Genetics of Growth and Quality Characteristics of Eucalyptus camaldulensis Dehnh.

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Abstract

Genetic parameters were estimated for 10 growth and quality characteristics of *Eucalyptus camaldulensis* grown at two sites within the Northern Guinea Savanna Zone of Nigeria. The characteristics are tree height, diameter at breast height, number of forks, first fork height, number of stems/fork, stem form, branch diameter, branch angle, number of branches and taper. Phenotypic variance was higher than its corresponding genetic variance. Tree height had the greatest genetic component and the highest phenotypic and provenance coefficients of variation while taper had the least values. High phenotypic coefficient of variation was associated with high provenance coefficient of variation.

High provenance heritability estimates ranging from 0.667 for taper to 0.946 for height were recorded for the characteristics. However, high heritability was not generally associated with high provenance coefficient of variation. Expected genetic advance obtained ranged from 7.14% for taper to 58.14% for number of forks. High heritability was not generally associated with high genetic advance.

Key words: Eucalyptus camaldulensis, provenances, growth rate, forking characteristics, branching characteristics, taper, phenotypic coefficient of variation, provenance coefficient of variation, heritability, genetic advance.

Introduction

The tree species that naturally occur in the Savanna region of Nigeria are very slow in growth. It is therefore difficult to develop plantations that will quickly close canopy so as to protect the soil from degradation and prevent annual fires that ravage the region. Moreover, because of these annual fires, these tree species develop gnarled stems that make them practically useless for the production of sawn timber and poles. It is therefore not possible to meet the ever increasing demand of the people for wood and other wood products. There was therefore the need to identify exotic tree species that will exhibit rapid growth and desirable morphological characteristics. Eucatyptus camaldulensis, which is a species of savanna woodland, is among the exotic tree species that can be used for afforestation programmes in the region.

In order to identify the most suitable provenance(s) of E. camaldulensis for use in the Nigerian Savanna, a provenance trial was carried out on the species in 1967 at different sites within the region. Previous report (Otegber and Samarawira, 1989) has shown the variation patterns in the 18-year growth and quality characteristics

Table 1. — Form of combined analysis of variance over sites for each characteristic of 10 provenances of Eucalyptus camaldulensis examined at Kabama and Afaka.

Source of variation	df	Mean square	Expected mean square
Site	s-1	MS _s	$\delta_{\rm e}^2 + {\rm p}\delta_{\rm r(s)}^2 + {\rm pr}\delta_{\rm s}^2$
Replication (Site)	s (r-1)	MS _{r(s)}	$\delta_e^2 + p \delta_{r(s)}^2$
Provenance	p-1	мs _р	$\delta_{\rm e}^2 + {\rm r}\delta_{\rm ps}^2 + {\rm rs}\delta_{\rm p}^2$
Provenance x site	(p=1)(s-1)	MS _p s	$\delta_{\rm e}^2 + {\rm r} \delta_{\rm ps}^2$
Brror	s(p-1)(r-1)	NS _e	$\delta_{ m e}^2$

where,

 $\sigma_{\mathbf{p}}^{\mathbf{i}} = \sigma_{\mathbf{g}}^{\mathbf{i}} = \mathbf{genetic}$ variance among provenances.

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s = number of sites

r = number of replications

p = number of provenances

MS = observed mean s.uare of the corresponding subscripted source of variation

 $[\]sigma_{\theta}^2 = \text{error variance}$

 $[\]sigma_{n_{\alpha}}^{2} = \text{provenance } x \text{ site interaction variance}$

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						Mean Square	ופון ב				
Source of variation	df	df Height	Diameter at breast height	Number of forks	First fork height	Number of stems/ fork	Stem	Branch Brancl diameter angle	Branch angle	Number of branches	Taper
Site	-	17.808	484.88** 1.119** 16.646	1,119**	16.646	2,440** 0,010	0.010	19,369** 1,721** 32,604	1.721**	32.604	1,105**
Replication (Site)	ω	18,334**	5.904	0.082*	4.697** 0.110	0.110	0.209	1,111** 0,068	0,068	5.166	0.013
Proven ance	0	84.271**	40.846** 0.220*	0.220*	7.935*	0.439*	0.829**		2.007** 0.679** 14.679*	14,679*	0.040
Provenance x site	6	7.044*	5.541	0.045	2.133	0.125*	0.104	0.370	0.107	4.127	0.017
Residual	72	2.650	3,183	0.034	1,489	0.061	0.140	0.260	0.068	3.574	0.010

of the species. The aims of this study are therefore to: estimate some genetic parameters for the growth and quality characteristics of *E. camaldulensis*; show the degree to which provenance selection can be used in the improvement of this species.

