Genetic variation in shrinkage properties of *Eucalyptus pilularis* (Smith) assessed using increment cores: preliminary results.

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Summary

An important challenge facing the hardwood sawmilling industry in Australia is to manage the expanding eucalypt plantation resource to produce high quality standards required for appearance grade products. Plantation-grown logs tend to be smaller than those previously derived from native forest, they suffer increased drying degrade and hence decreased grade recovery. Since wood properties are normally under moderate to high genetic control and have high natural variability, genetic improvement through selection and breeding is one way of improving the wood quality of eucalypt plantations. Assessments of genetic variation in wood properties are difficult and expensive to carry out. As a consequence, the inclusion of wood quality traits in eucalypt breeding programs has to date been limited.

This study is part of a large investigation into the use of non-destructive methods of assessing wood properties by comparing the results with traditional destructive methods. This component of the study investigates the genetic variation in linear shrinkage of 152 open-pollinated families of *Eucalyptus pilularis* (Smith). Increment cores and test blocks were used to assess radial and tangential shrinkage as well as their ratio. Preliminary results at 17% MC and 12% MC are presented here. Heritability estimates were moderate for tangential shrinkage but not significant for radial shrinkage or the ratio of the two. The genetic correlation between shrinkage measured on cores and on blocks at this stage was not sufficient to justify the use of increment cores alone in genetic assessments. Basic density had a moderate and

negative correlation with tangential shrinkage, suggesting that selecting for higher basic density may help reduce tangential shrinkage. The increment core method was not successful at measuring radial shrinkage due to core distortion but an improved method is suggested. Measurements from scans and blocks showed that radial shrinkage was not heritable.

Keywords: shrinkage; increment cores; genetic improvement; *Eucalyptus pilularis,* wood properties.

1. Introduction

Large-scale eucalypt plantations are relatively recent in Australia. While most are being grown for pulpwood, increasing proportions are being managed for sawlog. Some of the plantation resource is expected to supply the growing demand for higher value products such as flooring, furniture and veneers (Nolan *et al*., 2005). This new plantation timber is however markedly different from the native forest regrowth timber it is replacing. Plantation logs are typically younger and smaller than native forest logs, and little is known about their wood properties. It is still uncertain how well the plantation resource can meet the high quality standards required for appearance grade products.

Most wood properties display high intra-specific variability, they are moderately to highly heritable and genetic improvement is one way of achieving high-value products from plantation wood (Donnelly *et al*., 2003). Breeding objectives for eucalypts are increasingly taking into account wood quality. Basic density has played an important role in genetic improvement of pulp regimes of *Eucalyptus urophylla* S.T. Blake*, E. globulus* Labill. and *E. nitens* (Deane and maiden) Maiden (Greaves *et al*., 1997; Wei and Borralho, 1997; Raymond, 2002; Kube and Raymond, 2002). Genetic improvement studies for improving quality of solid-wood products are only beginning.

Assessing wood quality for selection and breeding programs requires that a large number of families and sufficient number of individuals per family be investigated. Traditional methods of assessment are not only costly, they also involve the

destruction of the sample trees and the loss of genetic material (Raymond *et al*., 1998; Raymond, 2002; Downes *et al*., 1997). These factors are driving the development and evaluation of non-destructive methods of assessing wood quality.

Increment cores are the most common form of non-destructive sampling and they have long been used for growth assessments, dendrochronology and to establish forest stand histories. More recently they have been used to assess some wood properties in softwoods and hardwoods employing a wide range of methods. Basic density, pulp yield, grain angle, latewood proportion, extractives content, tracheid length and reaction wood proportion have been measured in increment cores by direct measurements, dissection, image analysis, NIRA (near-infrared reflectance analysis) and SilviScan (Cown *et al*., 1992; Harding and Copley, 2000; Washusen and Ilic, 2001; Raymond and Muneri, 2001; Kube and Raymond, 2002).

