addition of correlated errors, using PROC MIXED, also accounted for the apparent small-scale microsite variation. This led to the best description of our data. This model resulted in an error term that allowed us to detect significant differences among soil-moisture classes. Analysis including spatial autocorrelations, may be helpful for other examples with complicated spatial structure. When using common garden studies for provenance testing, information on the row and column position of each experimental unit should be recorded in order to make trend analysis and the inclusion of correlated errors possible.

PROC MIXED is also more versatile than PROC GLM for including several random factors. This can be particularly relevant in nested models. However, we wish to point out two drawbacks to PROC MIXED. First, running PROC MIXED can be very time consuming. Some of our programs took up to 45 minutes of CPU time to run (Hewlett Packard mainframe computer HP9000/H50, 128 Mb memory). The use of a grid of values for the PARMS statement and the use of the DDFM=SATTERTH option tend to be very time consuming. When appropriate, we found it useful for saving CPU time to provide single starting values instead of a grid of values for the PARMS statement (although a grid was sometimes necessary to avoid achieving a local maximum). In addition, it may be useful to omit the DDFM=SATTERTH option whenever it is not necessary (for example, when screening models or for reduced models). Second, we felt that the PROC MIXED release version 6.12 is somewhat cumbersome in that it does not automatically provide the likelihood ratio statistic for testing estimated variance components and spatial autocorrelation. Such tests required further runs with reduced models. Despite these concerns, PROC MIXED is strongly recommended for the types of analysis we considered.

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Interactions of Genotype with Site for Height and Stem Straightness in *Pinus taeda* in Zimbabwe

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Summary

The magnitude and importance of genotype x environment interactions (GXE) for stem height and straightness at 2, 10, 14 and 23 years of age were estimated for *Pinus taeda* L. planted at four sites in Zimbabwe. Genetic correlations between heights at different sites varied from low to high (0.18 to 0.95). They were not consistent across the different ages, but were generally high between all sites at younger ages and progressively diminished with age. These results suggest that early growth assessments may not be reliable for predicting GXE at maturity. Genetic correlations between stem straightness scores at different sites also varied from low to high (-0.13 to 0.95); those between sites A and C, and between sites B and D, were consistently high (>0.84) at ages greater than 2 years.

On the basis of the magnitude of genetic correlations, site B was generally the best selection site for height. At 23 years,

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there was no single best selection site for height. There did not appear to be any single environmental factor that influenced GXE for height, making it difficult to classify environments. Since GXE interactions were unpredictable for height, the value of the multiple population breeding strategy adopted for *P. taeda* in Zimbabwe may not be high. Genetic correlations for straightness were high between sites A and C and between sites B and D, suggesting similarity within these two pairs of sites.

On the basis of correlations between breeding values and weighted aggregate genetic merit, site A was the best single site for selection to improve the average performance across all four sites. Consequently, a single breeding population could be established at site A.

Key words: Genotype x environment interactions, genetic correlation, height, stem straightness, *Pinus taeda*.

Introduction

The presence of genotype x environment interactions complicates tree breeding programmes and may reduce the rate of genetic progress by selection. Heterogeneity between forest sites, due to variation in soil and/or climatic conditions, may cause genotype x environment interactions (GXE). The magnitude of the GXE affects decisions on testing, selection and deployment. At the species level, GXE is used in matching species to sites; at the family or individual level, it influences major elements of the breeding strategy such as the structure of the breeding population, and the selection of parents in the breeding population.

GXE may be due to heterogeneity of variances measured at each of the sites, where ranking of genotypes in the various environments is unaffected or due to both heterogeneity of variances and rank changes (DICKERSON, 1962). Only the latter will significantly influence any breeding strategy.

