



Hybrid effects on processing recovery, wood quality, and structural performance of engineered *Eucalyptus pellita* products

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Abstract

Eucalyptus pellita is cultivated for pulpwood in tropical and subtropical regions but remains underutilised for structural applications, particularly in dry tropical environments. Compared to well-studied species such as *Eucalyptus grandis* and *Eucalyptus globulus*, its potential in engineered wood products is poorly understood. As plantation industries seek to diversify products and increase wood value, understanding the structural suitability of *E. pellita* hybrids is critical. This study evaluated the performance of *E. pellita* and its F1 and backcross hybrids across two dry tropical sites, spanning log quality, product recovery, structural properties, and genetic associations. Billets were assessed for form, diameter, and defects. Sawing and peeling trials quantified recovery rates and defects. Laminated veneer lumber (LVL) was fabricated from hybrid veneers and tested for density, modulus of elasticity (MOE), modulus of rupture (MOR), and bond quality. The *E. pellita* × *Eucalyptus brassiana* hybrid achieved highest recoveries among the materials tested (sawn board recovery up to 49.2%; green veneer recovery up to 83.6%). The highest-performing LVL (layup 3) from this hybrid achieved an MOE of 18.8 GPa and MOR of 139 MPa. Genetic analysis using a targeted panel of ~5500 single nucleotide polymorphism (SNP) markers identified significant associations above the $-\log_{10}(p)=1.30$ threshold for end split (SNP1358), knot diameter (SNP3201), and heartwood proportion (SNP2187). Although statistical power was limited by sample size, these findings highlight the potential of *E. pellita* hybrids for structural applications and demonstrate the value of integrating phenotypic and molecular data to support tropical hardwood breeding and utilisation strategies.

1 Introduction

There is growing interest in utilising fast-growing *Eucalyptus* species in hardwood commercial tree plantations, due to their high productivity, adaptability, short rotations, economic returns (Li et al. 2015; Balasso et al. 2022; Vaknin

and Korol 2023; Baño et al. 2025), and suitability for pulp, paper, sawn timber, and fibreboard manufacturing (Wu et al. 2017; Japarudin et al. 2022; Hutapea et al. 2023). Traditionally, small-diameter logs from young *Eucalyptus* plantations were unsuitable for sawmilling and peeling due to low recovery rates, however, recent advancements in sawmilling

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and spindleless lathe technologies have enabled efficient processing, resulting in improved recovery (Leggate et al. 2017; Belleville et al. 2018, 2020; McGavin and Leggate 2019; Jimenez et al. 2021; McGavin et al. 2021). *Eucalyptus pellita* is gaining popularity as a tropical plantation species where it has been planted in countries such as Australia, Indonesia, Papua New Guinea, and parts of Southeast Asia. Fast-growing *Eucalyptus* trees grown without silvicultural or genetic improvement often exhibit wood with small diameters, low strength and stiffness, and branch defects, which negatively affect the recovery and quality of sawn timber and veneer (Balasso et al. 2022). Therefore, combining appropriate silvicultural practices with the breeding of genotypes possessing desirable wood traits is essential for improving product recovery and suitability for high-value applications.

Tree improvement offers a practical approach to enhance both the quality and quantity of *E. pellita* timber supply (Kien and Bien 2024). There has been a growing interest in *Eucalyptus* breeding programs worldwide. Clonal forestry has advanced significantly, leading to notable gains in plantation productivity and wood volume (Ramage et al. 2017; Nickolas et al. 2020). Genetic improvement efforts in *Eucalyptus* species have predominantly focused on pulpwood breeding objectives. However, there is growing interest in improving wood traits for solid wood applications, with recent studies examining the genetic control of traits such as density, stiffness, and pulp yield (Marco de Lima et al. 2019; Nickolas et al. 2020; Ho et al. 2021; Drew et al. 2022; Rashidi-Jouybari et al. 2022). In forest genetics, phenotypic traits result from the interaction between genetic and environmental factors, such as soil type, rainfall, temperature and site management practices (Jurcic et al. 2023). Comparative trials across diverse environments help disentangle these effects and guide breeding priorities (Nickolas et al. 2020; Iyiola et al. 2022). Blackburn et al. investigated genetic differences in sawn board stiffness and checking, highlighting their potential for improvement through selective breeding (Blackburn et al. 2010). Wood density, as one of the most studied wood properties, is an important indicator of strength, stiffness, and dimensional stability. It shows moderate to high heritability and is often used as a key selection trait in breeding programs (Hassegawa et al. 2019; Balasso et al. 2021; Yanez et al. 2021). Other wood traits such as acoustic velocity, lignin, pulp yield, microfibril angle (MFA), fibre length (FL), and fibre width (FW) have been investigated (Marco de Lima et al. 2019; Nadeau et al. 2023). In these studies, moderate to high heritability estimates have been observed for wood quality traits such as density and flexural stiffness, often exceeding those reported for growth traits (Marco de Lima et al. 2019; Thavamani-kumar et al. 2020; Kombi Kaviriri et al. 2021). However,

despite the strong genetic control of density, its relatively low genetic variance can limit achievable genetic gains. For instance, in clonal populations of *E. nitens* × *E. globulus*, genetic variances are generally high for volume and pulp yield, and moderate for basic density (Ibarra et al. 2023).

Effective selection depends on identifying end-use requirements, for instance, *E. globoides* has been evaluated for heartwood content and extractives related to wood durability (Iyiola et al. 2022). For sawn timber and veneer production, key traits include diameter at stump height, knot size, slope of grain, presence of reaction wood, and stem straightness, as these influence both strength and recovery (Wimmer and Johansson 2014; Ramage et al. 2017; Hassegawa et al. 2019; Purba et al. 2019; Japarudin et al. 2021a; McGavin et al. 2021; Barrette et al. 2023). High heritability and genetic variation for these traits have been reported in *E. globulus* (Nickolas et al. 2020). Genetic studies on processing recovery remain limited, particularly for sawing and peeling traits. In *E. nitens*, however, significant genetic variation has been reported for traits such as diameter, stem straightness, and log volume, which are linked to sawn timber recovery (Blackburn et al. 2011). A notable trade-off is the positive correlation observed between diameter at breast height (DBH) and log splitting, suggesting that larger trees may be more prone to splitting (Blackburn et al. 2011). Additionally, genetic correlations have been reported between acoustic traits and veneer sheet stiffness in *E. nitens* (Blackburn et al. 2012).

