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SUMMARY

Genetic parameters were estimated for diameter, basic density (using cores sample) and Pilodyn penetration from 12 year old *Eucalyptus nitens* progeny trials across three sites in Tasmania. In a combined site analysis, heritabilities for diameter, basic density and Pilodyn were 0.39, 0.55 and 0.47 respectively. There were adverse genetic correlations between diameter and basic density (–0.55) and between diameter and Pilodyn (0.63). Genetic correlations between basic density and Pilodyn penetration were very strong (-0.90). Pilodyn penetration was measured in both late summer and late winter and heritabilities and correlations did not vary between seasons.

Genetic gains in basic density were compared using different sampling strategies. The recommended strategy is a 2-stage process. Stage-1 is to take a random sample within families using either cores or Pilodyn. Stage-2 is to take core samples from the top ranked trees selected on an index constructed from diameter and family basic density data to address the adverse genetic correlation between diameter and basic density. Gains are greater if cores are used in the stage-1 sampling, however costs are also greater. The use of a Pilodyn in stage-1 can deliver reasonable gains at a low cost. However, selecting for basic density using Pilodyn alone is not recommended.

INTRODUCTION

Eucalyptus nitens (Deane & Maiden) Maiden is used as a hardwood plantation species in cool-temperate regions. The global plantation area was approximately 220,000 ha in 1999 and the main plantation areas were in Australia (Tasmania and Victoria), Chile, South Africa and New Zealand (Tibbits *et al*. 1997). *E. nitens* is mostly used for pulpwood although plantations of this species are now being grown for veneer, sawn timber and composite products (Neilsen and Pinkard 2000).

Basic density is recognised as important to product value and profitability for many different end uses. Improved basic density has been shown to be important to the profitability of kraft pulp production (Borralho *et al*. 1993, Greaves *et al*. 1997). Basic density is also important for cold caustic soda pulp production, although it appears low density is desirable (Banham *et al*. 1995, Jones and Richardson 1999). The importance of basic density to solid wood and composite products has not been precisely defined. However, in a review of the traits thought to be important for appearance grade timber, structural timber, veneer, and medium density fibreboard, basic density was flagged as important to all (Raymond 2000).

Tree breeding programs require large numbers of basic density measurements, and these need to be taken using low cost and non-destructive techniques. Basic density is commonly assessed using a core taken near breast height, which has been shown to be highly correlated to whole tree values (Lausberg *et al*. 1995, Kube and Raymond 2002, Raymond and Muneri 2001). Basic density has also been assessed using a Pilodyn, which is an instrument that drives a flat-nosed pin into a wood sample with a fixed force. The depth of penetration is negatively correlated with basic density (Greaves *et al*. 1996, Raymond and MacDonald 1998, Raymond *et al*. 1998). Some studies have found Pilodyn precision to be low and unreliable for selecting individual trees (Raymond *et al*. 1998) however the low cost and simplicity of this method remain strong advantages and, for this reason, it is still being used.

This report is part of a broader study evaluating the genetic control of wood properties in *E. nitens*. Genetic parameters for basic density, fibre length, fibre coarseness and cellulose content have been reported in Kube *et al*. (2001). This study concentrates on the relationships between basic density and Pilodyn penetration. There were three aims. Firstly, to measure genetic parameters (heritabilities and genetic correlations) for basic density of a core and Pilodyn penetration over three sites. Secondly, to determine if there are differences between summer and winter Pilodyn assessments (ie. shooting into early-wood or late-wood) in the accuracy of selection. And thirdly, to determine gains under different sampling strategies involving cores, Pilodyn, and combinations of both.

MATERIALS AND METHODS

Trial establishment and assessment

The genetic material used was open pollinated progeny from 40 native forest families from Toorongo Plateau in the central highlands of Victoria. Progeny trials were established on three sites in northern Tasmania in 1984 and site details are given in Table 1. The trial design was a randomised complete block with 16 replications per site and single tree plots spaced at 3 m by 3 m.

Table 1. Location and description of field sites.