The method most used by tree breeders for determining the magnitude of GXE and implications for gain treat a trait measured on two environments as analogous to two traits in a single environment. Genetic correlation across environments for a trait measured in two environments then provides a measure of the magnitude of GXE. Genetic correlations that do not differ significantly from unity suggest there is no GXE, while genetic correlations significantly less than 1 indicate the presence of GXE. This approach to detect the presence of GXE, first introduced in forestry by BURDON (1977), and referred to as "Type B correlations", has subsequently been widely used in tree breeding (e.g. CARSON, 1991; MATHESON and RAYMOND, 1984; JOHNSON, 1992; JOHNSON and BURDON, 1990; PSWARAYI *et al.*, 1997). The estimation of Type B correlations provides a means of determining the loss (or improvement) of potential gain in one environment from selection at another, using the method of indirect selection proposed by FALCONER (1989). It appears that many recent GXE studies in forestry have followed this approach, and examined the magnitude of genetic correlations and efficiency of selection across different sites when the trait has been assessed at the same age across sites.

When GXE is present, and considered important, the options – other than simply ignoring it – are to group environments, or to group genotypes (RAYMOND and LINDGREN, 1990). Ignoring GXE will result in the least direct cost, but may result in the largest losses in gain. The next option implies a multiple population or sub-line breeding strategy, where environments are grouped to those within which GXE is minimised. While this option will result in the largest gain in the short term, it is likely to be the most expensive, as sites will need to be classified to determine regions of minimum GXE, and more than one breeding population will need to be managed. The third option implies elimination of the most interactive families, and is likely to be less expensive than the first. However, some of the most productive families on average across all sites may be the most interactive, and their elimination may impact adversely on gain.

Most studies carried out in forest tree species report that, whilst there is often statistically significant GXE, it is not of practical significance (e.g. CARSON, 1991; JOHNSON, 1992; JOHNSON and BURDON, 1990; OWINO, 1977; PSWARAYI *et al.*, 1997). Such studies considered GXE to be of no practical significance when the genetic correlations were high, and hence the potential loss of gain from selecting at one site for planting at another was low (e.g. PSWARAYI *et al.*, 1997), or GXE to be due to heterogeneity of variances across sites (e.g. OWINO, 1977).

Pinus taeda is an important forest plantation species in Zimbabwe, where it has been established for industrial wood (principally sawlog) production. The environments in which *P. taeda* in Zimbabwe grows vary greatly in terms of rainfall and altitude; Zimbabwe is implementing a multiple population breeding strategy (MPBS) in *P. taeda*, largely to take advantage of GXE by selecting for specific adaptations (BARNES, 1989). However, this strategy was based primarily on the results from *P. patula* genetic tests, and GXE interactions in *P. taeda* in Zimbabwe have not been quantified; consequently, the MPBS's applicability to *P. taeda* is unknown. For the related species, *P. elliottii*, in Zimbabwe, PSWARAYI *et al.* (1997) concluded that GXE was not of sufficient practical significance to warrant sub-dividing the population. Using the same data set as that on which this paper is based, GWAZE *et al.* (1997) found that pooling data across sites reduced heritability estimates to less than those obtained at each of the individual sites, indicating the possible presence of GXE. There is clearly a need to quantify the magnitude of GXE, to assist in making informed decisions on the breeding strategy for *P. taeda* in Zimbabwe.

Genetic tests of *P. taeda* in Zimbabwe were established across a range of sites, representing the diverse plantation environments. The results should indicate whether or not breeding populations should be sub-divided; and, if so, which parents should be included in each of the sub-populations, and whether it is appropriate to use the same genetic parameters across sites.

The objective of this study is to evaluate the magnitude of GXE for stem height and straightness across four sites for *P. taeda* in Zimbabwe, and consider its implications for breeding strategy.

Materials and Methods

Data

Genetic material, the field tests and assessment procedures were described fully by GWAZE *et al.* (1997). Briefly, the genetic material comprised of 140 full-sib families that originated from an incomplete factorial mating design involving 8 male and 15 female parents. The 23 parents were selected phenotypically from unimproved plantations in Zimbabwe and South Africa.