While genetic correlations with veneer stiffness have been reported, little is known about how genetic variation influences recovery and product quality in *E. pellita* and its hybrids. Laminated veneer lumber (LVL) is a widely used EWP valued for its strength, dimensional stability, and efficient use of raw materials. Studies on laminated veneer lumber (LVL) from fast-growing *Eucalyptus* species have highlighted the influence of veneer and lamina quality, adhesive type, and pressing conditions on product strength and durability (Leggate et al. 2017; Belleville et al. 2020; McGavin et al. 2021). Recent work also emphasises the role of visual grading and veneer characteristics such as density and knots in determining structural performance (Purba et al. 2019; Barrette et al. 2023). While some research has considered the effects of log traits and genetic variation, the relationship between these factors and recovery outcomes remains underexplored. Although single nucleotide polymorphism (SNP) markers have been widely used in forest genetics, their application to understanding variation in processing traits, such as recovery rates and product quality, remains limited.

E. pellita is a fast-growing tropical hardwood valued for its moderate to high density, strength, and natural durability, making it suitable for both pulp and solid wood products.

Studies have reported basic densities ranging from 550 to 750 kg/m³, with air-dry modulus of elasticity (MOE) values between 14 and 20 GPa and modulus of rupture (MOR) values between 90 and 120 MPa, indicating strong mechanical performance (Japarudin et al. 2021b; Kien and Bien 2024; Falade et al. 2025). However, challenges such as dimensional instability, internal checking, and shrinkage variation have limited its broader utilisation in structural applications. Falade et al. (2025) reported significant variation in tangential and radial shrinkage among *E. pellita* and its hybrids, underscoring the need to improve dimensional stability for value-added uses. Despite its high growth potential, research on *E. pellita* has largely focused on pulping performance and plantation productivity, with limited understanding of how log traits and genetics influence processing recovery and engineered wood product performance.

This represents a critical knowledge gap, particularly for species, where aligning genetic improvement with end-product performance is essential for commercial viability and resource efficiency. This study addresses these gaps by linking log traits and genetic variation to sawing and peeling recovery, and by evaluating their impact on the quality of LVL products derived from *E. pellita* hybrids. This study aims to inform genetic selection strategies and contribute to improving the efficiency and sustainability of wood processing in plantation forestry. The specific objectives are to: (1) investigate the genetic relationship between SNP markers and key log traits influencing recovery in *E. pellita* and its hybrids; (2) assess the correlations between growth traits and wood recovery and (3) examine the performance of laminated veneer lumber (LVL) produced from *E. pellita* and its hybrids. The findings will inform genotype selection and drive more efficient, sustainable use of plantation-grown hardwoods.

2 Materials and methods

2.1 Plantation sites and tree selection

This study was conducted on 10-year-old *Eucalyptus pellita* and hybrid plantations located at Kilu Impini 64 and Yapilika 28 on Melville Island, Tiwi Islands (~80 km north of Darwin, Australia). Both sites experience a tropical monsoonal climate, with 1200–1400 mm annual rainfall and a temperature range of 19–33 °C. The plantations were established in 2012 at 3 × 3 m spacing and managed under standard silvicultural practices for pulp and paper production. Each site comprised 10 seedlots and 1,000 planted trees. By 2022, 763 trees remained at Kilu Impini 64 and 666 at Yapilika 28. Based on field measurements and tree health assessments at age 10, Kilu Impini 64 (11° 25' 6.00"

S, 130° 30' 0.00" E) was classified as a high-productivity site, characterised by larger trees (mean DBH ≈ 19 cm; mean height ≈ 19 m) and better overall health compared with Yapilika 28 (11°33'45.00"S, 130°34'39.00"E), which was classified as moderate in productivity (mean DBH ≈ 17 cm; mean height ≈ 18 m). Tree health assessments indicated good general condition at both sites; however, Kilu Impini 64 exhibited higher crown size (CSS=4.4, score on a 1–5 visual scale) and crown density (CD=6.3, score on a 1–9 visual scale), lower crown epicormic growth (EG=0, indicating nil epicormic development based on a standard visual ordinal scale), and reduced foliar damage (FD=4.4, score on a 1–5 visual damage scale) compared with Yapilika 28 (CSS=4.0, CD=5.7, EG=3, FD=4.6). Tree health attributes were assessed using established visual tree and crown health assessment protocols for eucalypt plantations (Stone et al. 2003), with crown epicormic growth scored according to the presence and extent of epicormic shoots within the crown and foliar damage scored based on the severity of leaf damage and defoliation. These indicators collectively confirm the greater vigour and productivity of Kilu Impini 64 compared with Yapilika 28. Kilu Impini 64 is characterised by deep red to grey-yellow sandy soils (> 2 m), while Yapilika 28 is underlain by Moonkinu Member sandstone exceeding 3 m in depth. A replicated trial design was used at both sites, with 25 trees per plot and four replications per seedlot.

DNA was extracted using a modified cetyltrimethylammonium bromide (CTAB) protocol, following Tibbits et al. (2006), which facilitates efficient tissue collection and high-yield DNA isolation from mature trees. Genotyping was performed by Gondwana Genomics using Targeted Genotyping-by-Sequencing (TGS) with a custom *E. pellita* single nucleotide polymorphism (SNP) panel (Thavamanikumar et al. 2020; Thumma et al. 2022). Sequencing was conducted on an Illumina platform (Illumina Inc., San Diego, USA) at an average read depth of 30× per locus. Five genetic groups were identified: *E. pellita*, *E. pellita* × *E. brassiana* (F1 and BC), and *E. pellita* × *E. urophylla* (F1 and BC), with *E. pellita* as the recurrent parent in backcrosses. The inclusion of BC generations captured a broader range of *E. pellita* genomic contribution and enabled evaluation of trait inheritance and heterosis relevant to productivity and product development. Hybrid material originated from ten seedlots representing controlled and open pollinated families used in operational breeding. Genetic clustering confirmed hybrid composition and backcross relationships, and the groups were treated as representative of their respective hybrid classes rather than pure species. A raw dataset of approximately 5500 SNP markers per individual was generated and provided for downstream genetic structure and association analyses. SNPs were aligned to the *Eucalyptus*

grandis reference genome (v2.0, Phytozome) for downstream analyses.