	Dial	Gog	Kamona
Latitude (South)	41° 10’	41° 29’	41° 08’
Longitude (East)	146° 04’	146° 23’	147° 40’
Altitude (m)	100	300	160
Rainfall (mm/year)	1060	1200	1150
Mean monthly maximum temp (°C)	22.3	21.8	23.4
Mean monthly minimum temp (°C)	3.8	2.4	2.5
Parent material	mudstone	basalt	granite

All trees were measured for diameter at breast height (1.3 m) at age 12.5 years. Basic density was also measured at 12.5 years and was assessed using a 12 mm diameter bark to bark core at a height of 0.9 m. Core sampling at this height has been shown to be a reliable predictor of whole tree values of basic density (Raymond and Muneri 2001, Kube and Raymond 2002). Basic density was defined as oven-dry wood mass per unit volume of green wood, and was measured using the water displacement method (TAPPI 1989). Between 5 and 13 trees per family per site were randomly sampled (average of 8). Following an initial analysis, 11 trees were excluded due to high residuals (greater than 3 standard deviations from mean). These trees had low diameters, very little diameter increment between 6 and 12 years, and very high density. The number of trees and range of values are shown in Table 2.

Pilodyn penetration was measured on two occasions. The first measurement was done in late February (late summer) at age 13.5 years and the second was near the end of August (late winter) at age 14 years. Measurements were taken at a height of 1.3 m and, at each sampling time, two readings were taken per tree from a single bark ‘window’. Measurements were taken on opposite sides of the tree for summer and winter samples. Sampling in this way has been found to give accurate results, and opposite cardinal aspects have high repeatability (Greaves *et al*. 1996, Raymond and MacDonald 1998). Pilodyn penetration was measured on all trees assessed for basic density however, for the winter measurement, only two sites (Dial and Gog) were assessed. The number of trees and range of values are shown in Table 2.

Trees less than 10 cm diameter were excluded from diameter and wood property assessments. Trees of this size were all strongly suppressed with no diameter increment between ages 6 and 12, and had atypical wood properties. These trees were found to inflate error variances.

Table 2. Description of data used in analyses.

Trait		Min.	Mean	Max.	SD	n
D	Diameter, age 12 (cm)	10.1	21.1	40.4	6.0	1160
BD	Core basic density, (kg m^{-3})	362	451	568	31	841
PD_S	Pilodyn penetration, summer (mm)	7.0	12.2	17.0	1.6	853
PD_W	Pilodyn penetration, winter (mm)	6.0	11.4	16.5	1.7	607

Estimation of genetic parameters

The traits analysed were stem diameter (D), basic density (BD), Pilodyn penetration summer (PD_s) and Pilodyn penetration winter (PD_w). Variances, covariances, correlations and errors for each site and each trait were estimated simultaneously by fitting multi-variate multi-site models. Multi-variate analyses use information more efficiently and can improve the precision of genetic parameters when selected subsets of data are used (Dieters *et al*. 1999). Multi-variate multi-site models allow all genetic correlations to be calculated directly, and use appropriate variance-covariance matrices for each site. These models treat measurements on different sites as different traits. Analyses were done using ASREML (Gilmour *et al*. 1999), and the model fitted was:

$$Y = \mu + SITE + REP(SITE) + FAM(SITE) + \mathbf{e} \qquad \textbf{(1)}$$

where Y is a vector of data for each trait; μ is a vector of means for each trait; SITE are site effects for each trait fitted as a fixed factor; REP(SITE) are within site replicate effects for each trait fitted as a fixed factor; FAM(SITE) are within site family effects for each trait fitted as a random factor; and $\mathbf{e}$ is a vector of residuals for each trait. Full inter-trait and inter-site variance and covariance matrices were fitted for the family and residual effects.

A second model was fitted (also for D, BD, PD_s and PD_w) to determine the importance of genotype by environment interactions and to estimate genetic correlations and heritabilities when data was pooled across sites. Error variances for each trait were all similar and therefore adjusting to a constant error variance was not considered necessary. This analysis was also done using ASREML and the model fitted was:

$$Y = \mu + SITE + REP(SITE) + FAM + FAM.SITE + \mathbf{e} \qquad \textbf{(2)}$$

where Y, μ, SITE, REP(SITE) and $\mathbf{e}$ are as previously defined; FAM are across site family effects for each trait fitted as a random factor; and FAM.SITE are site by family interaction effects for each trait fitted as a random factor. The model term FAM included an inter-trait variance and covariance matrix pooled across sites.