These families were planted in genetic tests located at 4 sites in Zimbabwe (*Table 1*), which differed mainly in altitude and rainfall. Twenty-two of the 23 parents, and 86 of the 140 families, were represented at all sites. Two tests were established at low altitude sites, Tarka (A) and Martin (C) in the Chimanimani area of Zimbabwe, and two were established at high altitude sites, Stapleford (B) and Nyangui (D). Three of the sites had high rainfall (1836 mm to 2364 mm per annum), while Martin had low rainfall (1016 mm). Any GXE reported here may reflect the differential responses of families to different altitudes or rainfall.

Table 1. – Details of the genetic tests.

Site	Tarka (A)	Stapleford (B)	Martin (C)	Nyangui (D)
Region	Chimanimani	Penalonga	Chimanimani	Nyanga
Latitude	19°59'S	18°44'S	19°59'S	17°58'S
Longitude	32°56'E	32°49'E	32°56'E	32°47'E
Altitude (m)	1005	1745	1250	1882
Rainfall (mm)	2156	1836	1016	2364
Soils	Dolerite/alluvial -derived; reddish brown clays; well drained	Dolerite-derived; brown red clays; well drained	Dolerite/siltstones- derived; reddish brown clays; well drained	Dolerite-derived; red-reddish brown clays; well drained

Trees were planted at 2.4 m x 2.4 m spacing, and each plot comprised ten trees. The tests comprised three replicates and ten to twelve blocks per replicate, in a triple lattice design. Tests were assessed for height and stem straightness at 1.5, 9.5, 13.5 and 22.5 years of age, referred in this paper as 2, 10, 14 and 23 years of age, respectively. Height was assessed using height poles at 2 years and thereafter height instruments, and stem straightness was assessed visually using the 7-point absolute scale (1 = crooked to 7 = very straight) described by BARRETT and MULLIN (1968). One team assessed height and straightness at sites A and C, and another team assessed both traits at sites B and D at all ages. At 10 years, only one replication was assessed at Stapleford (B).

Statistical analyses

To test the significance of GXE effects data pooled across the four sites were analysed using general linear model (GLM) procedure of SAS® (1985), with the model used accounting for the random effects of site, replication, female, male and their interactions. Genetic parameters were estimated using the individual tree model ASREML (GILMOUR, 1996). Unlike SAS, ASREML allows the pedigree information to be incorporated in the genetic analyses. Individual-tree heritabilities and their standard errors were estimated using a univariate model, and genetic correlations and their standard errors were estimated using a bivariate individual tree model on block-adjusted data. The general linear model was:

$$Y_{ijkl} = \mu + S_i + R_{ij} + FM_{ijk} + A_l + e_{ijkl} \qquad (1)$$

Where:

Y_{ijkl} = is the observation on the lth tree in the ith site in the jth replication and in the kth family,

μ = overall test mean,

S_i = fixed effect of the ith site,

R_j = fixed effect of the jth replication,

FMijk = random effect of the kth family, in the ith site and in the jth replication,

Al = additive genetic effect of the lth tree, and

e_{ijkl} = residual term.

In the case of the bivariate analyses, the traits were assessed on different, but genetically related, trees across sites. For these analyses, therefore, genetic covariances exist between any two traits, but there are no environmental covariances.

Rank changes

The analysis of rank changes as an indicator of GXE followed the approach developed by MATHESON and RAYMOND (1984), but used breeding values rather than phenotypic values as they did. In order to identify the parents which were most highly interactive (i.e. least stable) across sites, each of the 22 parents common to all sites was ranked on its breeding value for each trait at each site, and on its average over all sites. The absolute deviation of the ranking at each site from the overall ranking over all sites was calculated, and these were summed across the 4 sites. The mean rank deviation was calculated by dividing the total deviations by 4. The parents with the greatest mean rank deviations were considered most interactive.

