GENETIC PARAMETERS FOR GROWTH AND WOOD DENSITY TRAITS IN *EUCALYPTUS NITENS* IN NEW ZEALAND

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ABSTRACT

Genetic and phenotypic parameters for diameter at breast height, bole straightness, branching, pilodyn penetration, and basic wood density were estimated for two open-pollinated progeny tests at age 5 years, including first- and second-generation material of different provenances. Different values for coefficients of relationship (0.25 and 0.5) were applied in the heritability calculations for each generation, which accounted for the expected difference in their pollination behaviour and the observed difference in their variance component estimates.

Strong evidence was found for substantial realised gains from open-pollinated progenies from seedling seed orchards of North Forest Products (NFP) and AMCOR in Australia and a New Zealand Forest Research Institute progeny trial. Differences in diameter growth between the best seed orchard seedlot and the best native race were 0.67 standard deviations. In terms of wood density, the New Zealand progenies were clearly superior to those from Australian seed orchards. Families from AMCOR and NFP were of low to very low density.

Keywords: progeny trial, genetic parameters; *Eucalyptus nitens.*

INTRODUCTION

There are more than 500 different species of eucalypt of which only about 150 have been introduced into New Zealand and even fewer have been considered for production forestry. Eucalypts were planted in this country initially to provide naturally durable timber and then for shelter and amenity purposes. By the late 1970s a group of species, mainly monocalypts of the ash group and the southern blue gums, had been identified as having forestry potential on a range of sites in New Zealand. First-stage breeding programmes were initiated with these species by establishing combined provenance-progeny trials.

In the late 1980s there was an increase in interest in planting eucalypts as a source of short-fibre pulp in New Zealand. In response to this a Research-Industry Eucalypt Breeding

Co-operative was formed to develop a programme of breeding and research to improve three species (*E. nitens* (Deane et Maiden) Maiden, *E. fastigata* Deane et Maiden, *E. regnans* F. Mueller) for short-fibre pulp. The breeding programme focused initially on *E. nitens* which species occurs naturally in four widely separated locations in eastern Victoria and New South Wales, Australia. It is found between latitudes 30°23′ and 38°00′S and typically between 1000 and 1300 m altitude. In central Victoria there are three recognised *E. nitens* regions—Toorongo Plateau mainly south of the Great Dividing Range, Rubicon mainly to the north of the Great Dividing Range, and MacAlister mainly on the coastal side of the Great Dividing Range. These populations are isolated from those in southern New South Wales and very isolated from those in northern New South Wales (Boland *et al.* 1994).

The breeding strategy involved the subdivision of the open-pollinated breeding population into 10 sublines and two different trial designs. A sets-in-reps single-tree-plot trial design provided a precise ranking of the families in "forward-selection blocks", where the families were established in isolated sublines of eight-tree rows replicated at random five times (Cannon & Shelbourne 1993; Cannon & Low 1994). This allowed forwards-selection of new breeding population parents and collection of open-pollinated seed.

In 1990 a breeding population of open-pollinated families was established as a single-tree-plot progeny test on two sites—Kaingaroa and Kinleith. Families in the breeding population were divided into sublines and sets largely according to these provenance groupings.

This paper reports genetic and phenotypic parameter estimations based on the assessments of these two progeny tests at ages 5 and 6 years. The objective was to obtain from these trials reliable estimates of genetic parameters for growth, stem characteristics, pilodyn penetration, and basic wood density, and the relative merits of the different genetic groups. The implications for a selection strategy for pulpwood production in New Zealand are also discussed. The main output of this study was a ranking of families based on an individual selection index score (which remains as confidential information for the members of the co-operative). The ranking can be utilised to rogue existing orchards in New Zealand.

MATERIAL AND METHODS

Test Sites and Design

The open-pollinated families used in this study originated from three sources: seed collected in native *E. nitens* stands in Australia; selections from New Zealand land-race plantations; selections from open-pollinated tests that have been converted to seedling seed orchards in Australia (AMCOR and North Forest Products) and New Zealand (Rotoaira progeny trial). Two control seedlots were included in the trials—a native seedlot from Toorongo Plateau and a southern New South Wales provenance from Nimmitabel planted in 1974 in Cpt 905 in Kaingaroa Forest, New Zealand.