For each genetic group at each site, six trees were randomly selected to represent high, medium, and low wood density classes. Wood density was measured non-destructively using a Resistograph (IML Resi PD400, IML System GmbH, Wiesloch, Germany). A three-bar histogram, representing the distribution of density values, was used to classify trees into three categories (upper, middle, and lower thirds) corresponding to high, medium, and low-density classes. Of these, five trees per group from each site were used for sawing trials (50 trees in total). Additionally, four mature *E. pellita* trees (30 years old) from a separate site (Bremer) were included to assess the recovery rates in older trees. The sixth tree in each group was allocated for peeling trials; however, only a subset was selected for actual use. These included one tree from each of the following groups: *E. pellita*, *E. pellita* × *E. urophylla* (F1), *E. pellita* × *E. urophylla* (BC), and *E. pellita* × *E. brassiana* (BC) from Kilu Impini 64; and *E. pellita* × *E. brassiana* (BC) from Yapi-lika 28. Additionally, a mature *E. pellita* tree (30 years old) from the Bremer site was included. In total, six trees were selected for peeling. All harvested logs were stored under a water sprinkler system to minimise stress before processing. For the sawing trial, a 2.4 m billet was collected from the lower bole, approximately 1.5 m above the ground. The lower 1.5 m section of these trees was retained for a separate study on wood property characterisation. For the peeling trial, a 1.8 m billet was collected just above stump height. The top of each billet was defined by the small-end diameter (SED) after cross-cutting. On average, one billet per tree was processed for each method (Fig. 1).

2.2 Growth traits and single nucleotide polymorphism (SNP) marker data

This research was part of a larger project comprising related studies focusing on *Eucalyptus pellita* and its hybrids. This included assessment of growth traits, such as height and diameter at breast height (DBH), from 1,500 trees across the two plantation sites. DNA from these trees was individually genotyped using an *E. pellita* single nucleotide polymorphism (SNP) marker panel developed by Gondwana Genomics, applying the Targeted Genotyping-by-Sequencing method. A total of 5,500 SNP markers were generated per tree across all 1,500 trees (GondwanaGenomics 2025). For this study, genetic data corresponding to the selected trees were extracted from this larger SNP dataset.

2.3 Billet assessment

For each billet, large-end diameter (LED) and small-end diameter (SED) under bark were calculated from long- and short-axis measurements using Eqs. (1) and (2). This method estimates an equivalent circular diameter for oval cross-sections, following (Belleville et al. 2018, 2020)

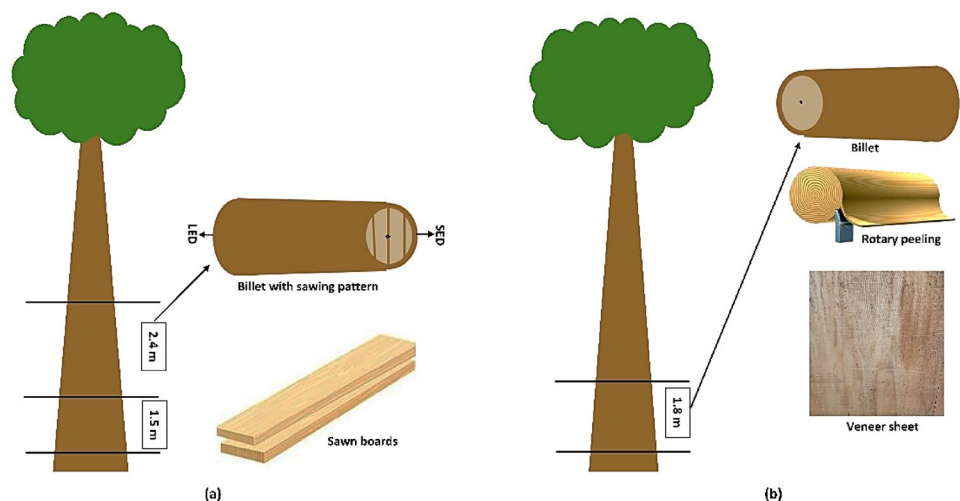
$$LED = \sqrt{\frac{LELD^2 + LESD^2}{2}} \quad (1)$$

$$SED = \sqrt{\frac{SELD^2 + SESD^2}{2}} \quad (2)$$

where *LELD* and *LESD* are the large-end long-axis diameter and large-end short-axis diameter (mm) respectively, *SELD* and *SESD* are the small-end long-axis diameter and short-axis diameter (mm) respectively.

Large-end heartwood diameter (LEHD) and small-end heartwood diameter (SEHD) were calculated using Eqs. (3) and (4), respectively.

Fig. 1 Schematic diagram for the collection of billets for **a** sawing, showing the large-end diameter (LED) and small-end diameter (SED), and **b** for peeling



$$LEHD = \sqrt{\frac{LELHD^2 + LESHD^2}{2}} \quad (3)$$

$$SEHD = \sqrt{\frac{SELHD^2 + SESHD^2}{2}} \quad (4)$$

where *LELHD* is the large-end long-axis heartwood diameter (mm), *LESHD* is the large-end short-axis heartwood diameter (mm), *SELHD* is the small-end long-axis heartwood diameter (mm), and *SESHD* is the small-end short-axis heartwood diameter (mm).

Billet volume was determined using Smalian's formula (Eq. 5).

$$V = \pi \times L \times \left(\frac{LED + SED}{4 \times 1000} \right)^2 \quad (5)$$

where *V* is the billet volume (m³), and *L* is the billet length (m).

Heartwood proportion (HP%) was calculated as the ratio of heartwood area (HA) to basal area (BA), as shown in Eqs. (6) to (8) (Belleville et al. 2018). This provides a relative measure of heartwood development among trees of similar diameter and allows comparison of genetic and site effects on heartwood formation.

$$HP = \frac{HA}{BA} \times 100 \quad (6)$$

where

$$HA = \pi \left(\frac{LEHD + SEHD}{2} \times \frac{1}{2} \right)^2 \quad (7)$$

and

$$BA = \pi \left(\frac{LED + SED}{2} \times \frac{1}{2} \right)^2 \quad (8)$$

Additional log characteristics recorded included sweep, number of knots, knot size, and end splits (Fig. 2). Sweep

(%) was measured as the maximum deviation from a straight line between log ends. Number of knots was the total count of visible knots on the billet surface. Knot size was the largest diameter measured perpendicular to the log. End splits were the longest surface cracks extending to the edge, expressed as a percentage of log length (Belleville et al. 2018). Measurements were taken immediately before milling to minimise variation due to post-felling changes.

