

Genetic Parameters and Gains expected from Selection in *Eucalyptus globulus* in Tasmania

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Summary

Genetic parameters for growth, stem form and branch size were estimated from measurements made at around six years in a seedling seed orchard of *Eucalyptus globulus* in north-west Tasmania. The orchard included 45 open-pollinated families collected from trees in 14 provenances across the natural range of the species.

Individual heritabilities for volume and stem form were moderate, with $h^2 = 0.19$ for volume and $h^2 = 0.24$ for stem form. The heritability of branch size was somewhat higher ($h^2 = 0.29$). Volume and stem form were poorly correlated both genetically and phenotypically. Volume was adversely correlated, both genetically and phenotypically, with branch size. Stem form and branch size showed strong positive correlations. Intensive selection for growth was found to lead to reduced gains in stem form and branch size and vice versa.

Key words: *Eucalyptus globulus*, heritability, genetic correlation, genetic gain, growth, form.

Introduction

Estimates of genetic parameters for growth traits in *Eucalyptus* species in general are not abundant in the literature. ELDRIDGE (1972) and GRIFFIN and COTTERILL (1988) have published heritabilities for *E. regnans*, PURNELL (1986) for *E. nitens*, MATHESON *et al.* (1986) for *E. obliqua* and KEDHARNATH and VAKSHASYA (1978) for *E. tereticornis*. There are no published estimates of heritability or genetic correlations for *E. globulus*. It is not possible to formulate optimum breeding strategies nor predict the likely outcome of selection without knowledge of these genetic parameters (COTTERILL and DEAN, 1988; Chapter 4).

The aim of this paper is therefore to present estimates of genetic parameters for growth and form traits in *E. globulus* on one site in Tasmania. The responses expected from selection on multi-trait selection indices constructed using these genetic parameters are presented and discussed in terms of breeding strategy for this population.

Materials and Methods

Trial Site and Design

The trial was established in November 1980 on a moderately fertile site at Woolnorth in north-western Tasmania (latitude 40°50' S, longitude 144°46' E, altitude 45 m). This region experiences a cool temperate climate with an average annual rainfall of 1100 mm.

Open-pollinated offspring collected from 45 naturally occurring trees within 14 provenances across the natural range of *E. globulus* LABILL. subsp. *globulus* were included in the trial. Provenances (and number of families) were

Bruny Island (5), Channel (4), Denison (1), Geeveston (3), Henty River (5), King Island (3), Leprena (5), Macquarie Harbour (5), North Flinders Island (1), Seymour (2), South Flinders Island (1), Swansea (1), Taranna (6) from Tasmania and Otway Ranges (3) from south-western Victoria. Details of the collection are given in VOLKER and ORME (1988). The trial design involves 22 randomised complete blocks. At planting each family was represented in each block by a plot of 5 trees. By age 3 years the plots had been thinned to leave single-tree plots at an average spacing of 6 m × 6 m. The wide spacing was adopted as it is intended to utilise the trial as a seedling seed orchard in future.

Measurement

In June 1986 (at around 6 years) trees were measured for stem diameter (at breast height over-bark) and total height. Volume was calculated as a simple conical function combining diameter and height. Ten months later, in April 1987, stem form and branch size were assessed visually on all trees. Stem form represents a composite score arising from the presence or absence of defects. The stem form score was actually assigned by starting with a score of six and deducting one point for the occurrence of each of basal sweep, stem curves, multiple leaders or single ramicorns, and two points for multiple ramicorns. Hence, 6 = best stem form and 0 = poorest stem form. Branch size was assessed on a five-point subjective scale with 1 = heavy branches and 5 = thin branches (after PEDERICK, 1979).