Index values

In order to make decisions on the best selection site at maturity, index values were calculated to estimate the aggregate genetic merit of the 22 parents at 23 years of age. The breeding values for each trait at each of the four sites estimated by ASREML univariate analyses were combined into appropriate index values. Each breeding value was weighted by the degree of importance. Here, the degree of importance was assumed to correspond to the extent to which the genetic test sites were representative of operational plantation areas. Since 80% of the plantations are found equally on sites similar to A and C, and very few plantations on sites similar to B (15%) and D (5%), the weights for tests A, B, C, D were assigned as 0.4:0.15:0.4:0.05, and the aggregate genetic merit (I) was determined by:

$$I = 0.4^{*}BV_{\text{site A}} + 0.15^{*}BV_{\text{site B}} + 0.4^{*}BV_{\text{site C}} + 0.05^{*}BV_{\text{site D}} \qquad (2)$$

Results

Analyses of variance

Site x female and site x male interactions for both height and straightness were highly significant, except straightness at 2 years (*Table 2*), indicating the presence additive genetic x environment interactions. Site x female x male interactions were highly significant at all ages in height, but were not significant in straightness at older ages. This indicates that dominance genetic x environmental interactions may be less important in straightness at older ages.

Means and heritability estimates

Height growth and stem straightness varied across sites, and there was no site at which performance was consistently superior across all ages assessed (*Table 3*). The heritability estimates for height ranged from 0.14 to 0.59, except for an unusually high estimate at site A at 10 years. Those for straightness generally ranged from 0.01 to 0.33, except for an unusually high estimate at site C at 23 years of age.

Genetic correlations

Genetic correlations (r_g) between heights assessed at the same age across sites were high at 2 years (0.77 to 0.95), and moderately high at 10 and 14 years (0.62-0.95) (*Table 4*). At 23 years, the r_g values between sites A and B and between sites D and B were high, at 0.90 and 0.73, respectively. The r_g between site A and D was low (0.18), indicating considerable family x

Table 2. – Mean squares for height and stem straightness from GLM analyses.

Trait	Source^{+}	df	2 yrs	df	10 yrs	df	14 yrs	df	23 yrs
HT	S	3	79.1	3	1588.4	3	1632.7	3	168.4
	R(S)	8	6.6	8	44.7	8	29.9	8	53.7
	F	20	1.9	20	44.7	20	87.0	20	9.8
	M	8	5.7	8	156.3	8	280.7	8	41.2
	FxM	112	0.3	112	5.9	112	12.3	112	3.9
	SxF	59	0.3	59	9.0	59	12.6	59	5.3
	SxM	18	0.5	18	12.3	18	15.1	18	4.3
	SxFxM	240	0.2	240	3.0	240	6.3	240	2.6
	Residual	13019	0.06	5967	1.9	5326	4.4	1978	2.5
ST	S	3	78.2	3	312.5	3	203.0	3	473.5
	R(S)	8	12.9	8	2.3	8	14.7	8	5.3
	F	20	1.4	20	5.9	20	5.4	20	2.8
	M	8	1.0**	8	3.9	8	5.0	8	1.6
	FxM	112	0.6	112	1.0	112	0.8*	112	0.5
	SxF	59	1.0	59	1.6	59	2.5	59	0.9
	SxM	18	0.5ns	18	3.2	18	4.7	18	1.3*
	SxFxM	240	0.6	240	0.6	240	0.7ns	240	0.4ns
	Residual	13019	0.3	5967	0.4	5326	0.6	1978	0.3

$^{+}$S = site, R = rep, F = female, M = male

All effects were significant at $P < 0.001$, except ** = significant at $P < 0.01$, except * = significant at $P < 0.05$, and ns = not significant.

Table 3. – Overall means (standard deviation) and heritability estimates (standard error) for height and straightness at four sites and four ages.