Materials and Methods

The provenance trial of Eucalyptus camaldulensis established in 1967 at Kabama (lat. 11°8'N, long. 7°42'E) and Afaka (lat 10°37'N, long. 7°17'E) which are both in the Northern Guinea Savanna Zone of Nigeria was used for the study. Ten provenances whose descriptions have been

given in earlier papers (Otegbeye, 1985; Otegbeye and Samarawira, 1989) involved in the study include three from Queensland (Petford, Bullock Creek and Eulo), four from Northern Territory (Katherine, Tennant Creek, Newcastle Waters and Alice Springs), two from Western Australia (Mundiwindi and Willuna) and one from New South Wales (Silverton), all in Australia. The nursery and field cultural practices followed have also been given (Otegbeye, 1985; Otegbeye and Samarawira, 1989). The experimental design used was a randomized complete block design with five replications and 36 trees per plot

Sixteen inner trees per plot were assessed for tree height, diameter at breast height (DBH,) number of forks, first fork height, number of stems/fork, stem form, branch diameter, branch angle, number of branches and taper in 1985 when trees were 18 years old. Details about the assessment procedure have been given (Otegbeve and Samarawira, 1989).

Combined analysis of variance over the two sites (*Table 1*) was carried out for each of the 10 characteristics using plot means since combined analysis reduces error and provides more valid estimates of variance components.

Phenotypic, provenance, provenance x site interaction and environmental components of variance for each characteristic were estimated using the appropriate mean square (MS) values as follows:

$$\begin{split} \sigma^2_{e} &= MS_{e} \\ \sigma^2_{p} &= \sigma^2_{g} = \frac{MS_{p} - MS_{ps}}{rs} = \text{Genetic variance among provenance means.} \\ \sigma^2_{ps} &= \sigma^2_{gs} = \frac{MS_{ps} - MS_{e}}{r} = \text{Provenance x site interaction variance.} \\ \sigma^2_{ph} &= \sigma^2_{p} + \sigma^2_{gs} + \sigma^2_{e} = \text{Phenotypic variance among provenance means.} \end{split}$$

Phenotypic coefficient of variation (P. C. V.) and provenance coefficient of variation (G. C. V.) were estimated for each of the 10 characteristics using the relationships suggested by Johnson *et al.* (1955) and Hanson *et al.* (1956).

P. C. V. (%) =
$$\sqrt{\frac{\sigma^2_{ph}}{\bar{x}}} \times 100$$

G. C. V. (%) = $\sqrt{\frac{\sigma^2_{ph}}{\bar{x}}} \times 100$

where $\sigma^2_{\,\mathrm{ph}}$ and $\sigma^2_{\,\mathrm{g}}$ are as defined above

 \bar{x} = mean of the characteristic.

A use of variance components in tree improvement studies is for predicting genetic gain through provenance selection (Burley and Wood, 1976). A ratio of variance that we call a heritability of provenance means (h^2_p) was therefore estimated for each of the characteristics using the relationship:

$$\begin{array}{ll} h^2_{\ p} \ = \ \frac{\sigma^2_{\ g}}{\sigma^2_{\ g} \ + \ \sigma^2_{\ gs/_{\ r}} + \ \sigma^2_{\ e/_{\ rs}}} \\ \text{where } \sigma^2_{\ g} \ \text{and} \ \sigma^2_{\ gs} \ \text{are as previously defined} \\ \sigma^2_{\ e} \ = \ \text{error variance} \\ \ r \ = \ \text{number of replications} \end{array}$$

s = number of sitesA genetic advance (GA) can also be estimated thus:

GA =
$$\frac{\sigma^2_g}{\sigma^2_{ph}}$$
 x K σ_{ph} (Burton and Devane, 1953; Johnson where: σ^2_g and σ^2_{ph} are as earlier defined

 $K \sigma_{ph} = \frac{\text{selection differential expressed in}}{\text{phenotypic standard deviation.}}$ K(selection intensity) was assumed to be 2.06 which is the

Table 3. — Estimates of phenotypic variance (σ^2_{pl}) , provenance variance (σ^2_{p}) , provenance x site interaction variance (σ^2_{ps}) and environmental variance (σ^2_{e}) for 10 characteristics of 18-year-old provenances of Eucalyptus camaldulensis grown at Kabama and Afaka.

Characteristics	$\mathcal{6}_{\mathrm{ph}}^{2}$	$\delta_{ m p}^2$	$\delta_{ m ps}^2$	$\delta_{\rm e}^2$
Height	8.164	7.723	0.879	2.650
Diameter at breast height	3.944	3.531	0.472	3.183
Number of forks	0.022	0.018	0.002	0.034
First fork height	0.755	0.580	0.129	1.489
Number of stems/fork	0.040	0.031	0.013	0.061
Stem form	0.087	0.073	-0.007	0.140
Branch diameter	0.194	0.164	0.022	0.260
Branch angle	0.065	0.057	0.008	0.068
Number of branches	1.435	1.055	0.111	3.574
Taper	0.003	0.002	0.001	0.010

Table 4. — General mean, estimates of phenotypic coefficient of variation (P.C.V.), provenance coefficient of variation (G.C.V.), provenance heritability (h_p^a), expected genetic advance ($\triangle G$) and expected genetic advance as percent of mean for 10 characteristics of 18-year-old Eucalyptus camaldulensis provenances grown at Kabama and Afaka.