The total end splits (ES), log taper (Tp), and ovality (O) were calculated using Eqs. (9) to (11), respectively.

$$ES (\%) = \frac{LEES + SEES}{L \times 1000} \times 100 \quad (9)$$

where *LEES* is the large-end end split (mm) and *SEES* is the small-end end split (mm).

$$Tp = \frac{LED - SED}{2L \times 1000} \quad (10)$$

$$O = \frac{1}{2} \times \left(\frac{LESD}{LELD} + \frac{SESD}{SELD} \right) \quad (11)$$

2.4 Billet processing, veneer recovery, and grading

Billets were peeled using a spindleless lathe with a targeted veneer thickness of 4 mm. The green recovery (GR%) for each billet was determined using Eq. (12).

$$GR (\%) = \frac{\sum_{i=1}^n (GL_i \times GW_i \times GT_i)}{V_{billet}} \quad (12)$$

where *GL_i*, *GW_i*, and *GT_i* are the length, width, and thickness of the *i*-th green veneer sheet, respectively, and *V_{billet}* is the billet volume. *n* is the total number of veneer sheets obtained from each billet.

Veneer sheets were air-dried under cover for 72 h to below 16% MC. They were then remeasured, and dry veneer recovery (DR%) was calculated using Eq. (13).

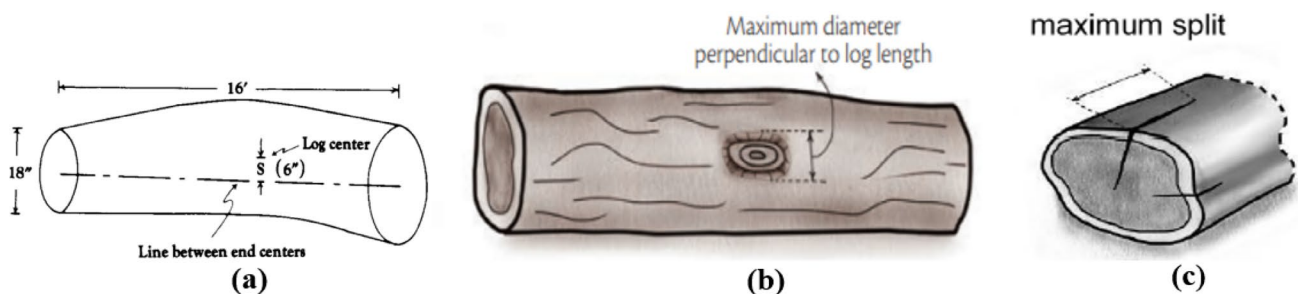


Fig. 2 Schematic illustration of sweep **a** (Graves 1986), knot **b**, and end split **c** measuring methods (Redman et al. 2015; Belleville et al. 2018)

$$DR(\%) = \frac{\sum_{i=1}^n (DL_i \times DW_i \times DT_i)}{V_{billet}} \quad (13)$$

where DL_i , DW_i , and DT_i are the length, width, and thickness of the i -th air-dried veneer sheet, respectively.

Dried veneers were visually graded according to the Australian/New Zealand grading standard (AS/NZS 2012). This standard classifies veneer sheets into six grades: A, S, B, C, D, and Reject. Gross veneer recovery (GSR%) was calculated as the ratio of the total volume of usable veneer sheets to the initial log volume (Eq. 14). Only sheets that met the A, S, B, C, or D grade classifications were included. Using Eq. (15), net recovery (NR%) was then estimated by applying a trimming factor (0.85) (Belleville et al. 2018).

$$GSR(\%) = \frac{\sum_{i=1}^n (L_i \times W_i \times DT_i)}{V_{billet}} \times 100 \quad (14)$$

Table 1 Veneer layup in 5-ply laminated veneer lumber (LVL) fabrication

LVL sample	Veneer sheet combination				
	Face veneer	Core veneer	Core veneer	Core veneer	Back veneer
Layup 1	Mature <i>E. pellita</i>	Mature <i>E. pellita</i>	<i>E. pellita</i> x <i>E. brassiana</i> (BC)	Mature <i>E. pellita</i>	Mature <i>E. pellita</i>
Layup 2	Mature <i>E. pellita</i>	Mature <i>E. pellita</i>	<i>E. pellita</i> x <i>E. urophylla</i> (F1)	Mature <i>E. pellita</i>	Mature <i>E. pellita</i>
Layup 3	Mature <i>E. pellita</i>	<i>E. pellita</i> x <i>E. brassiana</i> (BC)	<i>E. pellita</i> x <i>E. brassiana</i> (BC)	<i>E. pellita</i> x <i>E. brassiana</i> (BC)	Mature <i>E. pellita</i>
Layup 4	Mature <i>E. pellita</i>	<i>E. pellita</i> x <i>E. brassiana</i> (BC)	<i>E. pellita</i>	<i>E. pellita</i> x <i>E. brassiana</i> (BC)	Mature <i>E. pellita</i>
Layup 5	Mature <i>E. pellita</i>	<i>E. pellita</i>	<i>E. pellita</i>	<i>E. pellita</i>	Mature <i>E. pellita</i>
Layup 6	Mature <i>E. pellita</i>	<i>E. pellita</i> x <i>E. urophylla</i> (BC)	<i>E. pellita</i> x <i>E. urophylla</i> (BC)	<i>E. pellita</i> x <i>E. urophylla</i> (BC)	Mature <i>E. pellita</i>
Layup 7	Mature <i>E. pellita</i>	<i>E. pellita</i> x <i>E. urophylla</i> (F1)	<i>E. pellita</i> x <i>E. urophylla</i> (F1)	<i>E. pellita</i> x <i>E. urophylla</i> (F1)	Mature <i>E. pellita</i>
Layup 8	Mature <i>E. pellita</i>	<i>E. pellita</i> x <i>E. urophylla</i> (F1)	<i>E. pellita</i>	<i>E. pellita</i> x <i>E. urophylla</i> (F1)	Mature <i>E. pellita</i>

Face and back veneers from mature *E. pellita* were A and S grades, while core veneers from hybrids were D grade sheets; one panel per layup was fabricated

where L_i and W_i are the length and width of the i -th air-dried veneer sheet, respectively, while DT_i is the corresponding veneer thickness.

$$NR = GSR \times \text{trimming factor} \quad (15)$$

2.5 Fabrication of laminated veneer lumber (LVL) and evaluation of its physical and mechanical properties

Phenol formaldehyde (PF) adhesive, with a viscosity of 2000–3000 cP, was used to achieve a Type A bond suitable for structural and weather-exposed applications (AS/NZS 2016a). Adhesive preparation and application followed the manufacturer's specifications. Manufacture of LVL and material testing were done following AS/NZS 4357 (Structural laminated veneer lumber) and AS/NZS 2098 (Methods of tests for veneer and plywood). LVL panels were fabricated using five veneer plies, each measuring 400 mm × 400 mm × 4.0 mm. The veneer sheet for the configuration was selected from the mature *E. pellita* (face and back veneers) and hybrids (core layers) (Table 1). Veneers were conditioned in the conditioning chamber to a moisture content of 4–6%. Glue was applied to both sides of sheets 2 and 4, forming four glue lines. Layup time was 1 to 3 min, with a 5 min open and 20 min closed assembly time. Panels were cold-pressed at 1 MPa for 10 min, then hot-pressed at 135 °C and 1.3 MPa for 8 min. LVL panels were machined into test samples and conditioned to 12% MC before testing. Density of the LVL samples was determined. The bond quality was determined using Type A bond test following AS/NZS 2098. Mechanical properties (MOE and MOR) were tested according to AS/NZS 4357 (AS/NZS 2016b, c).