Progeny and their parents were allocated to nine different sets, generally grouped by provenance and previous selection effects. The genetic relationship between open-pollinated sibs in native stands (groups 1, 2, 3, 4, and 5) was assumed to be 0.5 (after Gea *et al.* 1997), and 0.25 between open-pollinated sibs from seedling seed orchards or plantations (groups 6, 7, 8, and 9) (Table 1).

TABLE 1–Provenances, number of families, and assumed intra-class correlation used in the analysis.

	Genetic grouping or provenances	No. of families	Genetic relationship
1	MacAlister, Victoria	65	0.5
2	Rubicon, Victoria	90	0.5
3	Toorongo Plateau, Victoria	129	0.5
4	Northern New South Wales	4	0.5
5	Southern New South Wales	6	0.5
6	New Zealand plantations	10	0.25
7	AMCOR seedling seed orchard	10	0.25
8	NFP seedling seed orchard	62	0.25
9	Rotoaira (NZ) seedling seed orchard	111	0.25

The progeny tests were established at two sites: Cpt 1060 in Kaingaroa Forest (denoted Kaingaroa hereafter) and Podocarp Road, Kinleith Forest (denoted Kinleith hereafter). The trial design was sets-in-reps, with single-tree-plots and nine sets of 30 families and two control seedlots per set. There were 30 replicates of each set at each site, making 300 blocks in total per site. The progenies were generally grouped by provenance in each set according to Table 1.

Both sites were pine cut-over and were prepared by v-blading. The seedlings were raised in root-trainers and established at a spacing of 3 × 3.5 m in November / December 1990.

Each site sustained post-planting damage shortly after establishment. At Kaingaroa seedlings were subject to fertiliser burn at the time of planting and survival was about 60%. The trial was blanked with stock of unidentified origin. This trial site also exhibited frost damage 10 months after establishment. Seedlings on the Kinleith site were severely browsed by animals, and as a result there was a high incidence of basal forking. Stems that had forked below 1 m were not included in the assessment.

Traits Assessed and Measured

Diameter was measured at breast height 1.4 m (dbh). Bole straightness and branching were assessed subjectively on a scale of 1 = poor to 6 = good at both sites.

Wood density shows useful correlation with important commercial traits such as wood consumption, moisture content, pulp and paper properties, and sawn timber properties (Kibblewhite *et al.* 1997; Greaves 1997; J.Richardson pers. comm.), but direct selection for density in breeding programmes requires the removal and analysis of timber samples either as increment cores or disks, work that can be very costly. The pilodyn is a hand-held tool which has shown promise as an indirect measure of wood density in standing trees (Greaves 1997; Cown 1978). It drives a high precision hardened-steel flat-nosed pin into a wood sample, and depth of pin penetration is read directly from a scale on the top of the instrument. In the present analysis, negative values implied high density and positive values low density.

Pilodyn penetrations at breast height were obtained for wood density estimates from about 10 trees per family on most families, while 5-mm cores (pith to bark at breast height) were obtained from two to five individuals per family on a sub-sample of 40 families with low pilodyn averages. Both measurements were taken only at the Kinleith site.

Statistical Analysis

The model used in the analysis, in matrix notation, was:

$$y = Xb + Za + ZQg + e \tag{1}$$

where y is the vector of records, $\boldsymbol{X}$ is an incidence matrix associating records with fixed effects, b is a vector of fixed effects (blocks), g is the vector of effects of groups to which parents have been assigned, $\boldsymbol{Z}$ is an incidence matrix associating records with genetic effects, a is a vector of genetic effects (breeding values), e is the vector of residuals, and $\boldsymbol{Q}$ the incidence matrix relating trees to groups (Westell *et al.* 1988). The elements of $\boldsymbol{Q}$, qjr, are fractions relating the contribution of the rth genetic group to the total genetic value of the jth tree. The total of genetic group effects for the jth individual is:

$$\sum_{r=1}^{n} q_{jr}g_r \tag{2}$$

and the estimated total genetic merit for the jth tree is:

$$\hat{u}_j = \hat{a}_j = \sum_{r=1}^{n} q_{jr}g_r \tag{3}$$

Estimates of variance components for a and e, and group and tree genetic merit were estimated using MTDFREML (Meyer 1989) and SAS.

