# GENETIC VARIATION IN SHRINKAGE PROPERTIES OF *EUCALYPTUS PILULARIS* ASSESSED USING INCREMENT CORES AND TEST BLOCKS*

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## ABSTRACT

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 programmes has to date been limited. This study was part of a large investigation into the use of non-destructive methods of assessing wood properties by comparing the results with those from traditional destructive methods. This component of the study investigated the genetic variation in linear shrinkage of 152 open-pollinated families of *Eucalyptus pilularis* (Smith) at 17% m.c., 12% m.c., and 5% m.c. Increment cores and test blocks were used to assess radial and tangential shrinkage as well as their ratio. Heritability estimates were moderate for tangential shrinkage but not significant for radial shrinkage or the ratios 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. Measurements from scans and blocks showed that radial shrinkage was not heritable.

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

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## INTRODUCTION

Large-scale eucalypt plantations are a relatively recent phenomenon in Australia. Most are being grown for pulpwood, but increasing numbers are being managed for sawlogs. 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). However, this new plantation timber is 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, and are moderately to highly heritable; 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 & Maiden) Maiden (Greaves *et al.* 1997; Wei & Borralho 1997; Raymond 2002; Kube & Raymond 2002). Genetic improvement studies for improving quality of solid-wood products are only beginning.

Assessing wood quality for selection and breeding programmes requires investigation of a large number of families and a sufficient number of individuals per family. Traditional methods of assessment are not only costly — they also involve the destruction of the sample trees and the loss of genetic material (Downes *et al.* 1997; Raymond *et al.* 1998; Raymond 2002). 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, for 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 & Copley 2000; Raymond & Muneri 2001; Washusen & Ilic 2001; Kube & 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 four discs per tree taken (destructively) at different heights explained 95–98% of the observed variation in basic density, compared to 50–53% for four pilodyn (non-destructive) readings per tree, and 81–82% for

a single increment core (non-destructive) taken per tree. Raymond *et al*. (1998) concluded that increment cores provided the cheapest and the most accurate non-destructive method of assessment, although the rate for pilodyn assessment appears conservative. If the core samples are used to measure other properties, then their cost effectiveness increases further.

Non-destructive methods for asssessing pulpwood quality, 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 & 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 list of studies that have used increment cores for shrinkage assessments is presented in Table 1.

The study reported here explored the use of increment cores to assess the genetic contribution to linear shrinkage in *E. pilularis*, an important commercial species of the New South Wales 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 & Smith 2007). They have recently initiated the largest inquiry ever undertaken into the genetics of various wood properties. The project involves assessing the genetic contribution to shrinkage and other wood properties in *E. pilularis*, 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 was part of the larger project. This study investigated the genetic contribution to basic density and shrinkage properties as measured in bark-to-bark increment cores. The purpose of the study was three-fold:

(1) Explore the use of increment cores to assess linear shrinkage in both tangential and radial directions;

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

| Source | Species | Properties measured | Method |
|---|---|---|---|
| Washusen & Ilic 2001 | *E. globulus* | T and R shrinkage<br>T and R collapse<br>Tension wood properties | 12 mm cores dried to 17% m.c.<br><br>Reconditioned 1 h |
| Yang & Pongracic 2004 | *E. globulus* | T and R shrinkage | Dried to 12% m.c. (30°C, 65% RH) |
| Hamilton *et al.* 2004 | *E. nitens* | Volumetric shrinkage | 12 mm cores dried to 12% m.c. (22°C, 30% RH) |
| Kube & Raymond 2002 | *E. nitens* | T collapse<br>Basic density<br>Cellulose content | 12 mm cores. Oven dried (105°C) |
| Harwood *et al.* 2005.<br>Bandara 2006 | *E. dunnii* | T shrinkage<br>Basic density | 12×12 mm flitches (pseudo-cores) dried at 70°C for 48 h. Reconditioned 0.5 h. |
| Bandara 2006 | *E.grandis* | T and R shrinkage | 15×15 mm flitches (pseudo-cores) dried at 25°C, 65%RH. Reconditioned 1 h. |

(2) Assess the genetic contribution to shrinkage properties and basic density in a 9-year-old *E. pilularis* progeny trial;