2.6 Billet processing, sawn timber recovery, and grading

Billets (2.4 m) from *E. pellita* and hybrids were back sawn using a LUCAS mill (Model 6–18) with a plain sawing pattern to maximise recovery and retain sapwood. Target board dimensions were 100 mm × 25 mm × 2200 mm and 150 mm × 25 mm × 2200 mm, with initial sawing approximately 5 mm more than the nominal size to allow for shrinkage and dressing. Boards were labelled and air-dried for 32 weeks, then kiln-dried from 40 to 60 °C over three weeks to reach 12% MC. The final dimensions after dressing were approximately 100 mm × 25 mm × 2200 mm and 150 mm × 25 mm × 2200 mm, respectively. On average, 2–5 boards were recovered per billet. However, in mature *E. pellita* trees, recovery was higher, averaging 5–10 boards per billet.

Sawn board recovery (SR), sawn-graded recovery (SGR), and dried-dressed recovery (DDR) were calculated

for each billet and then averaged by hybrid group within each site to assess variation among genetic groups and sites. These were calculated following McGavin et al. (2021). Sawn board recovery (SR%) measures the proportion of log volume converted into boards. SR (%) was calculated using Eq. (15).

$$SR = \frac{\sum_{board} (W \times T \times L)}{\sum_{log} V} \times 100 \quad (16)$$

where W is the sawn board nominal dried width (m), T is the sawn board nominal dried thickness (m), L is the sawn board length (m), and V is the log volume (m^3).

Sawn graded recovery (SGR%) accounts for losses from both sawing and grading, including defects, and was calculated using Eq. (16).

$$SGR = \frac{\sum_{board} (W \times T \times GL)}{\sum_{log} V} \times 100 \quad (17)$$

where W is the sawn board nominal dried width (m), T is the sawn board nominal dried thickness (m), GL is the sawn board length (m) that meets the grade requirements of Australian Standard (AS 2016), V is the log volume (m^3).

Dried-dressed recovery (DDR%) includes losses from sawing, grading, and final machining, and was calculated using Eq. (17).

$$DDR = \frac{\sum_{board} (DDW \times DDT \times GL)}{\sum_{log} V} \times 100 \quad (18)$$

where DDW is the board's nominal width (m) after drying and machining, DDT is the board's nominal thickness (m) after drying and machining, GL is the sawn board length (m) that meets the grade requirements of the Australian Standard (AS 2016), and V is the log volume (m^3).

After drying, boards were visually graded following Australian Standards AS 2082:2017 (Timber Hardwood-Visually stress-graded for structural purposes) (AS 2017) and AS 2796.2:2006 (Timber Hardwood sawn and milled products – Part 2: Grade description) (AS 2016). Defects contributing to board downgrading (e.g., knots, checks, wane, and distortion) were recorded during grading.

2.7 Data analysis

Variation in log traits among genotype groups (Hybrid) was analysed separately for each site using one-way analysis of variance (ANOVA) in R software (version 4.3.3). Within each site, the effect of Hybrid on each trait was tested, and post hoc comparisons were conducted using Tukey's Honest Significant Difference (HSD) test. Correlations between

growth traits and recovery measures were evaluated using Pearson correlation in RStudio. A SNP-based association analysis was conducted to examine the genetic basis of log traits using data from 55 *E. pellita* trees and ~5,500 SNPs generated by Gondwana Genomics (GondwanaGenomics 2025). All SNPs were mapped to Chromosome 1 of the *Eucalyptus grandis* reference genome, as provided in the dataset. To improve data quality, SNPs with multiple variants or a minor allele frequency (MAF) below 0.10 were excluded, yielding a final set of approximately 3,000 high-quality markers. Association testing was conducted using the Bayesian-information and Linkage-disequilibrium Iteratively Nested Keyway (BLINK) method implemented in GAPIT version 3 (Huang et al. 2018; Wang and Zhang 2021). A kinship matrix was calculated using the VanRaden (2008) method to account for genetic relatedness among individuals and control for population structure. In BLINK, markers identified as significant in the initial iteration are incorporated as fixed-effect covariates in subsequent iterations to reduce false positives and improve detection power (Huang et al. 2018). Multiple testing was controlled using the Benjamini-Hochberg False Discovery Rate (FDR) correction method (adjusted $p < 0.05$) (Huang et al. 2018). SNP positions were aligned to the *Eucalyptus grandis* reference genome (version 2.0) available on Phytozome (https://phytozome-next.jgi.doe.gov/info/Egrandis_v2_0). The *E. grandis* genome was used as a proxy due to its strong synteny and close evolutionary relationship with *E. pellita* (Rocha et al. 2022).

3 Results and discussion

3.1 Influence of genotype and site on log traits

To evaluate the effects of genotype and plantation site on form and quality, log traits were assessed across genotype groups at two plantation sites: Kilu Impini 64, characterised by higher productivity, and Yapilika 28, known for moderate productivity. Traits related to billet form included volume, small-end diameter (SED), small-end heartwood diameter (SEHD), and heartwood proportion (HP) (Table 2). In addition, the number of knots, knot diameter, end-split percentage (ES), taper, ovality, and log sweep were assessed to determine billet quality (Table 3).