Heritabilities (narrow sense) and their standard errors were calculated by ASREML. Heritabilities for the individual site and multisite analyses were calculated as shown in models 3 and 4 respectively.

$$h^2 = \sigma 2f / r\,(\sigma^2_f + \sigma^2_e) \qquad \textbf{(3)}$$

$$h^2 = \sigma^2_f / r\,(\sigma^2_f + \sigma^2_{f.s} + \sigma^2_e) \qquad \textbf{(4)}$$

Where h^2 is the narrow sense heritability; σ^2_f, $\sigma^2_{f.s}$ and σ^2_e are, respectively, the variance components for FAM, FAM.SITE and $\mathbf{e}$ estimated in the models above; and r is the

coefficient of relationship. The coefficient of relationship used was 0.4 which assumes a selfing rate of approximately 30% (Griffin and Cotterill 1988).

Evaluation of sampling strategies

Sampling strategies for basic density were evaluated by comparing genetic gains from different strategies. Four broad sampling strategies were evaluated and, within these, different sampling intensities tested (see Table 7). The sampling strategies were:

1. Random basic density samples from a set number of trees per family. The number of samples per family was either 6 or 12 and samples were taken using cores and Pilodyn.
2. Two-stage sampling using cores. In stage-1, random basic density samples were taken using cores from a set number of trees per family (either 6 or 12 cores per family). In stage-2, cores were taken from the top ranked trees on an index combining diameter and the family basic density (both the top 10% and 20% of trees).
3. Two-stage sampling using Pilodyn and cores. In stage-1, random within-family Pilodyn measurements were taken from a set number of trees per family (either 6 or 12). In stage-2, cores were taken from the top ranked trees as described in 2) above.
4. Two-stage sampling using Pilodyn only. In stage-1, random within-family Pilodyn measurements were taken (either 6 or 12 measurements per family). In stage-2, Pilodyn measurements were taken from the top ranked trees on an index combining diameter and the family Pilodyn data (either the top 10% or 20%).

The data used was diameter, core basic density and summer Pilodyn penetration (Table 2). Trees for which no basic density measurements had been taken were excluded from this part of the analysis. This allowed gain to be calculated after 100% sampling for basic density, which was the 'benchmark' used to compare all other sampling strategies. New data sets were created for each strategy using appropriate subsets of data.

Gains were estimated after calculating individual tree breeding values for diameter and basic density. Breeding values were calculated by fitting the following individual tree model using ASREML:

$$Y = \mathbf{m} + SITE + REP(SITE) + TREE + FAM.SITE + \mathbf{e} \qquad \textbf{(5)}$$

Where Y is a vector of the data for the traits appropriate to each sampling strategy (combinations of D, BD, PD_s); μ, SITE, REP(SITE), FAM.SITE and **e** are as previously defined; and TREE are individual tree breeding values for each trait. The model terms TREE and **e** included an inter-trait variance and covariance matrix pooled across sites. These were fixed to values calculated in model (2) in all breeding value calculations (see footnote on Table 7 for values). Therefore an assumption in this sampling simulation is that appropriate genetic parameters are known. Separate models were run for each sampling strategy.

Trees were ranked on a selection index and the top 30 trees selected (2.5% of trees). This was done for each selection strategy and the index used was:

$$\boldsymbol{I} = BV_D.W_D/\sigma_D + BV_{BD}.W_{BD}/\sigma_{BD} \qquad \textbf{(6)}$$

Where ***I*** is a unitless index value; BV_D, and BV_{BD} are, respectively, breeding values for diameter and core basic density calculated in equation 5; σ_D and σ_{BD} are additive genetic standard deviations for these traits; and W_D and W_{BD} are economic weights. The weights describe the relative importance of a standard deviation unit of each trait and were W_D=1 and W_{BD}=1. These are weights that approximate economic weights given by Borralho *et al*. (1993) and Greaves *et al*. (1997) when converted to standard deviation units. Each selection strategy had its own set of breeding values and these were used in the selection index. Genetic gains were calculated by averaging breeding values of the selected population and were expressed relative to gains that could be obtained using the 'maximum strategy' (ie. 100% core sampling).

The costs of sampling were calculated for each strategy. Core sampling for basic density is assumed to cost $10.5 per tree, which includes field collection and laboratory processing. The cost of Pilodyn measurements is assumed to be $1.5 per tree. These costs are based on the times taken during this study.