Raymond *et al.* (1998) compared the costs and accuracy of measuring basic density using destructive and non-destructive sampling methods in *E. globulus* and *E. nitens*. They found that 4 discs (destructive) per tree taken at different heights explained 95%-98% of the observed variation in basic density, compared to 50%-53% for 4 pilodyn (non-destructive) readings per tree, and 81%-82% for a single increment core (non-destructive) per tree taken. Raymond *et al.* (1998) concluded that increment cores provided the cheapest and the most accurate non-destructive method of assessment, although the rate of pilodyn assessment appears conservative. If the core samples are used to measure other properties, then their cost effectiveness increases further.

Methodologies to assess pulpwood quality using non-destructive methods such as pilodyn and near-infrared spectroscopy are well developed (Greaves *et al*., 1995; Laurence *et al*., 1999). There is a need however to develop similarly reliable methods of assessing wood properties relevant to solid-wood products. Recent studies have investigated the possibility of using increment cores to assess shrinkage in standing trees (Arnold *et al*., 2004; Yang and Pongracic, 2004; Harwood *et al*., 2005; Bandara, 2006). The properties tested included tangential shrinkage and collapse in cores as well as in sawn boards of *E. dunnii* Maiden and *E. globulus*. Cupping in backsawn boards was found to be widespread in one study, and it was suggested that future

assessments include the measurement of radial shrinkage (Harwood *et al*., 2005). The need to correlate core sample measurements to actual defects in sawn boards in order to validate the method was also highlighted (Hamilton *et al*., 2004). A review of studies that have used increment cores for shrinkage assessments is presented in Table 1.

Table 1: Published reports of tangential (T) and radial (R) shrinkage in eucalypts assessed using increment cores.

This study explores the use of increment cores to assess the genetic contribution to linear shrinkage in *E. pilularis* Smith (blackbutt), an important commercial species of the NSW north coast. In 2005-06 Forests NSW produced 217 000 m^3 of *E. pilularis*, of which 60% met the requirements for high quality wood products. The agency currently has 15 000 ha of *E. pilularis* plantations (Henson and Smith, 2006). They have recently initiated the largest inquiry into the genetics of various wood properties ever undertaken. The project involves assessing the genetic contribution to shrinkage and other wood properties in plantation blackbutt, as well as testing a range of non-destructive methods of assessing wood properties for breeding purposes. The non-destructive assessments (coring, pilodyn, longitudinal growth strain, acoustic velocity, NIRA, molecular genetics) are followed by traditional destructive methods of assessing the same properties on the same material, providing a unique and unprecedented opportunity to test each method's accuracy. Destructive assessments include shrinkage and collapse measurements on standard test blocks, mechanical properties testing on standard clear samples and a commercial sawing study to measure shrinkage on standard industrial-size boards.

The study presented here is part of this larger project. This study investigates the genetic contribution to basic density and shrinkage properties as measured in bark to bark increment cores. The purpose of the study is three-fold:

1. Explore the use of increment cores to assess linear shrinkage in both tangential and radial directions.
2. Assess the genetic contribution to shrinkage properties and basic density in a 9-year-old *Eucalyptus pilularis* progeny trial.

3. Identify material of superior dimensional stability to use for future propagation and tree improvement.

2. Methods

To assess the genetic variation in shrinkage properties of *E. pilularis,* 1165 increment cores representing 302 families were collected from a progeny trial. Amongst the trees cored, 599 were subsequently processed into standard size shrinkage blocks measured in the same manner as the increment cores. The ranking results obtained using the non-destructive method (increment cores) was tested against results from the shrinkage blocks (destructive method).

Study material

The genetic material used in this study is a progeny trial growing at Hannam Vale, approximately 40 km south-west of Port Macquarie, NSW (Latitude 31°40', Longitude 152°33', Elevation 150-170 m asl). Mean annual rainfall at the site is 1500 mm and soils are Deep Yellow Earths to Yellow Podzolics. The trial is one of three planted on the NSW north coast in 1997 and 1998 by Forests NSW as the first step in a *E. pilularis* genetic improvement program launched in 1994-95 (Johnson, 2002). An early selection based on growth and form assessment at age 3 years led to the establishment of clonal seed orchards. The study is part of the final selection based on wood quality which will further improve the seed orchards.

