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Genetic control of traits influencing sawn timber properties of plantation-grown *Eucalyptus urophylla*

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Abstract

Background: *Eucalyptus urophylla* S.T.Blake is a major plantation species in tropical and subtropical regions, mainly grown for pulpwood. Increasing interest in solid wood applications has highlighted the need to improve wood properties through genetic selection.

Methods: A subset of 200 trees representing 50 open-pollinated families from three seed sources in an eight-year-old progeny trial in northern Vietnam was sampled. Wood basic density, tangential, radial and longitudinal shrinkage, coefficient of anisotropy, and log end-splitting index (LESI) were assessed.

Results: Wood basic density showed high heritability ($h^2 = 0.90 \pm 0.24$). Tangential and radial shrinkage exhibited moderate heritability estimates (0.43 ± 0.22 and 0.34 ± 0.21, respectively), while longitudinal shrinkage showed no genetic variation. The coefficient of anisotropy and LESI also showed moderate heritability estimates (0.32 ± 0.21 and 0.31 ± 0.21). Genetic correlations between growth and wood traits were weak and non-significant, but a strong negative genetic correlation was observed between wood density and coefficient of anisotropy (–0.89 ± 0.37).

Conclusions: Substantial additive genetic variation exists for key wood properties in *E. urophylla*, indicating good potential for genetic improvement. Selection for higher wood density is expected to reduce anisotropy without compromising growth. These results support the integration of wood quality traits into breeding objectives to enhance solid wood recovery from plantation-grown *E. urophylla*.

Keywords: dimensional shrinkage, genetic correlation, heritability, log end-splitting, wood basic density

Introduction

Eucalyptus species are among the most widely planted hardwoods globally, covering an estimated 22.57 million hectares worldwide (Zhang & Wang 2021). Traditionally, the primary use of plantation-grown *Eucalyptus* wood has been for pulp and paper production, owing to its fast growth, disease resistance, high fibre yield, and suitability for short-rotation forestry systems. In particular, *E. urophylla* S.T.Blake and its interspecific hybrids such as *E. urophylla* × *E. grandis* and *E. urophylla* × *E. pellita* have been extensively adopted in tropical and subtropical regions for these purposes.

However, there is a growing demand for plantation-grown hardwoods suitable for higher-value solid wood applications, such as furniture manufacturing, veneer production, and engineered wood products (Luo et al. 2013, Guo & Altaner 2018). In many countries, including Vietnam, Brazil, China and Australia, the interest in using plantation-grown *Eucalyptus* wood for sawn timber and veneer has increased significantly in the last two decades.

This shift represents a critical opportunity for improving the economic returns of *Eucalyptus* plantations, moving from low-margin pulp production towards high-value markets.

Despite its potential, the utilisation of *Eucalyptus* wood for solid wood products faces technical challenges. Wood from short-rotation *Eucalyptus* plantations often exhibits substantial growth stresses and pronounced shrinkage anisotropy. Both phenomena, although associated with different wood characteristics, cause warping and checking of sawn timber. In their combination they can significantly reduce solid wood recovery and product quality (Thomas et al. 2009, Trung 2015, Japarudin et al. 2021).

The extent to which wood properties impacting solid wood production are under genetic control remains a crucial question for breeding programmes. Genetic variation and heritability of key wood traits such as wood basic density, stiffness, shrinkage, and growth stress-related defects have been reported in species such as *E. globulus, E. nitens*, *E. grandis, E. globoidea* and *E. pellita* (Santos et al. 2004, Hamilton et al. 2009a, Hamilton et al. 2009b, Bandara & Arnold 2017, Guo & Altaner 2018, Espey et al. 2021). These findings indicate that selective breeding could be an effective strategy to mitigate undesirable characteristics of plantation-grown *Eucalyptus* wood and enhance their value for solid wood uses.

However, comparatively fewer studies have focused on *E. urophylla*, a species of increasing importance for plantations in tropical regions and these have mainly focused on wood basic density (Wei & Borralho 1997, Nguyễn et al. 2008, Thomas et al. 2009). Given its adaptability and growth performance, understanding the genetic basis of wood properties in *E. urophylla* is critical to developing improved varieties that meet the rising demand for higher-value timber products.