RESULTS AND DISCUSSION

Site differences

There were statistically significant differences between sites for diameter, basic density and Pilodyn penetration (Table 3). The peak mean annual increments for each site were predicted using Farm Forestry Toolbox (Private Forests Tasmania 2001) from mean dominant height and basal area data. Growth rates on all sites were good and maximum growth rates are projected to be 25, 28 and 35 $m^3ha^{-1}year^{-1}$ for Dial, Gog and Kamona respectively. Basic density was similar at Dial and Kamona, but 5% higher at Gog. Similarly, Pilodyn penetration was 5% lower at Gog. Pilodyn penetration was significantly lower in winter when compared to summer but the magnitude of differences was not consistent across sites. At Dial, winter measurements were 3% lower but at Gog, winter measurements were 12% lower.

Table 3. Least square means (± standard error) for each site.

Trait		Dial	Gog	Kamona
D	cm	18.4 ± 1.0	20.8 ± 1.0	23.5 ± 1.1
BD	$kg\ m^{-3}$	441 ± 5	470 ± 5	449 ± 6
PD_s	mm	12.3 ± 0.3	11.7 ± 0.3	12.3 ± 0.3
PD_w	mm	11.9 ± 0.3	10.3 ± 0.3	

Genetic parameters

Heritabilities for diameter were moderate (0.39 in a combined site analysis) and differences between sites were not significant (Table 4). For basic density, heritabilities were high (0.55 in a combined site analysis) and estimates varied significantly across sites (0.47 to 0.96). One site (Gog) had a very high heritability due primarily to a substantially higher additive genetic variance. Heritabilities for Pilodyn penetration were also high (0.47 in a combined site analysis) but less variable across sites (0.47 to 0.59). For the Gog site, Pilodyn heritability was significantly less than that of basic density. Pilodyn heritabilities were not significantly different between summer and winter measurements.

There were strong adverse genetic correlations between diameter and basic density (Table 5). Values for individual sites ranged from –0.13 to –0.79, and in a pooled analysis the correlation was –0.55. Genetic correlations between diameter and Pilodyn penetration were positive, and very similar in magnitude to those for diameter and basic density with values ranging between 0.56 to 0.82. Genetic correlations between Pilodyn penetration and basic density were strongly negative and differences between sites were significant. The range of values was -0.79 to -0.98, and in a pooled analysis the correlation was -0.90 (Table 5).

There were no significant genotype by environment interactions for diameter or for Pilodyn penetration in either summer and winter. For these traits, family by site variance was zero (Table 4) and genetic correlations between sites were high (Table 6). Genotype by environment interaction for basic density was significant but relatively small, with family by site variance accounting for 6% of the total variation (Table 4), and between site genetic correlations ranging from 0.68 to 0.89 (Table 6). The interaction appeared to be caused by minor rank changes from many families and excluding groups of families did not substantially reduce the interaction.

Genetic parameters for *E. nitens* basic density and Pilodyn penetration have been published by Greaves *et al*. 1996, Gea *et al.* 1997, and Tibbits and Hodge 1998. Heritabilities for basic density (combined site analyses) range from 0.45 to 0.73 and the value from this study falls within the middle of that range. Similarly, the heritability for Pilodyn penetration from this study falls within the published range, which is 0.41 to 0.60. Genetic correlations between basic density and Pilodyn have always been found to be high (–0.92 to –1) and this study was no exception (–0.90). However genetic correlations for diameter-basic density and diameter-Pilodyn calculated in this study are very different to those found elsewhere. Diameter-Pilodyn correlations have been reported as being near zero (Gea *et al.* 1997, Tibbits and Hodge 1998) but in this study they were strongly adverse (0.63). The same authors report diameter-basic density correlations from zero to weakly negative (–0.24), but in this study the correlation was found to be strongly negative (–0.55).

Table 4. Variance components (± standard error) and heritabilities (± standard error) for diameter at breast height, basic density, and Pilodyn penetration.