Age (years)	Site	Height (m)		Straightness (score)	
		Mean (SD)	h^2 (SE)	Mean (SD)	h^2 (SE)
2	A	0.997 (0.255)	0.23 (0.08)	4.00 (0.600)	0.02 (0.02)
	B	1.13 (0.291)	0.32 (0.09)	3.85 (.484)	0.01 (0.02)
	C	1.01 (0.296)	0.35 (0.12)	3.95 (0.540)	0.08 (0.03)
	D	0.704 (0.227)	0.14 (0.05)	3.59 (0.755)	0.02 (0.02)
10	A	14.7 (1.60)	0.73 (0.27)	4.51 (0.682)	0.25 (0.08)
	B	12.1 (1.68)	0.41 (0.14)	4.64 (0.866)	0.22 (0.17)
	C	14.8 (1.73)	0.59 (0.12)	4.42 (0.640)	0.16 (0.14)
	D	13.2 (1.50)	0.39 (0.13)	4.49 (0.740)	0.18 (0.08)
14	A	19.4 (2.68)	0.24 (0.08)	3.91 (0.678)	0.16 (0.05)
	B	17.2 (2.37)	0.32 (0.11)	3.54 (0.746)	0.18 (0.07)
	C	19.9 (2.01)	0.49 (0.13)	4.68 (1.04)	0.27 (0.15)
	D	19.1 (2.01)	0.23 (0.11)	4.17 (0.800)	0.23 (0.12)
23	A	22.5 (1.92)	0.42 (0.16)	4.27 (0.645)	0.16 (0.13)
	B	24.2 (2.00)	0.26 (0.11)	6.66 (0.513)	0.33 (0.12)
	C	24.5 (1.42)	0.39 (0.19)	4.75 (0.693)	0.83 (0.19)
	D	25.1 (1.49)	0.40 (0.13)	5.89 (0.764)	0.32 (0.11)

site interactions. The correlations between other pairs of sites at age 23 were moderate (0.51 to 0.58), indicating likely significant parental rank changes. Although the best site for selection varied with age, site B generally had the highest average genetic correlations with the other sites, suggesting that it would be the preferred site for selection for height.

Genetic correlations between stem straightness scores were high at 2 years, except those involving site D, which were highly negative (*Table 4*). At ages 10, 14 and 23 years, genetic correlations between straightness scores were low, except for those between sites A and C, and sites B and D. This result appears to be associated with altitude: sites A and C are at low altitude, and sites B and D are at high altitude. It was not possible to identify single preferred site for selection for straightness, but – as discussed above – performance at sites A and C, and sites B and D, appeared related. The average genetic correlations across all sites (e.g. 0.15 for stem straightness and 0.86 for height at 2 years) suggested that stem straightness was more sensitive to environmental variation than height, particularly at younger ages.

Parental rank changes

Parental rank values were calculated for height and straightness only at 23 years, as the genetic correlations between sites were particularly low at this age, indicating considerable genotype x environment interactions (results not presented; available from senior author). Rank changes for height and straightness were large (mean rank deviation > 5) for six parents, suggesting large parent x site interactions. Although the most interactive parents were of average or poor performance across all sites, a few were of superior performance across all sites.

Index values

When breeding values for height and straightness at the individual sites were not weighted according to the relative importance of sites, the highest correlation with the aggregate genetic merit was with site B (*Table 5*), indicating it would be preferred for selection. When the breeding values were weighted according to importance of the sites, genetic correlations suggest that it is best to select at sites where most of the plantations are located – with site A being the best for selecting height and site C the best for selecting straightness. Although some of the correlations between individual site breeding values and the aggregate breeding values were low, all individual site heritability estimates were higher than those estimated across all four sites (pooled $h^2 = 0.24$ for height and 0.22 for straightness).

Discussion

In investigating GXE and its consequences, it is important to ascertain whether GXE is due to heterogeneity of variances across sites or to rank changes of the genotypes (DICKERSON, 1962). In this study, both the additive variance and heritability estimates varied across sites (GWAZE *et al.*, 1997), and genetic correlations across sites for height at 23 years were low, indicating rank changes of the genotypes. Furthermore, rank changes in breeding values were observed in both traits at 23 years of age. Therefore, the GXE observed in this study was due to both the heterogeneity of variances across sites and rank changes of genotypes across sites.