Data Analysis

(1) Analysis of variance and covariance

Individual tree data were analysed using a random model which included families nested within provenances — (1)

$$Y_{ijkl} = \mu + P_i + F_{ij} + B_k + e_{ijkl} \quad (1)$$

Where μ is the overall mean, P_i is the effect of the i th provenance, F_{ij} the effect of the j th family nested within the i th provenance, B_k the effect of the k th block, the e_{ijkl} residual error. Variance components due to provenances (σ_p^2), families-within-provenances ($\sigma_{f(p)}^2$) and the residual error (σ_e^2) were calculated using expectations of mean squares.

(2) Genetic parameters

Individual heritabilities (denoted h^2) were estimated as — (2)

$$h^2 = \text{additive variance} / \text{variance of individual phenotypes} \\ = 2.5 \sigma_p^2 / (\sigma_{f(p)}^2 + \sigma_e^2) \quad (2)$$

The coefficient of relationship of 2.5 in Equation 2 assumes an average rate of outcrossing of 70% for *Eucalyptus* species (MORAN and BELL, 1983; GRIFFIN and COTTERILL, 1988). It is likely that there are differences in the rate of outcrossing from one open-pollinated family to another, particularly for seed collected in native stands. GRIFFIN and COTTERILL (1988) draw attention to the fact that this variation in outcrossing may inflate heritabilities but there is no way of correcting for the effect.

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Standard errors of individual heritabilities were estimated according to SWIGER *et al.* (1964). Genetic correlations (r_A) were calculated from estimates of additive genetic variances and covariances following HAZEL *et al.* (1943) and the standard errors of these correlations according to TALLIS (1959). No assumption regarding the coefficient of relationship is required for estimating genetic correlations. Phenotypic correlations (r_p) were estimated as simple correlation coefficients.

(3) Selection indices

Volume, stem form and branch size were combined in selection indices using the computer program RESI. (Practical application of the program has been described in detail by COTTERILL and DEAN, 1988; Chapter 11.) The program uses individual heritabilities, phenotypic standard deviations and genetic and phenotypic correlations together with a range of economic weightings to first construct the indices and then to calculate the genetic gains expected in each trait as a consequence of selection on each index. Two indices were actually constructed, both integrating the same traits, but one index had 5 times more weighting on volume relative to the other index.

The RESI program routinely calculates gains expected in each trait following selection on each index (COTTERILL and DEAN, 1988; Chapter 8) as — (3)

$$A_m = \text{Cov}(A_m I) (i/\sigma_I) \quad (3)$$

Where A_m is the gain expected in the m th trait, $\text{Cov}(A_m I)$ the covariance of the breeding value A_m of the m th trait and the index value I , σ_I is the phenotypic standard deviation of I , and i is the standardised select on differential. Selection was assumed to be at an intensity of one tree in every 100 ($i = 2.665$; ВЕСК'Р, 1985) because this is approximately the intensity of selection which may be used in advanced generation selection of *E. globulus* from plantations in Tasmania.

Results and Discussion

Overall means and their standard deviations and variance components for provenance, family-within-provenance and residual effects are given in *Table 1*. Individual heritabilities and their standard errors and genetic and phenotypic correlations are presented in *Table 2*. Genetic gains following selection on multi-trait selection indices

combining volume, stem form and branch size with varying emphasis on volume are compared in *Table 3*.

Heritabilities

Individual heritabilities of growth traits ranged from $h^2 = 0.12 \pm 0.05$ for height to $h^2 = 0.24 \pm 0.07$ for diameter (*Table 2*). The heritability of volume was similar to diameter ($h^2 = 0.19 \pm 0.07$). The standard errors of the heritabilities of growth traits were consistently low. These heritabilities suggest that individual selection for growth traits should lead to substantial genetic gains (discussed later).

Stem form also had a moderate heritability of $h^2 = 0.22 \pm 0.07$. Branch size, however, had a higher heritability of $h^2 = 0.29 \pm 0.08$ (*Table 2*). Again the estimates for both traits had low standard errors. The lower heritability of stem form (compared with branching) may be due to the fact that the trait included characters such as forking and ramification which seem to be poorly inherited in trees (e.g. COTTERILL and ZED, 1980). If stem form had been assessed simply in terms of stem straightness the heritability may have been higher. COTTERILL and DEAN (1988; Chapter 5) argue against using composite traits such as the present stem form score because the inheritance of individual components is obscured. These authors recommend separate scores or measurements for each component of form (that is, separate scores for stem straightness, forking, ramification, branch quality and so on).