The Hannam Vale trial was planted in March 1997 and was 9 years old at the time of assessment. It is an alpha generalised lattice, row-column (18-row x 17-column) design (Williams *et al*., 2002) consisting of 6 replicates and 308 *E. pilularis* open-pollinated families established in 4-tree-row plots. Each replicate contained 308 plots (families) each represented by 4 individuals for a total 24 individuals per family across the replicates and in excess of 7000 trees across the trial. The trees were grown from open-pollinated seed collected from candidate trees from 36 provenances from the NSW central coast to South-east Queensland.

A total of 1165 trees were selected for assessment, 164 of which were used for molecular genetic analysis. The remainder 1001 individuals assessed comprised 152

families each represented by three to 14 individuals per family, with an average of 6.6 individuals per family.

Sample preparation

Bark to bark increment cores 12 mm in diameter were extracted at breast height using a motorised corer developed by Queensland DPI & Fisheries, Wood Quality Improvement Laboratory, Innovative Forest Products Program. All cores were extracted in the north-south direction. After extraction the cores were marked with the tree ID number and placed in aluminium channelling of 13mm internal width. The channels were intended to help keep the pieces of broken cores together, and restrain the cores as they dried. All cores and their channels were placed inside plastic bags immediately after extraction to minimise moisture loss. The bags were kept in refrigeration at the site, then weighed and placed in a freezer at the end of each day. Cores were kept frozen for the duration of the extraction process (24 days). The cores were then saturated by immersion in water until they reached a constant weight (8 days).

Basic density

Basic density was determined using the test method described in *Australian and New Zealand Satndard AS/NZS1080:3-2000 Timber – Method of test – Method 3: Density* (Standards Australia, 2000). Green volume was measured using the displacement method described by Heinricks and Lassen (1970). Cores were weighed on a top-loading analytic balance to 0.00 g accuracy (AS/NZS 1080.3). After completion of the shrinkage measurements, cores were dried in a testing oven at 103ºC for 24 hours. Oven-dried cores were weighed and basic density obtained using formula 1.

$$D_b = \frac{\text{Oven-dry weight (g)}}{\text{Green volume (cm}^3\text{)}} \times 1000 \qquad (1)$$

Where D_b is basic density.

Shrinkage assessment

Assessment of cores

Cores were marked with indelible pencil at each end for radial measurement and at 4 positions (60% and 80% of core length) along the radial length for tangential measurement (4 measurements per core, Figure 1). Measurements were recorded using digital callipers with automatic data entry at 0.01 mm accuracy.

Figure 1: Diagram showing the position of radial and tangential measurements on increment cores.

Cores were first measured in the green condition (saturated). They were then dried in conditioning cabinets at set temperature and relative humidity and measured again when they reached 17%MC, 12% MC and 5% MC so that unit shrinkage could be calculated. Shrinkage at each %MC was calculated for each position, and tangential shrinkage for each core was calculated by averaging the four measurements. All cores were also scanned at each stage of drying using a flatbed scanner. Cores were positioned on the scanner with the longitudinal direction at 90% from the line of scan so that the tangential dimension could be observed. The scanned images at 12%MC were assessed using the ImageJ software (National Institutes of Health) to measure changes in radial length between the two tangential marks on each half of the cores thus avoiding any distortion at the pith.

Assessment of blocks

599 of the 1165 cored trees representing 129 families were felled and 3.2 m logs transported to Southern Cross University for processing. Two shrinkage blocks (one from each of the northern and southern side of the tree) of 25 mm (radial) x 25 mm (tangential) x 100 mm (longitudinal) dimension were cut from each log at a height of 1.3 m. The blocks were cut from the outer heartwood (approximately 40 to 80%). The blocks were marked on the radial and tangential faces at three locations along the longitudinal axis as described in Kingston and Risdon (1961). Blocks were measured in the green condition and in similarity with the cores, they were dried in conditioning cabinets and measured at 17% MC, 12% MC and 5% MC.