The aim of this study was to investigate the genetic control of wood properties influencing solid wood performance in *E. urophylla*. Specifically, we quantified the heritability of wood basic density, dimensional shrinkage, coefficient of anisotropy, and end-splitting, and also examine genetic correlations among these traits. The results are expected to inform breeding strategies for *E. urophylla* aimed at improving both growth and wood quality traits, contributing to increasing the overall economic value of short-rotation *Eucalyptus* plantations.

Materials and methods

Materials and sampling strategy

A progeny trial of *E. urophylla* was established in 2008 near Nam Dan in the Nghe An province of Vietnam (13°40'N, 105°40'E, altitude 70 m, mean annual rainfall 1,900 mm and mean annual temperature 23.2°C) on Ferrosol soil. The trial evaluated 96 open-pollinated families of *E. urophylla* selected from three first generation progeny within provenance seedling seed orchards established in Ba Vi, Hanoi province (32 families), Van Xuan, Phu Tho province (33 families), and Sakaerat in Thailand (31 families). These orchards were originally established from multi-provenance open-pollinated families and share broadly comparable genetic backgrounds. As such, the material represents related operational breeding populations rather than genetically independent seed sources.

An incomplete block design with eight replicates of four tree row plots per family was used with row and column positions assigned to evaluate spatial variation. The trial was established with an initial spacing of 3 m between planting rows and 2 m between trees along the rows. At age five, two of the four trees per plot (bottom 50%) were removed during first thinning. At age eight, one of the remaining two trees was removed, leaving one tree per plot. Among the felled trees, a sub-set of 200 trees from 50 randomly selected families were used in this study. The sub-set of families included all three seed sources with 11 to 20 families each. The selected trees were felled with chainsaws 0.3 m above the ground line. One 50 mm thick disk was cut from the felled stem at 1.3 to 1.35 m tree height and disks were used to estimate basic density. From the billet between 0.3 m and 1.3 m tree height, a 20 mm thick, defect-free board was cut along the east-west axis from pith to bark. Samples were cut from each board using an adjustable table saw to produce a clear wood sample from midway between the cambium and the pith. Samples were resized to 20 mm (tangential) × 20 mm (radial) × 30 mm (longitudinal), for measurements of shrinkage traits. From the felled trees, one log per tree was cut from 1.4 m tree height upward to 2.7 m for the assessment of end-splitting.

Wood basic density assessment

Wood discs were debarked, stored in plastic zip-lock bags to avoid moisture loss, and maintained in cool conditions prior to the assessment of wood density. Wood basic density (BD) was determined, from the fresh volume of the sample (v), estimated by the mass of water displaced on immersion and oven dry mass (w), where BD = w/v (Olesen 1971).

Wood shrinkage

Sample preparation and measurement of shrinkage in different dimensions followed ISO standard 4469-1981. Samples were soaked in distilled water for 72 hours to ensure moisture content above the fibre saturation point. The dimensions were measured with a digital calliper to the nearest 0.01 mm at the mid-point on each axis of all three principal directions, with points marked for re-measurements. The samples were then placed in a conditioning chamber at 20 ± 2°C and 65 ± 5% relative humidity until they reached the equilibrium moisture content (EMC) in air-dry condition (EMC average = 12.4% ± 0.2%). Dimensional differences were used to estimate partial shrinkage (from green to 12% MC) in the tangential (S_T), radial (S_R), and longitudinal (S_L) dimensions and these values were used to calculate the partial coefficient of anisotropy (T/R).

End-splitting

Logs were placed horizontally, not stacked, isolated from the ground, and preserved in openly shaded areas to avoid direct sunlight. Splits on each end of the logs were counted and categorised as internal splits and surface cracks after 40 days from felling. Width and length of surface cracks at each end of the log were then measured in mm. To quantify the severity of defects, the Log End-Splitting Index suggested by Lima et al. (2002) was calculated:

$$LESI = 200(\frac{\sum_{i=1}^{n} o_i L_i}{\pi D^2})(\%)$$

Where LESI = Log End-Splitting Index (%), o_i is the maximum opening of a surface crack, L_i = length of the same crack, and D is the average diameter of the log.