RESULTS

Overall means and standard deviations for growth, stem characteristics, pilodyn penetration, and wood density for both sites were calculated using SAS (Table 2).

TABLE 2–Basic statistics for the four traits used in the analysis

Trait	Mean (std dev.)	No parents	No records
Kaingaroa			
Diameter	146.30 (30.94)	305	3590
Straightness	3.04 (0.98)	305	3590
Branching	3.04 (1.06)	305	3590
Kinleith			
Diameter	163.9 (36.67)	307	5649
Straightness	3.06 (0.87)	307	5649
Branching	3.07 (0.95)	307	5649
Pilodyn penetration	15.56 (1.62)	249	5649
Density (cores)	391 (27)	90	217

Variance components for open-pollinated sibs from seedling seed orchards or plantations were estimated separately from those for native stands, using SAS Proc Varcomp. Although both groups had almost the same number of families, family variance for the plantation material was almost half the size of variance for native stands for all traits except malformation (Table 3). Coefficients of relationships of 0.5 for native stands and 0.25 for plantations were then assumed and incorporated into MTDFREML to obtain comparable heritability values for both groups. Pooled estimates of narrow-sense heritability were 0.11 for diameter, 0.18 for straightness, 0.13 for branching, 0.41 for pilodyn penetration, and 0.61 for wood density cores (Table 4).

TABLE 3–Family variances for native provenances and plantations at Kinleith and Kaingaroa

Traits	Kinleith		Kaingaroa	
	Native provenances	Plantations	Native provenances	Plantations
Diameter	83.93	52.34	65.92	39.81
Straightness	0.07	0.03	0.08	0.05
Branching	0.06	0.02	0.06	0.06
Malformation	0.14	0.02	0.02	0.16

TABLE 4–Standardised pooled estimates of variance components using MTDFREML for the four traits across the two sites, and individual heritabilities

Trait	Additive variance	Family*site variance	Error variance	Individual h^2
Diameter	0.108	0.018	0.867	0.11
Straightness	0.177	0.012	0.799	0.18
Branching	0.131	0.011	0.846	0.13
Core density	0.137	–	0.465	0.45
Pilodyn penetration	0.408	–	0.578	0.41

The heritabilities were consistent with previous estimates for growth, stem characteristics, and wood density in Australia and New Zealand. Reported heritabilities for growth ranged between 0.09 and 0.44, with a mean of 0.25 (Whiteman *et al.* 1992; Woolaston *et al.* 1990; Johnson 1997; Hodge *et al.* 1996; King & Wilcox 1988; Kube *et al.* in prep.; McKimm 1985; Greaves *et al.* in press). For density reported heritability was 0.59 based on pilodyn measurement or 0.73 based on discs (Greaves 1997), and for stem straightness and branch thickness it was 0.44 (Greaves 1997).

Pilodyn-measured heritabilities are reportedly high; however, only a moderately strong phenotypic correlation with core density was obtained here ($r = -0.68$). This could be a reflection of the sample selection, as only higher density trees (low pilodyn values) were sampled. Greaves *et al.* (in press) obtained also a phenotypic correlation of –0.61 and a genetic correlation of 0.98.

A linear regression between pilodyn penetration and corewood density was produced (Eq. 4). Since the wood density cores were obtained from a sub-sample of families with low pilodyn scores (high density), the regression equation was expected to be poorly estimated.

$$\text{Corewood density} = 502.06 - 10.55 \text{ pilodyn penetration} \tag{4}$$

Genetic and phenotypic correlations between these traits are listed in Table 5. Diameter growth showed only low genetic correlation with straightness, pilodyn penetration, and density. The only previous estimates of genetic correlations for *E. nitens* were by Greaves *et al.* (in press) from a 7-year-old progeny trial in Australia, with an unfavourable genetic correlation between diameter and wood density of $r_G = -0.28$, and diameter and pilodyn penetration of $r_G = 0.24$.

Provenance Variation

The provenance or genetic group variations for growth, stem characteristics, and pilodyn penetration are shown in Table 6.

TABLE 5–Estimates of phenotypic (above diagonal) and genetic (below diagonal) correlations between different traits.