Statistical analysis

Family and provenance means analyses were generated using Microsoft Excel. Variance components, heritabilities and genetic correlations were calculated using

ASReml Version 2.00a (Gilmour *et al*., 2006). Although the trial was planted in a lattice, row-column design, not all individual trees in the trial were used for the wood properties assessment. The limited subset of trees cored did not allow the inclusion of Row, Column and Plot effects in the model. Therefore the model used was simplified to a Randomised Complete Block (Williams *et al*., 2002). The univariate mixed model fitted here (equation 2) used provenance and replicate as fixed effects and individual tree as random effect. A separate pedigree file was used to define the genetic relationships of individual trees. Individual-tree, narrow-sense heritability estimates were calculated using equation 3. An explanation of the abbreviations used to describe the results is presented in Table 2.

$$Y = \mu + PROV + REP + TREE + \varepsilon \quad (2)$$

Where Y is the vector for each trait

μ is the overfall mean for the trait

PROV is the fixed, provenance effect

REP is the fixed, replicate effect

TREE is the random, genetic effect

ε is the residual (random error)

$$h^2 = \sigma_t^2 \ / \ \sigma_a^2 \quad (3)$$

Where h^2 is the narrow sense heritability

σ_t^2 is the individual tree variance

σ_a^2 is the total phenotypic variance

Table 2: Description of abbreviations used to present wood traits investigated in *E. pilularis* progeny trial.

3. Results

Data summary

Since the drying of the shrinkage blocks is still in progress, results at 5% MC and unit shrinkage results are not presented here. Data summary for the preliminary results available to date is presented in Table 3. Distortion of the cores at the pith in the early stages of drying was sufficient to prevent subsequent radial measurements in most of the samples. While

tangential shrinkage was successfully measured from increment cores, radial shrinkage at 12% was obtained from scanned images.

Mean tangential shrinkage was higher than that reported for mature native forest *E. pilularis*, but radial shrinkage was lower (Bootle, 1983). The ratio of tangential to radial shrinkage was high for the cores (3:1) and higher for the blocks (4:1). Variability was high for all properties measured, with tangential shrinkage at 12% MC varying from 4.4% to 18.9% on cores and from 2.3% to 18.7% on blocks. The number of sample blocks available dropped from 599 to 354 because some of the logs were either too small for processing, their form was too poor, internal defects were such that no clear sample could be cut or the pith was so eccentric it was not possible to obtain blocks with true tangential and radial planes.

Table 3: Data summary for the properties assessed in the *E. pilularis* progeny trial including growth parameters assessed at 104 months age.

Genetic paraeters

Estimates of genetic parameters are presented in Tables 4 to 6. Tangential shrinkage was measured at three different stages of drying so that unit shrinkage could be measured. Shrinkage of blocks to 5% MC was not complete at the time of submission so unit shrinkage results will be presented later. The results presented here include shrinkage to 17% MC and 12% MC.

Table 4: Heritability estimates (diagonal), phenotypic correlations (below the diagonal) and genetic correlations (above the diagonal) for tangential shrinkage traits showing standard errors in brackets ( ) and significant estimates and genetic correlations in bold. Standard error is not reported where the analysis were bound (restricted to 1).

Table 5: Heritability estimates (diagonal), phenotypic correlations (below the diagonal) and genetic correlations (above the diagonal) for radial shrinkage traits showing standard errors in brackets ( ) and significant genetic correlation in bold.

Table 6: Heritability estimates (diagonal), phenotypic correlations (below the diagonal) and genetic correlations (above the diagonal) for core basic density and shrinkage at 12% MC. Standard errors are shown in brackets ( ) and significant estimates and genetic correlations in bold. Standard error is not reported where the analysis were bound (restricted to 1).