Statistical analysis

The statistical analysis was performed in two steps: (i) univariate analysis to estimate variance components for each trait; and
(ii) multivariate analysis to estimate covariances between traits.

Row and column within replicate effects were omitted in the model because the wood traits in this study were assessed using a sub-sample of less than one-quarter of the trees in the trial. In the case of diameter at breast height (DBH), values of all surviving trees in the trial were used for analysis.

The linear mixed-effects model for univariate analysis was:

$$\boldsymbol{y} = \boldsymbol{X_B b} + \boldsymbol{X_M m} + \boldsymbol{Z_F f} + \boldsymbol{e}$$

Where $\boldsymbol{y}$ is the vector of observations for phenotypes (DBH, BD, S_T, S_R, S_L, T/R, and LESI), $\boldsymbol{b}$ is the vector of fixed replicate effects, $\boldsymbol{m}$ is the vector of fixed seed source effect, $\boldsymbol{f}$ is the vector of random family effects, and $\boldsymbol{e}$ is the vector of random residuals. $\boldsymbol{X_B}$, $\boldsymbol{X_M}$ and $\boldsymbol{Z_F}$ are incidence matrix relating $\boldsymbol{b}$, $\boldsymbol{m}$, and $\boldsymbol{f}$ to $\boldsymbol{y}$

The coefficient of genetic relationship (r) was assumed to be 0.33 for open-pollinated families assuming there was a proportion of inbreeding in the seedling seed orchards where seed was collected from (Quang et al. 2013). Additive genetic variance (σ^2_A), phenotypic variance (σ^2_P), within provenance narrow-sense heritability (h^2), and genetic correlation (r_g) between traits were estimated as:

$$\sigma_A^2 = \frac{\sigma_f^2}{r} = 3\sigma_f^2$$

$$\sigma_P^2 = \sigma_f^2 + \sigma_e^2$$

$$h^2 = \frac{\sigma_A^2}{\sigma_P^2}$$

$$r_g = \frac{\sigma_{A_1 A_2}}{\sigma_{A_1}\sigma_{A_2}}$$

Where: σ^2_f is family within provenance variance and σ^2_e is the residual variance. Standard errors of the estimates of heritabilities and genetic correlations were calculated using a standard Taylor series approximation in the ASREML software (Gilmour et al. 2015).

Results

Wood properties of *E. urophylla*

Wood basic density of *E. urophylla* families ranged from 0.43 to 0.64 with an average of 0.51 g cm^{-3} at eight years of age. Wood shrinkage from green to air-dry (12%) moisture content in tangential and radial directions averaged 6.3% and 2.6%, respectively, and the average coefficient of anisotropy was 2.6 (Table 1). About 90.5% of all logs exhibited evidence of splitting on their cross-sectional surface, with an average of 4.3 splits per log. Significantly more splits were found on the small end and more were classified as internal than surface checks (Figure 1).

TABLE 1: Mean, phenotypic standard deviation (σ_p), family mean range and heritability (h^2) estimates of traits measured in an eight-year-old progeny trial of *E. urophylla* in Nam Dan

Trait	Mean	σ_P	Family mean range	$h^2 \pm se$
DBH (cm - all trees measured)	13.4	3.41	9.9 – 17.8	0.15 ± 0.06
BD (g cm^{-3})	0.51	0.06	0.43 – 0.64	0.90 ± 0.24
S_T (%)	6.3	1.63	4.1 – 8.5	0.43 ± 0.22
S_R (%)	2.6	0.9	1.8 – 4.0	0.34 ± 0.21
S_L (%)	0.17	0.13	0.07 – 0.37	0.00 ± 0.00
T/R	2.6	0.80	1.6 – 3.6	0.32 ± 0.21
LESI (%)	12.7	31.9	0.0 – 95.1	0.31 ± 0.21