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

## METHODS

### Study Material

The genetic material used in this study was from 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 a.s.l.). Mean annual rainfall at the site was 1500 mm and soils were Deep Yellow Earths to Yellow Podzolics. The trial was 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 programme launched in 1994–95 (I.G.Johnson unpubl. data). An early selection based on growth and form assessment at age 3 years lead to the establishment of clonal seed orchards. The study was 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 was an alpha generalised lattice, row-column (18-row × 17-column) design (Williams *et al*. 2002) consisting of six replicates and 308 *E. pilularis* open-pollinated families established in four-tree-row plots. Each replicate contained 308 plots (families) each represented by four individuals, for a total 24 individuals per family across the replicates and in excess of 7000 trees across the trial. However, at the time of measurement natural mortality had reduced this to 5465 trees. The trees were grown from open-pollinated seed collected from candidate trees from 36 provenances from the NSW central coast to south-east Queensland.

To assess genetic variation in shrinkage properties of *E. pilularis*, 958 increment cores representing 152 families were collected from a progeny trial, with each family represented by three to 14 individuals per family. A minimum of three individuals per family was used to increase the reliability of heritability estimates.

Amongst the trees cored, 419 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) were tested against results from the shrinkage blocks (destructive method).

### 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 13 mm 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 Standard 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 & 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 was obtained using Formula 1.

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

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 four positions (60% and 80% of core length) along the radial length for tangential measurement (four measurements per core, Fig. 1). Measurements were recorded using digital callipers with automatic data entry at 0.01 mm accuracy.

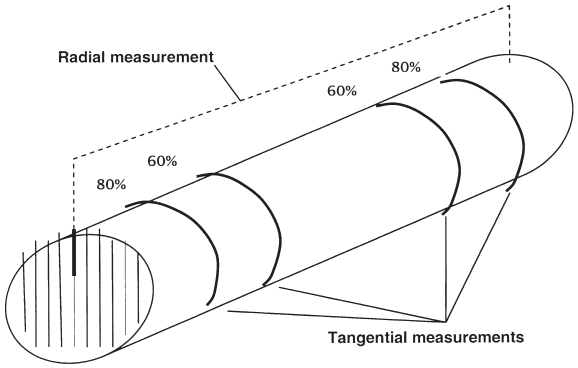


FIG. 1–Position of radial and tangential measurements on increment cores.

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% m.c., 12% m.c., and 5% m.c. so that unit shrinkage could be calculated. Shrinkage at each percentage moisture content 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% m.c. 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*

Of the 958 cored trees representing 152 families, 419 were felled and 3.2-m logs were transported to Southern Cross University for processing. Two shrinkage blocks (one from the northern and one from the southern side of the tree) of 25 mm (radial) × 25 mm (tangential) × 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%), and marked on the radial and tangential faces at three locations along the longitudinal axis (as described by Kingston & Risdon 1961). Blocks were measured in the green condition and, as were the cores, dried in conditioning cabinets and measured at 17% m.c., 12% m.c., and 5% m.c.

## Statistical Analysis

Family and provenance means analysis were generated using Microsoft Excel. Variance components, heritabilities, and genetic correlations were calculated using ASReml Version 2.00a (Gilmour *et al*. 2006). The model used in analysis constrained all variance components to be positive numbers, which meant calculated heritabilities were bound to be between –1.0 and 1.0. 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

TABLE 2–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% m.c., 12% m.c. |
| T:R | | Ratio of tangential to radial shrinkage at 12% m.c. |
| m.c. | % | Moisture content |
| $h^2$ | | Heritability estimate, narrow-sense, single-tree |
| s.e. | | Standard error |
| s.d. | | Standard deviation |
| CV | | Coefficient of variation |

$\mu$ 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
$\varepsilon$ is the residual (random error)

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

where $h^2$ is the narrow sense heritability
$\sigma_t^2$ is the individual tree variance
$\sigma_a^2$ is the total phenotypic variance

## RESULTS

### Data Summary

A summary of data 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. Tangential shrinkage was successfully measured from increment cores, but radial shrinkage at 12% was obtained from scanned images.