Heritability estimates were moderate for CT shrinkage, BT17 and CBD, but low for BT12 (Table 4). Heritability estimates are low for BR12 (0.17) and BR17 (0.17), and very low for CR12 (scans) (0.10) calculated from scan measurements, with no heritability estimates for radial shrinkage being significant (Table 5). Overall standard errors for blocks were higher than for cores, most probably because of a smaller sample size. The error for BT12 heritability estimate is too high to be considered reliable. The ratio of tangential to radial shrinkage had a low heritability estimate for the cores (0.14) and was nil for the blocks (Table 3).

Phenotypic correlations between core and block tangential shrinkage were very consistent and ranged from 0.56 to 0.57 (Table 4). CR12 (scans) and BR12 only had a weak phenotypic correlation (0.19), a moderate genetic correlation (0.63) but neither was significant (Table 5).

Genetic correlations were all significant for tangential shrinkage (Table 4). Standard error is not reported where the analyses were bound (restricted to 1). The highest genetic correlation was 0.999 between BT12 and all three CT stages (Table 5). CBD had a negative correlation with tangential shrinkage (Table 6).

Analysis of Sample selection

Analysis of growth traits for the Hannam Vale trial in early 2006 produced significant heritability estimates of 0.27 for height and 0.20 for diameter, confirming the quality of the progeny trial design (Forests NSW, unpublished report, 2006). However, the reduced variability in growth imposed by the pre-selection based on growth affected the current experimental design and potentially contributed to reduced heritability estimates observed in this study. Table 7 compares the estimates of genetic parameters obtained for the whole balanced trial with the estimates obtained for the reduced unbalanced design of the trees selected for wood quality assessment.

Table 7: Genetic parameter estimates of growth traits for the Hannam Vale progeny trial compared to the same estimates for the sample selected for the wood quality assessments.

4. Discussion

The use of increment cores

The method of assessing shrinkage tested in this study was based on past results and recommendations of studies involving eucalypts (Hamilton *et al*., 2004; Harwood *et al*., 2005; Bandara, 2006) and using whole increment cores for ease, speed and cost efficiency. Four tangential measurements per core proved to be sufficient to assess genetic variability in the

trial. Radial measurements using the length of whole cores, however were not successful. Future studies could explore the use of the tangential marks to measure radial shrinkage directly on the cores using callipers. A reduced accuracy is expected on such radial measurements because radial shrinkage is typically half that of tangential shrinkage. One way of alleviating this problem may be to take an extra tangential measurement closer to the pith (but making sure to avoid the pith where the distortion occurs). This would provide a longer distance for radial shrinkage measurement as well as an extra tangential measurement.

Genetic variability in shrinkage

Reports of heritability estimates for tangential and radial shrinkage vary widely, as shown in Table 8. Tangential shrinkage has consistently been found in several studies including this study to be heritable. However, heritability of tangential shrinkage measured on test blocks at 12% MC was not significant. Heritability estimates for tangential shrinkage measured on cores at all %MC, and for blocks at 17% MC is however within results reported in other studies (Table 4, 8).

Radial shrinkage measurements from scans did not correlate well with radial shrinkage measured on test blocks. Measuring radial shrinkage directly from tangential marks on cores may be worth investigating further, although the present study showed no indication of radial shrinkage (and therefore T:R) being controlled by genetic processes. This is consistent with at least one other study on *E. grandis* (Bandara, 2006).

Table 8: Reported heritability estimates for tangential and radial shrinkage in plantation eucalypts.

The strength of the genetic correlations found in this study between tangential shrinkage measured on increment cores and tangential shrinkage measured on shrinkage blocks are not sufficient to advocate the systematic use of increment cores in genetic assessments of linear shrinkage. Increment cores may however be used as a guide for testing relationships, but more accurate assessments using traditional methods are still required.

The motivation behind the present study came from a *E. dunnii* study conducted at Boambee State Forest, NSW in 2004 (Henson *et al*., 2004). Tangential shrinkage was measured in boards and in cores dried under harsh conditions in order to enhance differences between families in their tendency to collapse. Results from the two studies are compared in Table 9. The phenotypic correlation between the two methods was higher for *E. pilularis* at Hannam Vale than for *E. dunnii* at Boambee. The very high genetic correlation obtained for *E. dunnii* at Boambee is supported by the present results, despite the different drying schedules employed on the Boambee and Hannam Vale material. What remains to be ascertained, is

whether either of these methods correlates with actual drying performance in sawn boards dried under standard industrial conditions.