Genetic and Phenotypic Correlations

Strong genetic ($r_A = 0.82 \pm 0.06$; *Table 2*) and phenotypic ($r_p = 0.66$; *Table 2*) correlations were found between height and stem diameter. Volume showed very high genetic correlations with both height and, in particular, stem diameter with $r_A = 0.70 \pm 0.15$ and 0.98 ± 0.01 (*Table 2*) respectively. The standard errors of these correlations among growth traits are low. This same trend is apparent in the phenotypic correlations between these traits (*Table 2*) and reflects the stronger influence of diameter in the calculation of volume.

Stem form had moderate to low genetic correlations with diameter and volume ($r_A = 0.07$ and 0.13 ; *Table 2*). The genetic correlation between stem form and height was stronger ($r_A = 0.43$; *Table 2*). The standard errors of these correlations were large relative to the magnitude of the coefficients. This lack of precision may be attributable to the various components of the stem form score being dif-

Table 1. — Overall means (and their standard deviations) of all trees at age six years in the progeny trial and variance components relevant to heritability estimation for growth and form traits in *E. globulus* in Tasmania. The σ_p^2 represents variance due to provenances, $\sigma_{f(p)}^2$ families nested within provenances and σ_e^2 residual error.

Trait	Overall mean (\pm s.d.)	Variance components		
		σ_p^2	$\sigma_{f(p)}^2$	σ_e^2
Height (m)	19.0 \pm 2.99	0.017	0.077	1.462
Diameter (cm)	13.1 \pm 1.54	0.077	0.676	6.351
Volume (dm ³)	131 \pm 51	23.0	135.0	1662
Stem form (point)	4.8 \pm 0.95	0.000	0.084	0.890
Branch size (point)	2.6 \pm 0.88	0.002	0.100	0.770

Table 2. — Individual heritabilities ($h^2 \pm$ standard errors), genetic correlations ($r_A \pm$ standard errors) and phenotypic correlations (r_p) for growth and form traits in *E. globulus* in Tasmania.

Trait	$h^2 \pm$ s.e.	Correlations				
		Height	Diameter	Volume	Stem form	Branch size
Height	0.12 ± 0.05		0.55 ± 0.02^a	0.70 ± 0.15	0.43 ± 0.26	-0.38 ± 0.26
Diameter	0.24 ± 0.07	0.66^b		0.98 ± 0.01	0.07 ± 0.26	-0.45 ± 0.24
Volume	0.19 ± 0.07	0.75	0.95		0.13 ± 0.27	-0.28 ± 0.26
Stem form	0.22 ± 0.07	0.09	-0.03	0.0		0.76 ± 0.15
Branch size	0.29 ± 0.08	-0.04	-0.38	-0.33	0.21	

^a) Genetic correlations ($r_A \pm$ s.e.) in upper triangle.

^b) Phenotypic correlations (r_p) in lower triangle.

Table 3. — Genetic gains in volume, stem form and branch size expected from index selection in *E. globulus* in Tasmania with varying emphasis on growth and branching. The calculations are for selection of superior individuals (on the basis of their index values) at an intensity of one tree in every 100. Gains are expressed in both actual units of measurement and, in brackets, percentage changes in the mean for each trait.

Economic Weightings			Expected Genetic Gains		
Volume	Stem form	Branch size	Volume	Stem form	Branch size
			(dm ³)	(point)	(point)
0.02	1	1	9.1 ^a	0.68	0.65
			(7) ^b	(14)	(25)
0.10	1	1	22.9	0.43	0.25
			(17)	(9)	(10)

^a) Gain expressed in units of measurement (ie dm³ for volume).