Table 4. – Estimates of genetic correlations for height and stem straightness at four ages across four sites. Standard errors are in parenthesis.

Age (years)	Site	Height A	Height B	Height C	Straightness A	Straightness B	Straightness C
2	B	0.9			0.86		
		(0.09)			(0.46)		
	C	0.95*	0.95*		0.95*	0.94	
		(0.13)	(0.08)		(0.23)	(0.24)	
	D	0.88	0.77	0.78	-0.81	-0.95*	-0.82
		(0.10)	(0.13)	(0.14)	(0.55)	(1.00)	(0.44)
10	B	0.89			0.35		
		(0.10)			(0.29)		
	C	0.90	0.94		0.91	0.41	
		(0.05)	(0.10)		(0.08)	(0.30)	
	D	0.66	0.95*	0.73	-0.11	0.87	0.14
		(0.15)	(0.09)	(0.13)	(0.28)	(0.17)	(0.29)
14	B	0.64			-0.25		
		(0.17)			(0.28)		
	C	0.79	0.65		0.88	0.05	
		(0.11)	(0.16)		(0.10)	(0.29)	
	D	0.62	0.77	0.72	-0.24	0.95*	0.04
		(0.21)	(0.14)	(0.16)	(0.26)	(0.05)	(0.27)
23	B	0.90			0.66		
		(0.15)			(0.30)		
	C	0.51	0.58		0.84	0.44	
		(0.25)	(0.25)		(0.19)	(0.23)	
	D	0.18	0.73	0.52	0.06	0.95*	0.22
		(0.28)	(0.17)	(0.24)	(0.38)	(0.11)	(0.29)

*) Constrained by the program to 0.95.

Table 5. – Estimates of correlations of breeding values for height and stem straightness at each site without (r_A) and with weighting (r_A*) at 23 years

Trait	Site	r_A	r_A*
Height	A	0.70	0.88
	B	0.90	0.69
	C	0.59	0.74
	D	0.71	0.43
Stem Straightness	A	0.57	0.75
	B	0.83	0.43
	C	0.58	0.95
	D	0.74	0.24

For height, GXE was more pronounced as the trees aged. Genetic correlations were high at 2 and 10 years, indicating that if selections are made at one site there will be little loss in potential genetic progress at the other site. However, when selections were made at later ages the genetic correlations were low to moderate, indicating that there were significant rank changes between sites. Therefore, achieving maximum gain for a specific site would require that selection be conducted in tests planted at that site.

Because of the long rotation periods of forest tree species, results and conclusions regarding GXE are usually drawn from tests evaluated at a young age. For example, PSWARAYI *et al.* (1997) found across site genetic correlations in *P. elliottii* assessed up to 15 years in Zimbabwe to be higher than 0.8, indicating little GXE. Similarly, studies of GXE in *P. radiata*, based on tests assessed up to 12 years, found GXE not to be of practical importance (JOHNSON, 1992; MATHESON and RAYMOND, 1984; JOHNSON and BURDON, 1990). These conclusions are supported by our results up to 10 years, and to a lesser extent by those at 14 years. In contrast, results at 23 years indicate that, while GXE in this population was small at young ages, it was large at mature ages. Therefore, early growth assessments may not be reliable for assessing GXE at maturity. This implies a critical need to evaluate GXE at mature ages in forest trees. It is therefore important to verify, for the other species where inferences about GXE are based on early growth assessments, the trend in GXE over time to maturity.

Genetic correlations for stem straightness at the same age across sites were high between sites A and C, and between sites B and D. If straightness is the main selection criterion, sites A and C could form one breeding population and sites B and D another. However, the interpretation of these results is complicated because one team assessed sites A and C, and another assessed sites B and D. Although the assessment scale used is meant to be invariant across sites, it remains possible that differences of interpretation by the two assessment teams could confound these results, resulting in GXE effects in this study being inflated by different assessment criteria.