Table 9: Comparison of phenotypic and genetic correlations between the present study and *E. dunnii* progeny trial growing at Boambee State Forest, NSW.

There are only limited reports on relationships between basic density and linear shrinkage. Both positive and negative correlations have been found, sometimes for the same species (Bandara, 2006; Wu *et al*., 2006; Chafe, 1994; Chafe, 1985; Sesbou and Nepveu, 1978). In the present study basic density had a mild but negative impact on tangential shrinkage, a favourable situation indicating that selecting for increased basic density will also reduce somewhat tangential shrinkage. Pilodyn measurement had a high negative genetic correlation (-0.999 (bound)) with core basic density (Data not shown), pointing to the possibility of using pilodyn readings as an indirect measure for both density and tangential shrinkage.

Economic benefits of using core samples for wood quality assessment

Increment cores are already established as a reliable, cost-efficient method of assessing basic density in standing trees (Raymond *et al*., 1998). The present study provided the opportunity to assess their cost-efficiency in measuring shrinkage properties. Table 10 compares the number of person-days required in this study to process the equivalent number of increment cores and shrinkage blocks. It was assumed, for the purpose of the comparison, that genetic assessments require the investigation of 120 families and 10 individuals per family. One sample per tree was collected from 1200 trees for the increment core method, but two samples per tree were obtained from 1200 trees for the test block method. One hundred increment cores can be obtained per day with a team of three people using a motorised corer, for a total of 36 work days. In contrast, standard test blocks require a team of three people to fall, label and cut 1 metre billets from 40 trees per day, for a total of 90 work days to obtain the 1200 billets. Additionally, a team of four people is needed to process 1-metre billets into standard test blocks (100 mm x 25 mm x 25 mm) averaging 60 billets per day, giving a total of 80 work days for the 1200 logs. Measurements at 17%, 12% and 5% MC including weighing of samples took a comparable amount of time at each stage, but in the green condition samples also had to be marked.

Table 10: Comparison of person-days required for collecting and processing 1200 samples for shrinkage assessments using increment cores and standard test blocks.

The analysis presented in Table 10 shows that labour costs for the destructive method are expected to be around three and a half times those of the non-destructive method. The higher cost of transport of logs to the processing facility compared to transport of cores was

not included in the above analysis. If the value of the retained trees is also taken into account, then the cost efficiency of increment cores increases further. Superior trees can thus be assessed and retained in the breeding population to produce offspring in the future. The reduced cost of this non-destructive assessment method however has to be balanced against the method's accuracy.

5. Conclusions

The present study found moderate heritability estimates for tangential shrinkage measured on increment cores and on shrinkage blocks in a *E. pilularis* progeny trial, consistent with estimates found in other studies. The strength of the genetic correlation however was not sufficient to eliminate the need for destructive assessment, despite the much lower cost of the non-destructive method. However it was found that selecting for higher basic density using pilodyn may indirectly contribute to reducing tangential shrinkage. Less linear shrinkage and less variability in shrinkage reduces the need for over-cutting in sawmills, improving recovery and product uniformity. Radial shrinkage and the ratio of tangential to radial shrinkage were not heritable. Further investigations are required to establish a reliable, cost-effective and non-destructive method of measuring radial shrinkage, if a reduction in the occurrence of cupping when backsawing young plantation logs is to be achieved.

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Table 1: Published reports of tangential (T) and radial (R) shrinkage in eucalypts assessed using increment cores.