Trait	Site	σ^2 family	σ^2 family.site	σ^2 error	h^2
Diameter (cm)	Dial	4.29 ± 1.52		25.03 ± 1.83	0.37 ± 0.12
	Gog	5.97 ± 2.07		28.04 ± 2.17	0.44 ± 0.13
	Kamona	5.45 ± 2.24		38.70 ± 3.12	0.31 ± 0.12
	All sites	5.58 ± 1.55	0	29.88 ± 1.29	0.39 ± 0.09
Basic density (kg m^{-3})	Dial	168 ± 60		720 ± 64	0.47 ± 0.15
	Gog	377 ± 111		605 ± 55	0.96 ± 0.19
	Kamona	201 ± 72		590 ± 59	0.64 ± 0.18
	All sites	202 ± 59	59 ± 26	689 ± 37	0.55 ± 0.13
Pilodyn, summer (mm)	Dial	0.475 ± 0.173		2.040 ± 0.176	0.47 ± 0.15
	Gog	0.486 ± 0.168		1.561 ± 0.141	0.59 ± 0.17
	Kamona	0.435 ± 0.163		1.575 ± 0.158	0.54 ± 0.17
	All sites	0.434 ± 0.124	0	1.858 ± 0.095	0.47 ± 0.11
Pilodyn, winter (mm)	Dial	0.581 ± 0.211		2.511 ± 0.216	0.47 ± 0.15
	Gog	0.345 ± 0.130		1.629 ± 0.147	0.44 ± 0.14
	All sites	0.436 ± 0.131	0	2.142 ± 0.125	0.42 ± 0.11

Table 5. Genetic correlations (r_G) with standard errors above diagonal and phenotypic correlations (r) below diagonal.

Site		D	BD	PD_S	PD_W
Dial	D		-0.13 ± 0.25	0.56 ± 0.20	0.60 ± 0.21
	BD	-0.17 *		-0.79 ± 0.13	-0.71 ± 0.14
	PD_S	0.12	-0.45 *		0.98 ± 0.05
	PD_W	-0.04	-0.45 *	0.70 *	
Gog	D		-0.79 ± 0.12	0.68 ± 0.17	0.51 ± 0.23
	BD	-0.12		-0.98 ± 0.04	-0.95 ± 0.06
	PD_S	0.04	-0.64 *		0.98 ± 0.05
	PD_W	-0.12	-0.60 *	0.66 *	
Kamona	D		-0.72 ± 0.20	0.82 ± 0.19	
	BD	-0.03		-0.81 ± 0.11	
	PD_S	0.07	-0.58 *		
All sites	D		-0.55 ± 0.15	0.63 ± 0.14	0.52 ± 0.16
	BD	-0.11		-0.90 ± 0.06	-0.87 ± 0.07
	PD_S	0.03	-0.53 *		0.96 ± 0.03
	PD_W	-0.08	-0.54 *	0.68 *	

* Significantly different from 0 at 0.05.

Table 6. Genetic correlations (± standard error) between sites.

Trait	Dial & Gog	Dial & Kamona	Gog & Kamona
D	1.09 ± 0.10	0.95 ± 0.15	1.15 ± 0.12
BD	0.76 ± 0.14	0.68 ± 0.19	0.89 ± 0.11
PD_s	0.76 ± 0.17	0.99 ± 0.13	0.88 ± 0.14
PD_w	0.99 ± 0.13		

Comparing sampling strategies

Basic density was predicted to increase by 26 kg m^{-3} under the most intensive sampling strategy (sampling approximately 24 trees per family and 40 families). This represents an increase in the mean value of nearly 6% (from 451 to 477 kg m^{-3}). The cost of this sampling strategy is estimated to be AUD$10 K. A range of alternate basic density sampling strategies was evaluated and the gains and costs are shown in Table 7. The gains have been expressed as a percentage of this value (ie. 100% is a gain of 26 kg m^{-3}).

A two-stage core sampling strategy can deliver at least 74% of potential gains at a much lower cost (strategy 2 in Table 7). This strategy involves randomly sampling all families, making initial selections using diameter and family basic density, and then re-sampling highly ranked trees. Differences between sampling the top 10% and top 20% are not large; 13% of the total potential gain (or about 3 kg m^{-3}) is foregone by taking a smaller 'top' sample. Increasing the size of the random sample within families from 6 to 12 did not substantially increase gains. Therefore an efficient use of a limited sampling budget would be to sample fewer trees per family in 'stage-1' (6 trees appears adequate) and more 'top' trees in stage-2.

A two-stage sampling strategy involving Pilodyn for the stage-1 family sample and cores for the stage-2 individual tree sample also gave reasonable gains provided the family sample was sufficiently large (strategy 3 Table 7). Up to 70% of potential gains can be achieved under this sampling strategy. This strategy costs about half that of a two-stage coring strategy and would be suitable if the sampling budget is limited. However gains were considerably less with only 6 Pilodyn readings per family which suggests that this number of Pilodyn readings does not reliably rank families.