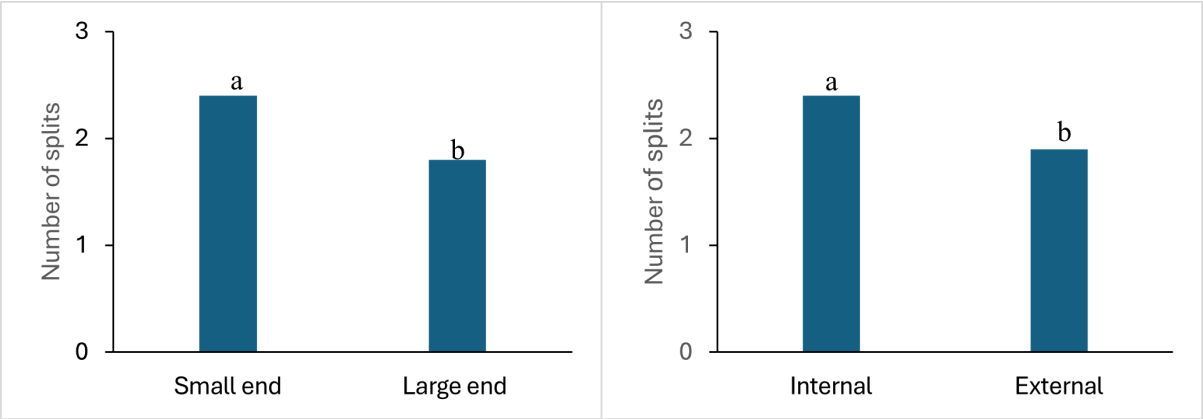

FIGURE 1: Log end splits in eight-year-old *E. urophylla*. Number of splits on the small end and large end surface of the logs (left); Number of internal splits and external splits (right) (Distinct letters in columns differ statistically by Tukey's test)

Seed source variation

There were no significant differences among the three seed sources (Ba Vi, Van Xuan, and Sakaerat) for most of the traits that were evaluated (Wald F-test P > 0.05). The exceptions were for tangential shrinkage (P < 0.05), where seed source means ranged from 7.8 to 9.1% (data not shown).

Heritability estimates

The within-source heritability estimates varied by trait and were high for wood basic density (0.90±0.24), moderately high for T/R, log end-splitting index, radial and tangential shrinkages (0.31-0.43), and low for DBH (0.15 ± 0.06) (Table 1). Longitudinal shrinkage was not heritable. The standard errors of the heritability estimates for these wood traits were large, at least in part due to the small sample size.

Genetic and phenotypic correlations between traits

No significant genetic correlations were observed between DBH and wood property traits (Table 2). In addition, genetic correlations among wood property traits themselves were not significantly different from zero, except for the genetic correlation between BD and coefficient of anisotropy. Similarly, the phenotypic correlations between DBH and wood properties were not significantly different from zero. Phenotypic correlations between wood property traits were largely insignificant, except for those between tangential shrinkage (S_T), radial shrinkage (S_R), and coefficient of anisotropy (T/R).

Discussion

This study investigated the genetic control of wood basic density, dimensional stability, and log end-splitting which are critical for the production of solid-wood products from plantation-grown *E. urophylla*. In an eight-year-old progeny trial, substantial additive genetic variation was observed for growth, wood basic density, dimensional stability, and splitting properties, indicating the potential for genetic improvement to be delivered through a selective breeding programme.

Wood properties of *E. urophylla*

The observed basic density of 0.51 g cm^{-3} at eight years of age was similar to other studies of similar-aged *E. urophylla* (ranging from 0.43 to 0.64 kg m^{-3}) (Wei & Borralho 1997, Nguyễn et al. 2008) and there was no significant difference between seed sources for this highly heritable trait. The tangential and radial shrinkage values determined in this study also aligned closely with

TABLE 2: Genetic (above diagonal) and phenotypic correlations (below diagonal) between traits measured in the 8-year progeny trial of *E. urophylla* at Nam Dan **(± standard error)**

	DBH	BD	S_T	S_R	T/R	LESI
DBH		0.05±0.35	0.04±0.41	0.28±0.51	-0.32±0.59	-0.94±0.58
BD	0.06±0.07		-0.47±0.26	0.29±0.31	-0.89±0.37	-0.22±0.35
S_T	0.04±0.07	-0.03±0.08		0.58±0.26	0.39±0.35	0.49±0.40
S_R	-0.14±0.07	0.01±0.08	0.46±0.06		-0.48±0.34	0.59±0.49
T/R	0.20±0.07	-0.08±0.08	0.33±0.07	-0.63±0.04		-0.28±0.54
LESI	-0.08±0.07	0.01±0.07	0.09±0.07	0.02±0.07	0.05±0.07	

those reported for ten-year-old *E. urophylla* specimens (5.8% and 2.7%, respectively) (Thomas et al. 2009). The same applied to the coefficient of anisotropy (2.3).