Log traits varied across genotypes and plantation sites. At Kilu Impini 64, growth conditions were favourable, resulting in minimal variation among hybrids. Billet volume ranged from 0.03 m^3 (*E. pellita* × *E. brassiana* (F1) to 0.05 m^3 (*E. pellita*), with SED values of 124.9–162.7 mm, and SEHD ranged from 102.1 to 129.9 mm, respectively. Heartwood proportion ranged from 60.4% to 70.3%. Among

Table 2 Mean variation among sawn log traits: volume, small-end diameter (SED), small-end Heartwood diameter (SEHD), and Heartwood proportion (HP)

Hybrid/plantation site	No of billet	Volume (m ³)	SED (mm)	SEHD (mm)	HP (%)
Kilu Impini 64					
<i>E. pellita</i>	5	0.0512 ^a (0.0108)	162.7 ^a (18.5)	129.9 ^a (16.8)	66.1 ^a (3.8)
<i>E. pellita</i> × <i>E. brassiana</i> (F1)	5	0.0333 ^a (0.0248)	124.9 ^a (48.02)	102.2 ^a (52.2)	65.7 ^a (15.2)
<i>E. pellita</i> × <i>E. brassiana</i> (BC)	5	0.0499 ^a (0.0085)	161.5 ^a (19.8)	129.3 ^a (18.9)	68.0 ^a (10.7)
<i>E. pellita</i> × <i>E. urophylla</i> (F1)	5	0.0465 ^a (0.0150)	147.1 ^a (10.8)	115.1 ^a (6.6)	60.4 ^a (14.1)
<i>E. pellita</i> × <i>E. urophylla</i> (BC)	5	0.0495 ^a (0.0137)	157.8 ^a (23.4)	129.5 ^a (18.0)	70.5 ^a (8.8)
<i>p</i> value		0.381	0.196	0.420	0.707
<i>F</i> value		1.106	1.671	1.021	0.542
Yapilika 28					
<i>E. pellita</i>	5	0.0441 ^a (0.0184)	148.7 ^a (31.8)	126.5 ^a (28.6)	73.9 ^a (13.8)
<i>E. pellita</i> × <i>E. brassiana</i> (F1)	5	0.0146 ^b (0.0052)	85.7 ^b (12.7)	71.2 ^c (15.7)	72.1 ^a (16.4)
<i>E. pellita</i> × <i>E. brassiana</i> (BC)	5	0.0470 ^a (0.0066)	150.1 ^a (17.4)	123.7 ^a (14.3)	71.2 ^a (5.2)
<i>E. pellita</i> × <i>E. urophylla</i> (F1)	5	0.0262 ^{ab} (0.0097)	113.2 ^{ab} (21.1)	82.6 ^{bc} (19.6)	60.7 ^{ab} (7.6)
<i>E. pellita</i> × <i>E. urophylla</i> (BC)	5	0.0468 ^a (0.0102)	152.5 ^a (17.2)	119.6 ^{ab} (16.3)	56.2 ^b (6.0)
<i>p</i> value		0.002*	0.001*	0.002*	0.049*
<i>F</i> value		6.289	6.966	6.840	2.952

Standard deviation in parentheses. Different letters indicate significant differences between means ($p < 0.05$) within each site; first-generation (F1) and backcross (BC) hybrids. Each hybrid group comprised five billets per site, and volume represents mean billet volume (m³)

the assessed traits, log sweep showed relatively low variation among hybrids within each site, as indicated by its low coefficient of variation (CV%) in Supplementary Table. *E. pellita* had the largest average knot diameter (55.12 mm). Only end-split percentage differed significantly among hybrids ($p = 0.041$), suggesting uniform tree form likely due to the site's high productivity (McGavin et al. 2021).

Yapilika 28 exhibited more pronounced genotype differences. Volume, SED and SEHD varied significantly among hybrids ($p \leq 0.002$) (Table 2), with ranges of 0.02–0.05 m³, 85.7–152.5 mm, and 71.2–126.5 mm, respectively. Hybrids involving *E. brassiana* (BC) generally had the highest values, while *E. pellita* × *E. brassiana* (F1) recorded the lowest. Heartwood proportion differed slightly ($p = 0.049$), ranging from 56.2% (*E. pellita* × *E. urophylla* (BC)) to 73.9% (*E. pellita*). Knot diameter also differed significantly ($p = 0.008$), with the smallest average in *E. pellita* × *E. brassiana* (F1) (11.6 mm). No significant differences were observed for log taper, ovality, and sweep among hybrids. Minor sweep (up to 14 mm) was observed in a few billets,

contributing to higher variability, but this variation was not statistically significant ($p = 0.564$ at Kilu Impini 64 and $p = 0.319$ at Yapilika 28).

Log trait variation across genotype groups and sites reflected both genetic and environmental influences. At Kilu Impini 64, hybrids showed relatively uniform log form and quality, with no significant differences for most traits. This suggested that the growing conditions at this site, including soil properties, moisture availability, or microclimate, may have influenced tree form and contributed to more uniform development across genotypes (Shi et al. 2024). At Yapilika 28, substantial differences emerged among hybrids in key traits such as volume, diameters, and heartwood dimensions. This indicated a stronger expression of genotypic variation, potentially influenced by more challenging environmental conditions. This could be due to differences in soil type and rainfall between the sites, as reported in a related study from adjacent plots within the same plantations (Hutapea et al. 2024). Interestingly, F1 hybrids, which are often expected to express hybrid vigour, did not consistently outperform the pure *E. pellita* or BCs. For example, *E. pellita* × *E. brassiana* (F1) recorded the lowest log volumes and diameters at Yapilika 28. This suggested that the expression of heterosis in log traits may be trait-specific and influenced by genotype combinations and environmental conditions, consistent with Gwaze et al. (2000), who observed variable growth and straightness among *Eucalyptus* hybrids across rainfall zones, and Luo (2023), who reported that hybrid performance and heterosis magnitude vary across single, three-way, and double crosses.

Similar findings have been reported in studies examining log traits in *Eucalyptus* species. For instance, research on *Eucalyptus nitens* logs found that environmental conditions significantly impacted log quality traits, with variations in volume and diameter affecting the recovery of structural sawn boards (Blackburn et al. 2011; Balasso et al. 2022). Additionally, studies on hardwood veneer logs have highlighted the importance of site-specific conditions in determining log quality, with better soil and moisture conditions leading to higher-quality logs (McGavin et al. 2021; Barrette et al. 2023). Differences in heartwood proportion, knot characteristics, and log sweep also have implications for processing (Purnell 1988). Larger diameters and higher heartwood content in *E. pellita* may support higher recovery rates and better durability in solid wood applications, while smaller knot diameters observed in some hybrids may be advantageous for appearance-grade products (Cown et al. 2013).