	Diameter	Straightness	Branching	Core density	Pilodyn penetration
Diameter		**0.56**	**–0.31**	**0.06**	**–0.05**
Straightness	–0.13		**–0.01**	**0.02**	**–0.08**
Branching	–0.10	0.40		**0.01**	**–0.01**
Core density	0.08	0.10	0.09		**–0.68**
Pilodyn penetration	–0.14	0.13	0.11	–0.92	

TABLE 6–Genetic group estimates, in units of phenotypic standard deviations, as deviations from the trial mean.

Genetic grouping	Diameter	Straightness	Branching	Pilodyn penetration
1 MacAlister	–0.29	–0.02	0.27	–0.01
2 Rubicon	–0.08	0.07	0.24	0.15
3 Toorongo	–0.19	0.11	0.22	–0.05
4 Northern New South Wales	–0.32	–0.44	–0.78	–
5 Southern New South Wales	–0.15	–0.11	–0.20	0.46
6 New Zealand plantations	–0.20	0.08	0.23	–0.05
7 AMCOR seed orchard	0.59	0.03	–0.37	–0.07
8 NFP seed orchard	0.49	–0.18	–0.05	0.25
9 Forest Research progeny trial	0.18	0.43	0.41	–0.69

Differences between the five native provenances were small for growth but more marked for straightness, branching, and pilodyn penetration. Victorian provenances and the New Zealand land-race had better growth and stem characteristics than those from northern and southern New South Wales, a result also apparent in previous studies in Australia (Johnson 1996). However, only a small number of families were sampled from southern and northern New South Wales provenances. The northern provenance from New South Wales was notably inferior in all traits. Southern New South Wales showed significantly lower density, whereas Toorongo, MacAlister, and the New Zealand land race had higher density. This result was consistent with the wood density results of W.N.Tibbits (pers. comm.).

There was strong evidence for substantial realised gains in material originating from seed orchards—NFP, AMCOR, and the Forest Research progeny trial. Growth differential between the best seed orchard seed and the best native race was 0.67 standard deviations. Superiority in straightness and branching was apparent only in the Forest Research trial material. This is consistent with the selection criteria used (New Zealand had a strong selection pressure on stem characteristics). In terms of wood density, the New Zealand (Rotoaira) progenies were clearly superior, though no selection for density had been applied. Families from AMCOR and NFP were of low to very low density (with positive pilodyn penetration values). The differences in density between the different groups are hard to explain given that selections in all the orchards ignored wood properties.

Superior growth and form of seed orchard seed have also been reported recently by Johnson (1996), although gain differentials were smaller (between 8% for growth and 15% for straightness).

CONCLUSIONS

The analysis of both progeny tests has produced provenance effects and genetic parameters that are highly useful for the breeding efforts applied to this species. It may be possible to re-design the breeding strategy of *E. nitens* to facilitate cross-breeding among the best families in all provenances. The best provenance source was Rubicon, although the difference compared with other seed sources was not large (Cannon & Shelbourne 1993; Gea *et al.* 1997). Northern and southern New South Wales provenances were poorly represented among the best, however.

Family variances for plantations were almost half the size of those for native provenances. The use of different coefficients of relationships in the MTDFREML analysis proved to be efficient for comparing heritabilities among native provenances and plantation provenances. Heritabilities calculated in this way showed similar trends at both sites. The amount of family × site variance was relatively small, accounting for low levels of genotype × environment interaction.

The regression equation presented here between pilodyn penetration and corewood density should be verified with data that include the whole range of Pilodyn values. The low negative correlation between growth and wood density allows the selection of individuals for specific-use seed orchards and promises a bright future for selection of breeding and production populations.

Seed from any Australian seed orchard or New Zealand progeny trial was approximately 0.6 standard deviations for growth over the best provenance. The implications for the New Zealand plantations are far-reaching. Both Australian orchards (AMCOR and NFP) had low pilodyn penetration values while the New Zealand selection showed high values that translated to higher density values.

The breeding values predicted as a consequence of the present analysis are powerful enough to facilitate a confident selection of families and individuals for breeding and production populations. Roguing of existing seed-stands based on these breeding values is recommended.

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