In this study, *E. urophylla* logs exhibited a high level of end-splitting. Log end-splitting is generally associated with the release of growth stresses present in standing trees. Log end-splitting is a concern to the timber industry as it results in substantial yield losses (Maree & Malan 2000, Yang 2005, McGavin et al. 2014). For instance, Maree and Malan (2000) estimated that end-splitting caused losses of up to 10% of sawn timber production for *E. grandis* in South Africa, and McGavin et al. (2014) reported that up to 28% of the veneer from various *Eucalyptus* species in Australia was down-graded to low-value 'D' grade due to end-splitting of logs.

Additive genetic variation

High heritability estimates for wood density have been widely reported in *Eucalyptus* and other forest tree species (Cornelius 1994). The heritability values for wood density estimated in this study were notably higher than those reported in previous studies on *E. urophylla* (Nguyễn et al. 2008, Wei & Borralho 1997) and other *Eucalyptus* species such as *E. dunnii* and *E. nitens* (Hamilton & Potts 2008, Henson et al. 2004). This can be a result of the study design discussed at the end of this section. However, they are comparable to those reported for *E. pilularis* (Raymond et al. 2008).

The heritabilities for tangential and radial shrinkage were moderately high. These findings are higher than those reported for the same species (Thomas et al. 2009) and *E. pilularis* (Pelletier et al. 2008) but align well with other eucalypt species such as *E. grandis* (Bandara 2006), *E. pellita* (Kien & Bien 2024) and *E. dunnii* (Henson et al. 2004). In contrast, the heritability for longitudinal shrinkage was negligible in our study, indicating minimal genetic variation detected among families in this population.

Heritability for the coefficient of anisotropy was moderate and non-significant. Heritability for the coefficient of anisotropy varied between studies on the same species or other *Eucalyptus* species. In a study in northern Vietnam for the same species, Thomas et al. (2009) reported zero heritability for coefficient of anisotropy. Similarly, Pelletier et al. (2008) also non-significant heritabilities of the trait, regardless of whether it was assessed using 12 mm increment cores (0.15±0.12) or wood blocks (zero). However, Kien & Bien (2024) found a significant and high heritability for the coefficient of anisotropy in *E. pellita*.

The heritability estimates for LESI in this study were moderate, while estimates for log end-splitting, measured by various methods ranged from low to high and were significant across different *Eucalyptus* species. In *E. grandis*, Santos et al. (2004) reported a heritability of 0.31 for LESI at age 9-years-old, while Bandara & Arnold (2017) found low and non-significant heritability for end-splitting at age 5-years-old. In *E. nitens,* Blackburn et al. (2011) reported heritability values of 0.28 and 0.46 for Yang's log end-splitting index for the lower and upper end of the log, respectively. Espey et al. (2021) reported moderate and significant heritability for split severity (h^2 = 0.24) in *E. pellita*. Murphy et al. (2005) reported a heritability of 0.32 for growth stress in *E. dunnii*. These findings reinforce that variation in log end-splitting can be reduced by selection of genotypes with favourable characteristics. However, environmental factors such as site conditions may also influence stress development and crack expression, contributing to the variability observed across studies.

The genetic correlations between DBH and wood properties were weak and non-significant, indicating that selection for increased growth would have little indirect impact on wood properties. This also implied that gains in wood quality traits will require their direct inclusion in the breeding objective. These results also support the feasibility of developing balanced selection strategies targeting both productivity and solid-wood performance.

Our findings of weak and non-significant genetic correlations between wood density and shrinkage differs somewhat from the results of other studies in *Eucalyptus* species. Bandara (2006) reported a significant positive genetic correlation between basic density and tangential shrinkage in *E. grandis* (0.67±0.22), but the correlation between density and radial shrinkage was not significant. Conversely, Pelletier et al. (2008) reported a significant negative genetic correlation between wood density and an increment core-based measurement of tangential shrinkage (-0.57±0.19) in *E. pilularis*. Inconsistency of these results might be attributed to the confoundment of drying collapse and normal shrinkage in the measurements, which are negatively and positively correlated to basic density, respectively.