^b) Gain expressed as a percentage change in the mean.

ferently associated with growth traits. Phenotypic correlations between growth traits and stem form were around zero (Table 2).

Consistently negative genetic correlations were found between all growth traits and branch size ranging from $r_A = -0.28 \pm 0.26$ to -0.45 ± 0.24 (Table 2). These genetic correlations suggest that it will be necessary to reach a compromise between selection for rapid growth and selection for fine branching in *E. globulus*. Phenotypic correlations between growth traits and branch size were also negative (Table 2).

The genetic correlation between branch size and stem form was strong and positive with a low standard error ($r_A = 0.76 \pm 0.15$; Table 2) suggesting that improvement in one of these form traits would lead to a correlated im-

provement in the other. The phenotypic correlation between the two traits was also positive but much lower in magnitude ($r_p = 0.21$).

Gains Expected from Index Selection

In the first index in Table 3, emphasis is placed equally on all traits. Selection on this index is expected to yield a moderate improvement of 9.1 dm³ (or 7%; Table 3) in volume and more substantial gains of 0.68 point (or 14%; Table 3) in stem form and 0.65 point (or 25%; Table 3) in branch size. Increasing the emphasis on growth by a factor of five (the second index in Table 3) leads to a corresponding increase in the gain expected in volume (7% to 17%; Table 3). This increase in expected gain for volume is, however, accompanied by a decrease in the gains expected

for both stem form (14% to 9%; Table 3) and branch size (25% to 10%; Table 3).

Neither of the selection strategies studied here were expected to lead to a deterioration in any of the traits considered. This result is surprising given the fact that there was an adverse association between growth and branch size. For example, DEAN *et al.* (1983) and DEAN *et al.* (1986) have found that it is not possible to simultaneously improve two adversely associated traits in one population. In this case, however, selection should be quite straightforward. *E. globulus* is being planted in Tasmania primarily for pulp and paper production, therefore, until more is known about wood quality traits, improvement in growth is likely to be the main concern of the breeding program, at least in the first generation. Since it appears that substantial improvements can be made in growth whilst suffering no deterioration in stem form or branch size such a strategy should be easily implemented.

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Genetic Parameter Estimates for *Pinus caribaea* var. *hondurensis* in Coastal Queensland, Australia

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Summary

Nineteen open pollinated progeny trials, comprising about 32 000 trees of *Pinus caribaea* var. *hondurensis* in Queensland, Australia, were assessed for growth and stem straightness at about five years after planting, and for windfirmness following cyclone damage. Mean weighted narrow-sense heritabilities on an individual tree basis were 0.30 for diameter, 0.20 for height, 0.24 for straightness, and 0.08 for windfirmness. The magnitudes of heritability estimates were independent of site quality. Mean weighted genetic correlations were 0.82 between diameter and height, 0.21 between diameter and straightness, –0.15 between height and straightness, and 0.21, –0.10 and 0.18 between windfirmness and each of diameter, height and straightness, respectively. Selection for volume should not adversely affect windfirmness, which might best be improved by selection on family mean values at wind damaged sites.

Key words: *Pinus caribaea*, heritability, genetic correlation, growth, stem straightness, windfirmness.

Introduction

Genetic improvement of *Pinus caribaea* MORELET var. *hondurensis* BARRETT and GOLFARI (Pch) in Queensland, Australia, has been undertaken by the Queensland Department of Forestry (QDF) since the early 1960s. In the past decade, Pch has become the exotic plantation species of greatest importance in Queensland, with annual plantings currently approximating 4 500 ha. Some 40 000 ha, concentrated in three discrete coastal regions around latitudes 18° S, 22° S and 27° S, were established by 1987 (Queensland Department of Forestry, 1987). Much greater areas of Pch have been planted elsewhere in the tropics. Reliable estimates are difficult to obtain: DAVIDSON (1988) estimated that 456 500 ha were established by 1980, and NIKLES (1979) suggested an annual planting rate of about 90 000 ha. Trials in Queensland currently represent one of

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