Source	*Species*	*Properties measured*	*Method*
Washusen and Ilic, 2001	*E. globulus*	T and R shrinkage T and R collapse Tension wood properties	12 mm cores Dried to 17%MC Reconditioned 1hr
Yang and Pongracic, 2004	*E. globulus*	T and R shrinkage	Dried to 12%MC (30C 65%r.h.)
Hamilton *et al*., 2004	*E. nitens*	Volumetric shrinkage	12 mm cores Dried to 12%MC (22C 30%r.h.)
Kube and Raymond, 2005	*E. nitens*	T collapse Basic density Cellulose content	12 mm cores Oven-dried (105C)
Harwood *et al*., 2005 Bandara, 2006	*E. dunnii*	T shrinkage Basic density	12x12 mm flitches (pseudo-cores) Dried at 70C for 48 hrs Reconditioned 1/2 hr
Bandara, 2006	*E. grandis*	T and R shrinkage	15x15 mm flitches (pseudo-cores) Dried at 25C 65%r.h. Reconditioned 1 hr

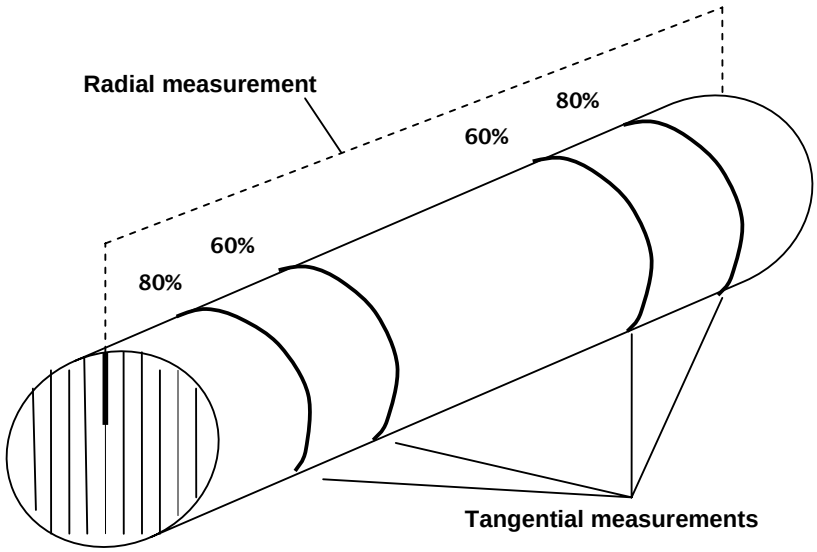

Figure 1: Diagram showing the position of radial and tangential measurements on increment cores.

Table 2: Description of abbreviations used to present wood traits investigated in *E. pilularis* progeny trial.

Abbreviation	Unit	Trait
CBD	kg/m^3	Core basic density
C		Core
B		Block
T	%	Tangential shrinkage
R	%	Radial shrinkage
17, 12	%	17% MC, 12% MC
T:R		Ratio of tangential to radial shrinkage at 12% MC
MC	%	Moisture content
h^2		Heritability estimate, narrow-sense, single-tree
SE		Standard error
SD		Standard deviation
CV		Coefficient of variation

Table 3: Data summary for the properties assessed in the *E. pilularis* progeny trial including growth parameters assessed at 104 months age.

Tree	n	Mean	SD	CV	h^2	SE
DBH (104 months)	1001	20.94	2.84	0.14	0.02	0.08
HT (104 months)	1001	22.99	2.42	0.11	0.12	0.10
VOL (104 months)	1001	0.29	0.10	0.33	0.03	0.08
Pilodyn	999	14.61	1.64	0.11	0.54	0.13
CBD	994	470.20	44.63	0.09	0.33	0.10
CT17	999	7.73	2.25	0.29	0.32	0.10
CT12	999	9.42	2.03	0.22	0.36	0.10
CR12 (scans)	880	3.91	1.78	0.45	0.10	0.09
T:R core	878	3.04	2.51	0.82	0.14	0.11
BT17	356	7.87	2.85	0.36	0.43	0.23
BT12	353	8.62	2.62	0.30	0.11	0.21
BR17	355	2.42	1.33	0.55	0.17	0.21
BR12	354	2.73	1.28	0.47	0.17	0.21
T:R block	353	4.07	3.81	0.94	0.00	0.00

Table 4: Heritability estimates (diagonal), phenotypic correlations (below the diagonal) and genetic correlations (above the diagonal) for tangential shrinkage traits showing standard errors in brackets ( ) and significant estimates and genetic correlations in **bold**. Standard error is not reported where the analysis were bound (restricted to 1).