Characteristics	General mean	P.C.V. %	G.C.V. %	h _p ²	∆G	ΔG as percent of mean
Height	18.87m	65.78	63.97	0.946	5.568	29,51
Diameter at breast height	18.20cm	46.53	44.05	0.895	3.663	20.13
Number of forks	0.43	22.62	20.46	0.818	0.250	58.14
First fork height	2.41m	55.97	49.06	0.768	1.375	57.05
Number of stems/fork	0.69	24.08	21.20	0.775	0.319	46.23
Stem form	3.14	16.65	15.25	0.839	0.510	16.24
Branch diameter	3.00cm	25.43	23.38	0.845	0.767	25.57
Branch angle	3.00	14.72	13.78	0.877	0.461	15.37
Number of branches	11.51	35.31	30.28	0.735	1.814	15.76
Taper	1.05	5.35	4.36	0.667	0.075	7.14

ecpectation when 5% of provenances are selected. Since many breeders prefer to think of advance as percent of population mean (Burton and Devane, 1953), the advance obtained for each characteristic was expressed as percent of the population mean (\bar{x}) for the characteristic thus:

GA as
$$^{0}/_{0}$$
 of mean $=\frac{GA}{\overline{x}} \times 100$.

Results and Discussion

The results of the combined analysis of variance (Table 2) show that, except for taper, there were detectable provenance differences in all the characteristics. Pheno-

typic, provenance, provenance x site interaction and environmental variance components estimated are presented in *table 3*. The phenotypic variance was a little higher than its corresponding provenance variance in all cases showing that the characteristics were slightly more influenced by environmental influences than by genetic effects.

The heritability of provenance effects was estimated for each of the characteristics and presented in *table 4*. High heritability estimates ranging from 0.667 for taper to 0.946 for tree height were obtained.

By itself, the provenance heritability does not indicate the amount of genetic improvement that can be achieved

through provenance selection (Johnson et al., 1955). It has therefore been suggested that high heritability coupled with high genetic advance is the true index for effective selection (Johnson et al., 1955; Swarup and Chaugale, 1962). The genetic advance estimated for the first generation from provenance selection ranged from 0.075 for taper to 5.568 for tree height (Table 4). When expressed as percent of mean, the values obtained ranged from 7.14% for taper to 58.14% for number of forks. High provenance heritability was not in most cases associated with high genetic advance, which is very much in agreement with the observation of Swarup and Chaugale (1962). The provenance heritability estimated for any one characteristic is useful when high selection gain in that characteristic is also feasible (Kaul and Bahn, 1974). In the present study, a genetic advance as percent of mean of 15.00 would be considered high. For instance, a 10% increase in DBH will, in strict mathematical terms, result in approximately a 20% increase in basal area, hence in volume (Lauridsen et al., 1987). Even small improvements become economically important in large planting programmes (ZOBEL, 1977). Over 15% genetic gain was recorded for all the characteristics except taper. Coupled with their high provenance heritability estimates, a reasonable level of genetic improvement can be achieved through provenance selection for each of the characteristics. Although taper had a fairly high provenance heritability, its genetic advance was low.

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Genetic Parameter Estimates for Growth Traits at Different Ages in Slash Pine and Some Implications for Breeding¹)

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Abstract

Data from 57 slash pine open-pollinated progeny tests, 585 different families and approximately 70,000 trees were used to estimate genetic parameters (heritabilities, Type B genetic correlations between measures of a trait on two sites, and genetic correlations between two different traits) for cumulative growth traits at ages 5, 10 and 15, and incremental and relative growth rates between ages. A modification of an analytical approach discussed by Burdon (1977) made use of all possible pairs of progeny tests with common families to estimate parameters. Heritabilities for cumulative growth traits (height, DBH, volume) in slash pine at age 5 are low, on the order of

0.05 to 0.10, and increase to 0.12 to 0.16 by ages 10 and 15. Genetic correlations of age 5 growth traits with the same trait at age 10 or 15 were moderate (0.5 to 0.7), while age 10 and 15 growth had extremely high correlations (approximately 1). Finally, Type B genetic correlations were higher between pairs of locations of similar site indices (< 2.6 m different) than between pairs of locations with very different site indices (\ge 2.6 m different). This indicates that genotype x environment interaction arises from differences in site quality, and suggests that large site index differences between progeny test sites and commercial production land will decrease the reliability of progeny test data in predicting breeding values.

Key words: Heritability, genetic correlation, Type B genetic correlation, genotype x environment interaction, juvenile-mature correlation, Pinus elliottii Engelm. var. elliottii.

Introduction

Precise and accurate genetic parameter estimates are crucial for making sound decisions in many stages of a tree

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