Sampling using a Pilodyn alone delivered substantially less gain (strategy 4 Table 7). At best, only 29% of potential gains were achieved. Pilodyn readings cannot accurately rank an individual tree for basic density and sampling more 'top' trees using a Pilodyn gave only a marginal increase in gains. If the sampling budget is limited then a stage-1 Pilodyn sampling and stage-2 core sampling will always give substantially better gains for virtually the same expenditure.

Differences in genetic gains for summer and winter Pilodyn assessments were compared for the two-stage Pilodyn plus cores sampling procedure (ie. strategies 3.1 and 3.2). It was thought that shooting a Pilodyn into a band of late-wood may give different results than when shooting into a band of early-wood. Gains were almost identical and therefore Pilodyn assessments in different seasons do not appear to alter the discriminating power of measurements.

Table 7. Comparison of genetic gains in basic density and costs (x AUD$1000) for different sampling strategies. Data is expressed as the percentage of gain obtained relative to sampling all trees using cores.

Sampling strategy		Samples per family			
		12		6	
1	**Random within family sample** [1]				
1.1	Cores	56%	($5.0)	33%	($2.5)
1.2	Pilodyn	22%	($0.7)	9%	($0.4)
2	**Two-stage, cores + cores** [1]				
2.1	Family cores + cores top 10% D-BD index	76%	($6.0)	74%	($3.5)
2.2	Family cores + cores top 20% D-BD index	89%	($7.0)	87%	($4.5)
3	**Two-stage, Pilodyn + cores** [1]				
3.1	Family Pilodyn + cores top 10% D-BD index	65%	($1.7)	39%	($1.4)
3.2	Family Pilodyn + cores top 20% D-BD index	70%	($2.7)	57%	($2.4)
4	**Two-stage, Pilodyn + Pilodyn** [1]				
4.1	Family Pilodyn + Pilodyn top 10% D-PD index	20%	($0.9)	12%	($0.5)
4.2	Family Pilodyn + Pilodyn top 20% D-PD index	29%	($1.0)	16%	($0.6)

[1] Trees selected on an index combining diameter and basic density with equal weighting per standard deviation unit on each trait.

In the strategies described above the second stage sample (ie. the top 10 or 20% of trees) was selected using both the diameter data and family basic density data. A second stage sample is sometimes selected using diameter data only, the assumption being that select trees will only come from trees with very good growth rates. However, in this study, at least 20% of potential gain in basic density (or 5 kg m^{-3}) was foregone when selecting the stage-2 sample using diameter data only (Table 8). This reflects the

strongly negative genetic correlation between diameter and basic density – selected trees are not necessarily limited to those with large breeding values for diameter.

Table 8: Comparison of genetic gains in basic density using different stage-2 sampling procedures. Data is expressed as the percentage of gain obtained relative to sampling all trees using cores.

Sampling strategy		Stage-2 selection method	
		D only	D-BD index
2	**Two-stage, cores + cores**		
2.1	Family cores (12 per family) + cores top 10%	56%	76%
2.2	Family cores (12 per family) + cores top 20%	59%	89%
3	**Two-stage, Pilodyn + cores**		
3.1	Family Pilodyn (12 per family) + cores top 10%	36%	65%
3.2	Family Pilodyn (12 per family) + cores top 20%	38%	70%

CONCLUSION

Heritabilities for basic density and Pilodyn penetration were high and the two traits were highly correlated at the genetic level. However for both traits there were strong and adverse genetic correlations with stem diameter. Heritabilities and genetic correlations for Pilodyn assessed in summer (shooting into early-wood) and winter (shooting into late-wood) were not significantly different.

Genetic gains are highest using core samples. An efficient two-stage core sampling strategy is to sample relatively low numbers per family (as few as 6 individuals) in stage-1 and sample up to 20% of the top trees ranked on a diameter-basic density index in stage-2. This strategy delivered 87% of the gains possible by core sampling all trees. A two-stage sampling strategy using Pilodyn to assess random individuals from each family and cores to assess selected individuals can deliver up to 70% of gains at a much lower cost. If using this strategy larger numbers of individuals per family need to be sampled in stage-1 (12 was substantially better than 6 in this study). Selecting for basic density using Pilodyn alone is not recommended despite the very high genetic correlations between basic density and Pilodyn. Pilodyn alone delivered no more than 29% of potential gains, even when large samples were taken.

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