Table 3 Mean variation in log traits (number of knots, knot diameter, end splits (ES), taper, ovality, and log sweep) among five sawn logs

Hybrid/plantation site	No of knot	Knot diameter (mm)	ES (%)	Taper	Ovality (mm)	Log sweep (mm)
Kilu Impini 64						
<i>E. pellita</i>	4.2 ^a (3.5)	55.1 ^a (19.7)	3.9 ^a (5.6)	0.004 ^a (0.001)	0.94 ^a (0.04)	0.0 ^a (0.0)
<i>E. pellita</i> × <i>E. brassiana</i> (F1)	3.6 ^a (2.9)	40.1 ^a (25.2)	13.1 ^a (10.0)	0.003 ^a (0.001)	0.97 ^a (0.02)	5.0 ^a (11.2)
<i>E. pellita</i> × <i>E. brassiana</i> (BC)	4.8 ^a (3.0)	45.7 ^a (13.2)	17.6 ^a (12.3)	0.004 ^a (0.002)	0.98 ^a (0.02)	0.0 ^a (0.0)
<i>E. pellita</i> × <i>E. urophylla</i> (F1)	6.0 ^a (3.1)	42.4 ^a (3.9)	2.2 ^b (5.0)	0.007 ^a (0.002)	0.94 ^a (0.03)	3.8 ^a (8.5)
<i>E. pellita</i> × <i>E. urophylla</i> (BC)	6.2 ^a (5.6)	38.8 ^a (23.6)	6.7 ^a (6.2)	0.004 ^a (0.002)	0.94 ^a (0.03)	0.0 ^a (0.0)
<i>p</i> value	0.778	0.590	0.041*	0.480	0.149	0.564
<i>F</i> value	0.441	0.717	3.055	0.904	1.906	0.759
Yapilika 28						
<i>E. pellita</i>	6.8 ^a (5.2)	49.4 ^a (8.8)	33.6 ^a (38.8)	0.003 ^a (0.002)	0.92 ^a (0.81)	0.0 ^a (0.0)
<i>E. pellita</i> × <i>E. brassiana</i> (F1)	5.0 ^a (8.7)	11.6 ^b (20.1)	9.3 ^a (8.5)	0.002 ^a (0.001)	0.95 ^a (0.05)	0.0 ^a (0.0)
<i>E. pellita</i> × <i>E. brassiana</i> (BC)	7.2 ^a (8.9)	24.9 ^{ab} (23.5)	12.6 ^a (9.5)	0.006 ^a (0.004)	0.95 ^a (0.02)	14.0 ^a (26.1)
<i>E. pellita</i> × <i>E. urophylla</i> (F1)	4.6 ^a (4.7)	32.4 ^{ab} (18.5)	8.4 ^a (12.4)	0.003 ^a (0.001)	0.96 ^a (0.02)	0.0 ^a (0.0)
<i>E. pellita</i> × <i>E. urophylla</i> (BC)	7.2 ^a (3.3)	55.8 ^a (8.6)	6.2 ^a (9.3)	0.004 ^a (0.002)	0.94 ^a (0.04)	0.0 ^a (0.0)
<i>p</i> value	0.945	0.008*	0.251	0.136	0.735	0.319
<i>F</i> value	0.182	4.773	1.475	2.008	0.501	1.269

Standard deviation in parentheses. Different letters indicate significant differences between means ($p < 0.05$) within each site; First-generation (F1) and backcross (BC) hybrids

Table 4 Summary of sawn (SR), sawn graded (SGR), and dried dressed (DDR) recoveries, and visual grading of sawn boards for genotypes at Kilu Impini 64 and Yapilika 28

Plantation/hybrid	DBH (mm)	No of boards	Sawn board recovery (%)			Grade proportion (%)			
			SR	SGR	DDR	G1	G2	G3	G4
Kilu Impini 64									
<i>E. pellita</i>	199	10	45.1	36.0	19.7	23.5	20.9	10.7	45.0
<i>E. pellita</i> x <i>E. brassiana</i> (F1)	156	8	49.2	37.4	20.8	10.0	29.9	11.2	48.9
<i>E. pellita</i> x <i>E. brassiana</i> (BC)	192	11	42.5	21.4	11.8	10.4	29.9	15.7	44.1
<i>E. pellita</i> x <i>E. urophylla</i> (F1)	186	11	40.1	25.8	14.3	0.0	33.1	29.4	37.5
<i>E. pellita</i> x <i>E. urophylla</i> (BC)	197	9	45.2	29.5	16.1	21.4	30.0	37.0	11.7
Yapilika 28									
<i>E. pellita</i>	195	9	43.2	27.8	15.7	15.0	0.0	0.0	85.0
<i>E. pellita</i> x <i>E. brassiana</i> (F1)	114	0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
<i>E. pellita</i> x <i>E. brassiana</i> (BC)	187	11	48.4	22.8	13.7	0.0	10.9	21.0	68.1
<i>E. pellita</i> x <i>E. urophylla</i> (F1)	154	10	50.8	27.1	15.0	0.0	0.0	0.0	100.0
<i>E. pellita</i> x <i>E. urophylla</i> (BC)	191	3	44.7	24.6	14.5	19.7	8.1	8.1	64.1
Bremer									
Mature <i>E. pellita</i>	362	25	40.0	35.6	21.1	58.8	6.0	9.9	25.3

3.2 Sawn board recovery (SR), sawn-graded recovery (SGR), dried-dressed recovery (DDR), and board quality across genotypes and plantation sites

Sawn board recovery (SR), sawn-graded recovery (SGR), and dried-dressed recovery (DDR) varied across genotypes and sites (Table 4). At Kilu Impini 64, *E. pellita* ×

E. brassiana (F1) recorded the highest SR (49.2%), SGR (37.4%), and DDR (20.8%), reflecting its efficient conversion into usable timber at this site. *E. pellita* × *E. urophylla* (F1) had the lowest SR (40.1%), while *E. pellita* × *E. brassiana* (BC) recorded the lowest SGR (21.4%) and DDR (11.8%).

At Yapilika 28, *E. pellita* × *E. urophylla* (F1) achieved the highest SR (50.8%), while *E. pellita* had the highest SGR (27.8%) and DDR (15.7%). *E. pellita* × *E. brassiana* (F1) recorded zero recovery at this site due to small log diameters falling below the sawmill's operational threshold. This does not imply hybrid or site unsuitability for sawn timber but reflects log size limitations at the time of sampling. The smaller population sizes for F1 groups reduced the pool of trees available for sampling, increasing the likelihood of including smaller or less representative logs. While F1 hybrids are often associated with heterosis, in this study, the BC hybrids demonstrated better recovery performance at the same age, suggesting that trait expression is influenced by both genetic background and developmental stage.