These results also suggest that strong influence of altitude on performance at the species level, which has been used to match tree species to environments in Zimbabwe, may not be applied at a population within species level. Sites A and C are low altitude sites, less than 5 km apart, while sites B and D were high altitude sites, more than 100 km from both sites A and C; nevertheless, the genetic correlation for height at 23 years between sites A and B was 0.90 while that between sites A and C was 0.51 (*Table 4*). Assuming it is not a Type II error, this result complicates breeding and deployment strategies, as there is no apparent environmental factor that explains this result.

The use of index values was helpful in determining the most appropriate site for selection after assigning weights to performance at each site. The use of genetic correlations did not offer clear guidance on the best selection site for height, particularly at maturity, and the index approach offered an alternative to optimal site selection.

Implications for breeding P. taeda in Zimbabwe

The multiple-population breeding strategy is being used in *P. taeda* in Zimbabwe, due in part to the possibility of utilizing GXE. However, there were no apparent consistent patterns of genotype response to environment in this study, implying that the value of the multiple population breeding strategy for *P. taeda* in Zimbabwe is probably not high.

The index values indicate that it is best to select at sites where most of the plantations are located (i.e. sites A & C), and that selections for height should be made at site A while that for straightness at site C. Given that height is a more important selection criteria than straightness in the Zimbabwe breeding program, a single breeding population may be established, tested and selected at sites similar to A. This strategy will not significantly affect selections for straightness, since selections made at site A predicted fairly well performance of straightness at site C. Since results of a single test are likely to overestimate gain across a region, as it ignores possible GXE, tests established should be replicated within the region represented by site A. Nursery period in *P. taeda* varies with altitude, being shorter at low altitudes, and therefore locating the nursery and genetic tests at site A, which is the lowest in elevation, should result in savings both in nursery and transport costs.

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Analyzing Parameters of Growth and Yield Models for Chinese Fir Provenances with a Linear Mixed Model Approach

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Abstract

Chinese fir is the preferred species for tree farm plantations in south Asia. Height growth and basal-area growth models were used to test the growth performance of Chinese fir originating from 26 provenances grown on two separate plantations in southern China. Parameters of the height growth and the basal-area growth models were statistically tested by way of a linear mixed-effects model approach in order to identify the growth parameters that are influenced by site and provenance. For the stand height growth model, it was found trees originating from the 26 provenances have different site indices when planted at similar sites. However, the slope coefficient was similar across provenances. Similarly for the basal-area growth model, the model intercept and the density-age related parameter showed no significant differences among provenances. No conclusive inference could be drawn concerning the site index-related parameter in the basal-area growth model.

Key words: basal area, Chinese fir provenances, growth and yield models, height, mixed-model approach, plantation, statistics.

Introduction

Chinese fir (*Cunninghamia lanceolata*) is a fast growing species that produces high quality lumber and attractive revenues up to 30 years. First commercial thinning can be done at about 8 years to 10 years following planting. As a result, Chinese fir constitutes one of the main commercial tree species in south Asia. As part of tree improvement research, many experimental plantations have been established in the past 20 years, with seed originating from many different geographic regions (BUFORD, 1986; MONTENEGRO *et al.*, 1997; YING, 1997). Growth and yield models are commonly used to evaluate growth performance. Parameters used in such models are normally site specific in nature. As a rule, these growth models need re-calibration (model parameter re-estimation) every time they are applied to new provenances or sites.

In theory, it is possible to design a growth and yield model to estimate stand growth for a single-species plantation. In designing such a model, efforts are required to determine which parameters in the growth and yield models are sensitive to provenance and site conditions, and which are not so sensitive.

Adequate testing of growth and yield models requires that repeated measurements be taken over many years. For data-

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