The significant negative genetic correlation between BD and coefficient of anisotropy obtained in our study was comparable to earlier reports in *E. pellita* (Kien & Bien 2024) and is favourable for breeding and should lead to reduced distortion of the sawn board during the drying process.

As genetic correlations between LESI and both wood density and diameter were non-significant in our study, none of these traits can reliably predict end-splitting properties in *E. urophylla*. These results contrast with those reported for *E. grandis*, where the genetic correlation between LESI and wood density was 0.44, and between LESI and log volume under bark was 0.40 (Santos et al. 2004). Similarly, although the genetic correlations between LESI and shrinkage properties were favourable, they were not significant, indicating that improving shrinkage properties would not affect end-splitting in *E. urophylla*. This was in line with the reported positive, but non-significant, genetic correlations between the scoring-based log-end-splitting severity and tree volume for 5-year-old *E. grandis* grown in Sri Lanka (Bandara & Arnold 2017).

All genetic correlations in our study were estimated with high standard errors, which was not unexpected for several reasons. The relatively small sample size of 50 families employed in this study could be one of the explanations. White et al. (2007) note that large numbers of genotypes (N≥ 100) should be sampled to

obtain reliable estimates of genetic variance, and hence genetic correlations.

Several factors may also have led to upward bias in heritability estimates. White et al. (2007) stated that heritability estimates made from a single site may be subject to upwards bias, a fact also true for this study. Selective thinning conducted during the development of the trial would have also inflated genetic parameter estimates, particularly those related to growth traits (Matheson & Raymond, 1984). In addition, the three seed sources for this trial originated from related breeding populations with a shared germplasm history, implying some level of relatedness among families. If deeper pedigree relationships were not fully accounted for, heritability estimates could be overestimated (Bush et al. 2025). Lastly, sampling of inferior (i.e. thinned) trees may also have contributed to upward bias if the removed trees had a higher proportion of inbred individuals than assumed in the model.

Implications for improving solid wood production

The rotation age of *E. urophylla* for sawn timber production in Vietnam is typically 10-15 years, depending on site productivity. This rotation aims to achieve an average DBH of 20-25 cm at harvest (Thuyet 2010). Wood density, modulus of elasticity (MoE), and modulus of rupture (MoR) are adequate for general uses at this harvest age (Thomas et al. 2009). Therefore, breeding for wood quality should prioritise improving shrinkage, and end-splitting severity, which have been shown to impact solid-wood product recovery. A breeding objective should further include increased volume and stem straightness. This can be achieved with a selection index that accounts for the relative importance of different traits, the level of additive genetic variance and the genetic correlations among traits (Missanjo & Matsumura 2017). Such an index, including stem volume, stem straightness and wood stiffness as assessed by dynamic MoE of standing trees has been proposed for *E. pellita* breeding in Sabah (Japarudin et al. 2022), with the expectation that gain in all three traits would be achieved.

Examination of family breeding values for DBH and wood traits from our study indicated that several families exhibit favourable breeding value combinations, suggesting potential candidates for further evaluation in the breeding programme (Figure 2).

Interspecific hybrids between *E. urophylla* and other eucalypt species have demonstrated superior growth rates and adaptability to various soil and climatic conditions compared to parental species (Thinh 2011, Kien 2015). These hybrid varieties may also enhance