Mean tangential shrinkage was higher than that reported for mature native *E. pilularis* forest, 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% m.c. 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 419 to 340 because some of the logs were 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 of age.

| Trait | n | Mean | s.d. | CV (%) | $h^2$ | s.e. |
|---|---|---|---|---|---|---|
| Dbh | 5465 | 18.59 | 4.82 | 0.26 | 0.20 | 0.04 |
| HT | 5462 | 20.73 | 4.45 | 0.21 | 0.27 | 0.04 |
| Vol | 5462 | 0.23 | 0.13 | 0.56 | 0.22 | 0.04 |
| CBD | 953 | 470.03 | 44.16 | 0.09 | 0.33 | 0.11 |
| CT17 | 958 | 7.70 | 2.23 | 0.29 | 0.35 | 0.11 |
| CT12 | 958 | 9.37 | 2.01 | 0.21 | 0.38 | 0.12 |
| CT5 | 957 | 11.07 | 2.04 | 0.18 | 0.37 | 0.11 |
| CR12 (scans) | 849 | 3.89 | 1.77 | 0.46 | 0.02 | 0.10 |
| T:R core | 847 | 3.05 | 2.54 | 0.83 | 0.15 | 0.12 |
| BT17 | 340 | 7.89 | 2.84 | 0.36 | 0.48 | 0.26 |
| BT12 | 336 | 8.65 | 2.62 | 0.30 | 0.12 | 0.24 |
| BT5 | 334 | 12.75 | 3.24 | 0.25 | 0.27 | 0.27 |
| BR17 | 339 | 2.44 | 1.35 | 0.55 | 0.11 | 0.25 |
| BR12 | 337 | 2.73 | 1.29 | 0.47 | 0.08 | 0.24 |
| BR5 | 334 | 5.02 | 1.75 | 0.35 | 0.21 | 0.26 |
| T:R block | 336 | 4.11 | 3.89 | 0.95 | 0.00 | 0.00 |

## Genetic Parameters

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.

Heritability estimates were moderate for CT shrinkage (range from 0.35 to 0.37 depending on moisture content) and CBD (0.33), and very low for CR12 (scans) (0.02, Table 5) calculated from scan measurements. No heritability estimates for radial shrinkage measured on cores were significant. Overall standard errors for blocks were higher than for cores, probably because a smaller sample size of blocks was measured. Although heritabilities for shrinkage using blocks were high, these high standard errors meant only the estimate for BT17 was significant. The ratio of tangential to radial shrinkage had a low heritability estimate for the cores (0.15) 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 0.61 (Table 4). CR12 (scans) and BR12 had only a weak phenotypic correlation (0.19) (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).

TABLE 4–Heritability estimates (diagonal), phenotypic correlations (below the diagonal), and genetic correlations (above the diagonal) for tangential shrinkage traits with standard errors in parentheses and significant genetic correlations in bold type. Standard error is not reported where the analyses were bound (restricted to 1).

| | | Cores | | | Blocks | | |
|---|---|---|---|---|---|---|---|
| | | CT17 | CT12 | CT5 | BT17 | BT12 | BT5 |
| Cores | CT17 | **0.35 (0.11)** | **0.90 (0.05)** | **0.94 (0.03)** | **0.63 (0.26)** | 0.99 (bound) | **0.90 (0.43)** |
| | CT12 | 0.91 | **0.38 (0.12)** | **0.98 (0.01)** | 0.99 (bound) | 0.99 (bound) | 0.99 (bound) |
| | CT5 | 0.91 | 0.96 | **0.37 (0.11)** | **0.87 (0.22)** | 0.99 (bound) | 0.99 (bound) |
| Blocks | BT17 | 0.56 | 0.58 | 0.59 | **0.48 (0.26)** | 0.99 (bound) | **0.88 (0.13)** |
| | BT12 | 0.55 | 0.56 | 0.57 | 0.86 | 0.12 (0.24) | 0.99 (bound) |
| | BT5 | 0.59 | 0.60 | 0.61 | 0.82 | 0.82 | 0.27 (0.26) |

TABLE 5–Heritability estimates (diagonal), phenotypic correlations (below the diagonal), and genetic correlations (above the diagonal) for radial shrinkage traits; standard errors in parentheses. There were no significant genetic correlations.

| | | Cores | Blocks | | |
|---|---|---|---|---|---|
| | | CR12 (scans) | BR17 | BR12 | BR5 |
| Cores | CR12 (scans) | 0.02 (0.09) | | | |
| Blocks | BR17 | 0.25 | 0.11 (0.25) | 0.65 (0.85) | 0.72 (0.60) |
| | BR12 | 0.19 | 0.79 | 0.08 (0.24) | 0.65 (0.72) |
| | BR5 | 0.17 | 0.65 | 0.68 | 0.21 (0.26) |

