995) age adjustment.

$$V_{adj} = V + \omega_1 A^{\omega_2} \exp\{\omega_3 A\} \qquad (8)$$

where V_{adj}=merchantable green weight with an overall or family-specific age adjustment, V=merchantable green weight in equation 7, and other terms as previously defined. As with height-age-site index, three sets of age adjustments were considered in the merchantable green weight prediction equation: No adjustment, which consists of the merchantable green weight model fit to only the data for the unimproved check; Overall adjustment, which consists of one adjustment for all improved families combined; and Family adjustments, which consist of fitting six different values of ω_1 in equation 6 for specific improved families.

Comparisons

In all, nine possible combinations of three height-age-site index and three age adjustments were evaluated (table 2) and goodness-of-fit statistics were compared. Bias (mean predicted/mean observed), fit index, average deviation, absolute deviation, and error mean square (MSE) of the basal area and merchantable green weight prediction equations were compared for each combination of height-age-site index curve and age adjustment. For bias and fit index, values closer to 1.0 were considered to be best. For average deviation, absolute deviation, and MSE, smaller values were considered better than larger values.

RESULTS AND DISCUSSION

Goodness-of-fit statistics for the basal area prediction equation (equation 6) with height-age-site index and age adjustments to account for genetic effects are compared in table 3.With few exceptions; the differences in fit statistics among methods are small. This suggests that genetic effects are either unimportant or that none of the modeling approaches were particularly effective in predicting differences in yield for open-pollinated families of loblolly pine. Using the height-age-site index curve for the unimproved check lot in combination with the overall age adjustment resulted in the least bias and smallest mean deviation in predicted basal area. The highest fit index, smallest absolute deviation, and smallest MSE was obtained by using the height-age-site index curve for overall improved families in combination with family-specific age adjustments. Using the height-age-site index curve for the unimproved check lot in combination with the family-specific age adjustments resulted in fit statistics that were consistently among the best for predicted basal area. In contrast, using the family-specific height-age-site index curves in combination with no age adjustment resulted in fit statistics that were consistently among the worst. This result is cause for some concern because this approach has been frequently used to account for genetic effects in yield models for loblolly pine (Buford and Burkhart 1987, Knowe and Foster 1989, Nance and Wells 1981, Sprinz and others 1987).

Goodness-of-fit statistics for the merchantable green weight prediction equation (equation 6) with height-age-site index and age adjustments to account for genetic effects are compared in table 4. As with basal area, the differences in fit statistics among methods are small. Using the height-age-site index curve for the unimproved check lot in combination with the overall age adjustment resulted in the least bias and smallest mean deviation in predicted merchantable green weight. The highest fit index, smallest absolute deviation, and smallest MSE was obtained by using the family-specific height-age-site index curves in combination with family-specific age adjustments. Using the height-age-site index curve for overall improved families in combination with the family-specific age adjustments resulted in fit statistics that were consistently among the best for predicted merchantable green weight. However, using the height-age-site index curve for overall improved families in combination with no age adjustment resulted in fit statistics that were consistently among the worst. As with predicted basal area, using the family-specific height-age-site index curves in combination with no age adjustment for merchantable green weight resulted in fit statistics that were consistently among the worst.

Table 2—Nine possible combinations of height-age-site index curves and age adjustments that were considered for incorporating genetic effects into basal area and merchantable green weight prediction equations for open-pollinated families of loblolly pine

	Height-Age-Site Index Curve		
Age Adjustment	Check	Overall	Family
No Adjustment	Check SI No Adj	Overall SI No Adj	Family SI No Adj
Overall Adjustment	Check SI Overall Adj	Overall SI Overall Adj	Family SI Overall Adj
Family Adjustment	Check SI Family Adj	Overall SI Family Adj	Family SI Family Adj

Table 3—Goodness-of-fit statistics for basal area equations using various combinations of site index curves and age adjustments to account for genetic effects represented by open pollinated families of loblolly pine. Statistics include bias, fit index, mean deviation (Dev), mean absolute deviation (Dev), and mean squared error (MSE)

Height-site index curve	Age adjustment	Bias	Fit index	Dev	Dev	MSE
Check	No adjustment	0.9883	0.8858	0.5886	11.0734	228.0427
	Overall adjustment	0.9958	0.8875	0.2099	11.0251	224.7512
	Family adjustment	0.9949	0.8901	0.2565	10.8397	219.4458
Overall	No adjustment	0.9874	0.8865	0.6365	11.0506	226.7683
	Overall adjustment	0.9927	0.8875	0.3652	11.0252	224.7740
	Family adjustment	0.9928	0.8903	0.3645	10.8351	219.1271
Family	No adjustment	0.9876	0.8852	0.6218	11.1131	229.3619
	Overall adjustment	0.9930	0.8861	0.3548	11.0877	227.4295
	Family adjustment	0.9930	0.8899	0.3539	10.8514	219.9447

Table 4—Goodness-of-fit statistics for merchantable green weight equations using various combinations of site index curves and age adjustments to account for genetic effects represented by open pollinated families of loblolly pine. Statistics include bias, fit index, mean deviation (Dev), mean absolute deviation (Dev), and mean squared error (MSE)

Height-site index curve	Age adjustment	Bias	Fit index	Dev	Dev	MSE
Check	No adjustment	0.9699	0.9118	0.4121	4.1457	57.0041
	Overall adjustment	1.0029	0.9137	-0.0396	4.1721	55.7926
	Family adjustment	0.9867	0.9178	0.1822	4.0019	53.0997
Overall	No adjustment	0.9687	0.9108	0.4285	4.1522	57.6335
	Overall adjustment	0.9895	0.9143	0.1436	4.0847	55.3786
	Family adjustment	0.9900	0.9182	0.1368	3.9936	52.8857
Family	No adjustment	0.9691	0.9116	0.4228	4.1423	57.1326
	Overall adjustment	0.9897	0.9150	0.1407	4.0674	54.9202
	Family adjustment	0.9900	0.9182	0.1362	3.9912	52.8618

CONCLUSIONS

For this level of genetic improvement (open-pollinated half-sib families), age adjustments were more effective than using height-age-site index curves to account for differences in yield among families. Fitting age adjustments for individual improved families was slightly better than fitting an overall adjustment for all improved families, and both age adjustments were better than no adjustment. Compared to the height-age curve fit to the unimproved check lot, using height-age-site index curves fit to all improved families combined or to individual improved families resulted in only slight improvements in many of the measures of fit. All three sets of height-age curves resulted in similar fit statistics for both basal area and merchantable green weight. Furthermore, the family specific height-age-site index curves resulted in fit statistics that were consistently among the worst.

Based on these results for open-pollinated families of loblolly pine, a height-age-site index curve for overall improved families should be combined with either overall or family-specific-age adjustments. Refinements in the prediction equations, specifically in the expression for thinning, may improve the fit statistics. The open-pollinated families used in this study represent a wide spectrum of performance, with yields ranging from lower to higher than the unimproved check lot. More detailed examination of these models among individual families is planned.

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