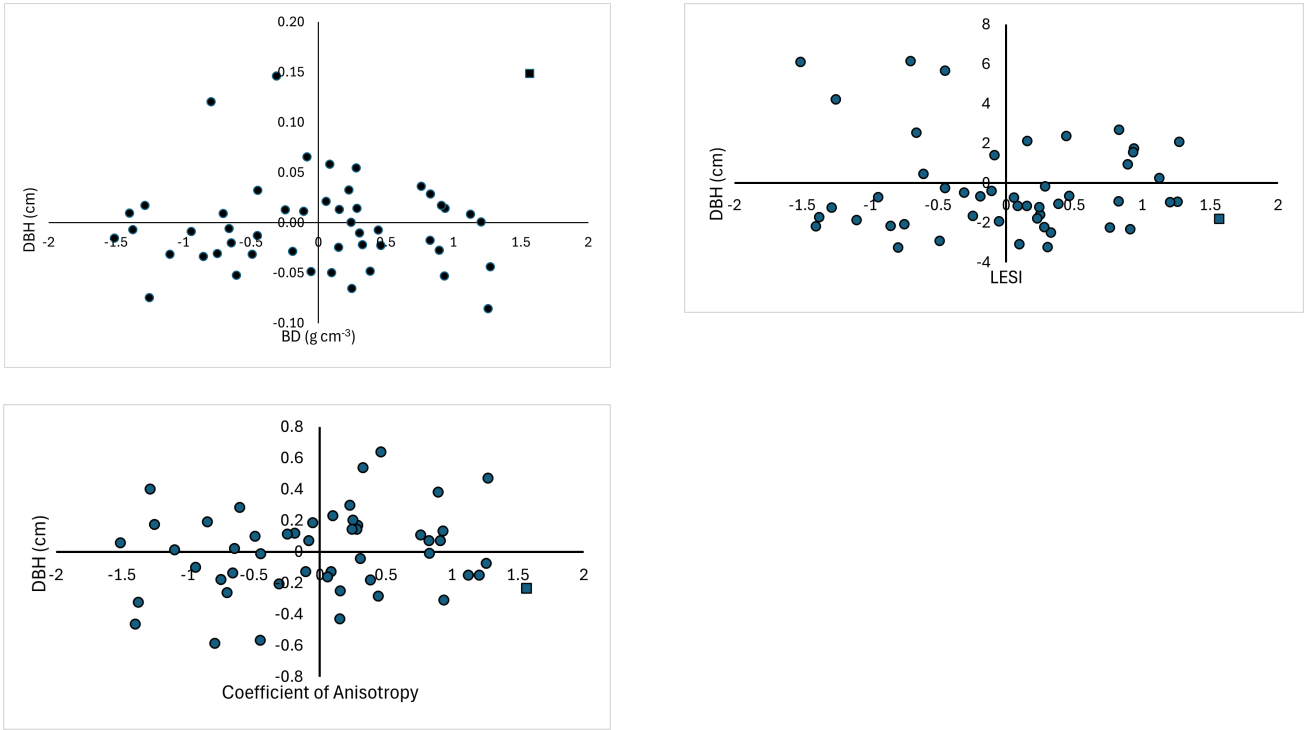

FIGURE 2: Plot of *E. urophylla* family breeding value expressed as deviation from mean for DBH and wood basic density (BD), Coefficient of anisotropy, and log-end-splitting index (LESI). (Note: squared point showing the same family of highest breeding value for DBH and desired breeding values for BD, Coefficient of anisotropy and LESI).

wood quality traits, such as reduced log end-splitting. In China, the use *E. urophylla* × *E. grandis* hybrids has increased the recovery of higher-value veneer grades (Peng et al. 2014). The best individuals identified in our study, with outstanding breeding values for growth and wood traits may be used as parents in hybrid eucalypt breeding programmes.

Conclusions

We have found that *E. urophylla* has substantial genetic variation, and selection may be used to increase the volume and quality of solid wood products. By integrating wood quality traits such as density and shrinkage into selection indices, the resulting selections will allow growers to significantly increase the recovery of high-quality sawn timber. We show that genetic variation in several wood properties relevant to solid wood production is substantial and under moderate to high genetic control. The results suggest breeding to improve wood properties in *E. urophylla* should lead to improvements in solid wood recovery and will be compatible with selection for improved growth. Selection of the best individual for each trait as well as individuals identified using different selection indices have been made so that individuals may be captured for evaluation in clonal trials and for the establishment in hybridisation orchards.

Competing interests

The authors declare that they have no competing interests related to the publication of this article.

Author contributions

KDN developed the research concept, designed the study, analysed the data, and drafted the manuscript. SL, SHN, HTTP, STN and NBTN were responsible for sample collection and preparation, data collection, and contributed to revising the manuscript. JB contributed to the preparation and revision of all manuscript versions. All authors reviewed the manuscript and approved the final version for publication.

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