TABLE 6–Heritability estimates (diagonal), phenotypic correlations (below the diagonal), and genetic correlations (above the diagonal) for core basic density and shrinkage at 12% m.c. Standard errors are given in parentheses, and significant estimates and genetic correlations in bold type. Standard error is not reported where the analyses 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)** |

## Analysis of Sample Selection

Analysis of growth traits for the Hannam Vale trial in early 2006 produced significant heritability estimates of 0.27 for tree height and 0.20 for diameter at breast height, confirming the quality of the progeny trial design (Forests NSW, unpubl. data). However, the reduced variability in growth imposed by the pre-selection based on growth affected the current experimental design and potentially contributed to the reduced heritability estimates observed. Estimates of genetic parameters obtained for the whole balanced trial are compared in Table 7 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.

| Trait | Whole trial | Wood quality selection |
|---|---|---|
| *n* ind/fam | 24 | 3–14 (6.6 av.) |
| Total *n* ind | 5465 | 958 |
| Height $h^2$ (s.e.) | 0.27 (0.04) | 0.12 (0.10) |
| Diameter $h^2$ (s.e.) | 0.20 (0.04) | 0.02 (0.08) |

## DISCUSSION

### 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. It is conceivable that more than four tangential measurements per core, or measurements representing particular growth stages within a year, or minimum tangential diameter in addition to the set percentages of core radius could improve accuracy of the data; and these would be recommended in future studies. Despite this, significant heritability estimates were achieved with four tangential measurements per core. However, radial measurements using the length of whole cores were not successful in assessing heritability of this trait. Future studies could explore the use of the tangential marks to measure radial shrinkage directly on the cores using callipers. 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. In several studies, including this one, tangential shrinkage has consistently been found to be heritable. However, heritability of tangential shrinkage measured on test blocks at 12% m.c. was not significant. Heritability estimates for tangential shrinkage measured on cores at all moisture contents, and for blocks at 17% m.c. was consistent with results reported in other studies (Tables 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).

The strength of the genetic correlations found in this study between tangential shrinkage measured on increment cores and tangential shrinkage measured on shrinkage blocks is 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.

TABLE 8–Reported heritability estimates for tangential and radial shrinkage in plantation eucalypts.

| Source (fam.) | Species | T shrinkage | R shrinkage | n (ind.) | n |
|---|---|---|---|---|---|
| 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)*<br>0.30 (0.18)† | –<br>– | 215 | 47 |
| Bandara 2006 | *E. grandis* | 0.29 (0.15) | 0.06 (0.13) | 320 | 50 |
| S.D.Verryn & P.Turner unpubl. data | *E. grandis* | – | 0.41 (0.14) | 472 | 90 |
| *This study* | | | | | |
| *– Cores (12% m.c.)E. pilularis* | | 0.36 (0.10) | 0.10 (0.09) | 999 | 153 |
| *– Blocks (12% m.c.)* | | 0.11 (0.21) | 0.17 (0.21) | 354 | 129 |

* Before reconditioning,
† After reconditioning

The motivation behind the present study came from a *E. dunnii* trial 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.

There are only limited reports on relationships between basic density and linear shrinkage. Both positive and negative correlations have been found, sometimes

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 (s.e.) |
|---|---|---|
| Boambee *E. dunnii*<br>Tangential shrinkage<br>(Core and 25 × 100 mm board) | 0.480 | 0.996 (0.13) |
| HannamVale *E. pilularis*<br>Tangential shrinkage<br>( Core and shrinkage block) | 0.559 | 0.999 (bound) |

for the same species (Bandara 2006; Wu *et al.* 2006; Chafe 1985, 1994; Sesbou & 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 tend to somewhat reduce 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. The numbers of person-days required in this study to process the equivalent number of increment cores and shrinkage blocks are compared in Table 10. 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 fell, label, and cut 1-m 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-m billets into standard test blocks (100 × 25 × 25 mm) averaging 60 billets per day, giving a total of 80 work days for the 1200 logs. Measurements at 17%, 12%, and 5% m.c., including weighing of samples, took a comparable amount of time at each stage, but in the green condition samples also had to be marked.

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 for the non-destructive method. The higher cost for 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

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 |

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.

## 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 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 reduce 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 is to be achieved when young plantation logs are being backsawn.

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