		Cores		**Blocks**	
		CT17	**CT12**	**BT17**	**BT12**
Cores	**CT17**	**0.32 (0.10)**	**0.90 (0.04)**	**0.53 (0.24)**	0.99 (bound)
	CT12	0.91	**0.36 (0.10)**	**0.90 (0.26)**	0.99 (bound)
Blocks	**BT17**	0.56	0.57	**0.43 (0.23)**	0.99 (bound)
	BT12	0.56	0.56	0.88	0.11 (0.21)

Table 5: Heritability estimates (diagonal), phenotypic correlations (below the diagonal) and genetic correlations (above the diagonal) for radial shrinkage traits showing standard errors in brackets ( ) and significant genetic correlation in **bold**.

		Cores	Blocks	
		CR12 (scans)	**BR17**	**BR12**
Cores	**CR12 (sca**	0.10 (0.09)	-0.07 (0.94)	0.63 (0.84)
Blocks	**BR17**	0.23	0.17 (0.21)	**0.89 (0.29)**
	BR12	0.19	0.79	0.17 (0.21)

Table 6: Heritability estimates (diagonal), phenotypic correlations (below the diagonal) and genetic correlations (above the diagonal) for core basic density and shrinkage at 12% MC. Standard errors are shown in brackets ( ) and significant estimates and genetic correlations in **bold.** Standard error is not reported where the analysis were bound (restricted to 1).

	BT12	**CT12**	**CBD**
BT12	**0.11 (0.21)**	0.99 (bound)	-0.99 (bound)
CT12	0.56	**0.36 (0.10)**	**-0.57 (0.19)**
CBD	-0.13	-0.12	**0.33 (0.10)**

Table 7: Genetic parameter estimates of growth traits for the Hannam Vale progeny trial compared to the same estimates for the sample selected for the wood quality assessments.

Trait	Whole trial	Wood quality selection
n ind/fam	24	3-14 (6.6 av.)
Total n ind	7350	1001
Height h^2 (SE)	0.27 (0.04)	0.17 (0.10)
Diameter h^2 (SE)	0.20 (0.04)	0.07 (0.09)

Table 8: Reported heritability estimates for tangential and radial shrinkage in plantation eucalypts.

		Heritability estimate (SE)			
Source	***Species***	**T shr**	**R shr**	***n* (ind.)**	***n* (fam.)**
Henson *et al*., 2004	*E. dunnii*	0.70 (0.31)	0.56 (0.31)	179	47
Harwood *et al*., 2005	*E. dunnii*	0.63 (0.24)[1] 0.30 (0.18)[2]	- -	215	47
Bandara, 2006	*E. grandis*	0.29 (0.15)	0.06 (0.13)	320	50
Verryn and Turner, 2000	*E. grandis*	-	0.41 (0.14)	472	90
This study - Cores (12%MC)	*E. pilularis*	0.36 (0.10)	0.10 (0.09)	999	152
- Blocks (12% MC)		0.11 (0.21)	0.17 (0.21)	354	129
- Blocks (17% MC)		0.43 (0.23)	0.17 (0.21)	356	129

Table 9: Comparison of phenotypic and genetic correlations between the present study and *E. dunnii* progeny trial growing at Boambee State Forest, NSW.

	Phenotypic correlation	Genetic correlation (SE)
Boambee *E.dunnii* Tangential shrinkage (Core and 25 mm x 100mm board)	0.480	0.996 (0.13)
HannamVale *E. pilularis* Tangential shrinkage (Core and shrinkage block)	0.559	0.999 (bound)

Table 10: Comparison of person-days required for collecting and processing 1200 samples for shrinkage assessments using increment cores and standard test blocks.

	Sample collection	Sample preparation	Measuring and weighing	**Total**
Increment cores	36		29	**65**
Shrinkage blocks	90	80	58	**228**