Visual grading patterns also reflected genotype and site effects. At Kilu Impini 64, *E. pellita* × *E. urophylla* showed the widest grade spread, with a notable G3 proportion (37.0%), while *E. pellita* and *E. pellita* × *E. brassiana* (F1) displayed more balanced grade distributions. In contrast, at Yapilika 28, visual grades skewed heavily toward G4, especially in *E. pellita* (85.0%) and *E. pellita* × *E. urophylla* (F1) (100%), suggesting more defects or poorer form.

First-generation (F1) and backcross (BC) hybrids; Each hybrid group was represented by five billets (one per tree) at Kilu Impini 64 and Yapilika 28, and four billets (one per tree) from mature *E. pellita* trees at Bremer site. Statistical testing was not conducted for recovery and grading traits because the data were summarised as group means and proportions from five billets per hybrid per site ($n=5$), which were insufficient for valid ANOVA comparison.

The mature *E. pellita* from the Bremer site, despite a lower SR (40.0%), achieved the highest DDR (21.1%) and the highest proportion of G1 boards (58.8%). This performance is primarily attributed to larger stem diameters and improved form typical of mature trees, which enhance sawing recovery and grade yield by reducing taper and knot frequency (Hamilton et al. 2015).

Sawn board recovery (SR), sawn-graded recovery (SGR), dried-dressed recovery (DDR), and visual grade distributions varied among *E. pellita* and its hybrids. These differences were influenced by both genotype and plantation site. At Kilu Impini 64, *E. pellita* × *E. brassiana* (F1) recorded the highest SR and DDR. This supports previous findings that F1 hybrids can enhance processing efficiency through heterosis, that is, improved performance resulting from the genetic combination of two distinct parent species (Blackburn et al. 2011; Filipescu et al. 2018). The sawn recoveries in this study are comparable and slightly higher than the SR recorded in a 7.5–13-year-old African mahogany plantation (McGavin et al. 2021) and 7 to 23-year-old *E. pellita* in Malaysia (Japarudin et al. 2021a). These variations likely reflect both species and site differences as well as variations

in log size and processing technology used across studies (Chauhan 2025). Conversely, the observed result is lower than the lumber yield recorded in 21-year-old *Eucalyptus regnans* (Rozas et al. 2023), likely reflecting differences in log diameter as larger diameters generally yield higher sawn recoveries.

E. pellita and hybrids not only show moderate recovery rates but also produce a wide range of visual grades. Moderate grades were recorded, with most recoveries grouped as G4, followed by G3 and G2. This indicated limited potential for high-quality output from young *E. pellita* and hybrids, such as the mature *E. pellita* from the Bremer site, which achieved higher-grade recoveries due to their greater size and form quality. Additionally, mature *E. pellita* trees from Bremer produced the highest G1 proportions (58.8%), reinforcing the known advantages of mature wood in quality and form (Japarudin et al. 2021a; Balasso et al. 2022). The findings underscore the importance of considering both volume and quality traits in the selection of superior genotypes for solid wood production. While F1s may offer high recovery potential, this advantage can be limited by site constraints or poor silvicultural management (Gao et al. 2024). The contrast between sites highlights the need for integrated genotype × environment × management ($G \times E \times M$) approaches (Ibarra et al. 2023). Incorporating recovery and grade performance into breeding indices alongside traditional growth traits will improve the identification and deployment of elite material. A multi-trait, site-specific strategy would be essential to optimise genetic gain, wood quality, and processing efficiency in tropical *Eucalyptus* plantations.

Following the grading outcomes, the types and frequencies of defects contributing to board downgrading were examined across the plantation sites. Key defects such as bow, cup, splits, checks, shakes, wane, knots, and decay were identified and compared across hybrids at Kilu Impini 64 (Fig. 3) and Yapilika 28 (Fig. 4), as well as the mature *E. pellita* (Fig. 5). Defect frequencies were summarised as proportions of affected boards. Statistical testing was not performed due to the small sample size. This comparison provides deeper insights into wood quality variations and their impact on recovery performance. At Kilu Impini 64, knots were the most frequent defect, ranging from 38.6% to 53.9%, reflecting the high branching tendency of fast-growing hybrids without pruning (Fig. 3). Bow occurred in all hybrids, with values between 11.9% and 23.8%, highest in *E. pellita* × *E. brassiana* (F1). Total splits ranged from 11.2% to 26.2%, with higher values observed in backcross hybrids, suggesting that hybrid vigour may be linked to increased drying-related stress. Shake and check were moderate (up to 12.5% and 4.2–6.4%, respectively), while wane was largely absent, and no decay was observed, indicating good log soundness and conversion practices.

Fig. 3 Sawn board defects observed in *E. pellita* and hybrids, including first-generation (F1) and backcross (BC), at Kilu Impini 64 (Defect frequencies were summarized as proportions of affected boards within each hybrid group)

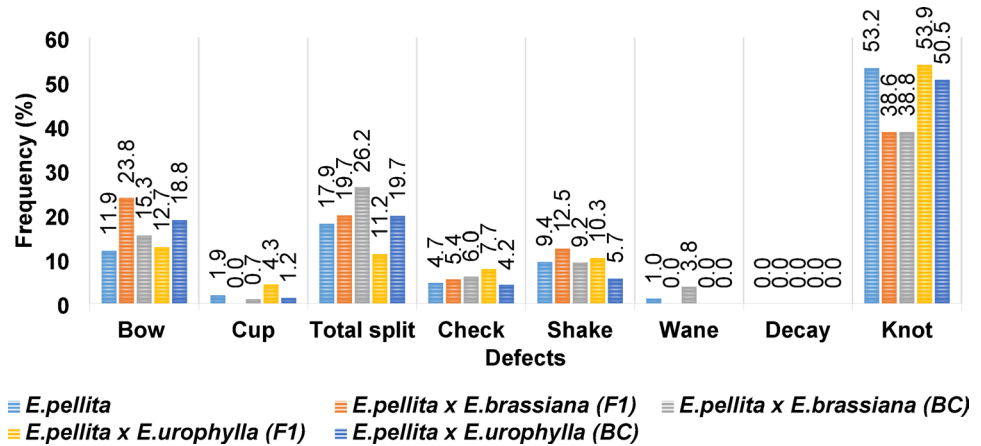


Fig. 4 Sawn board defects observed in *E. pellita* and hybrids, including first-generation (F1) and backcross (BC), in Yapilika 28 (Defect frequencies were summarized as proportions of affected boards within each hybrid group). The number of boards assessed per hybrid group ranged from 0–11

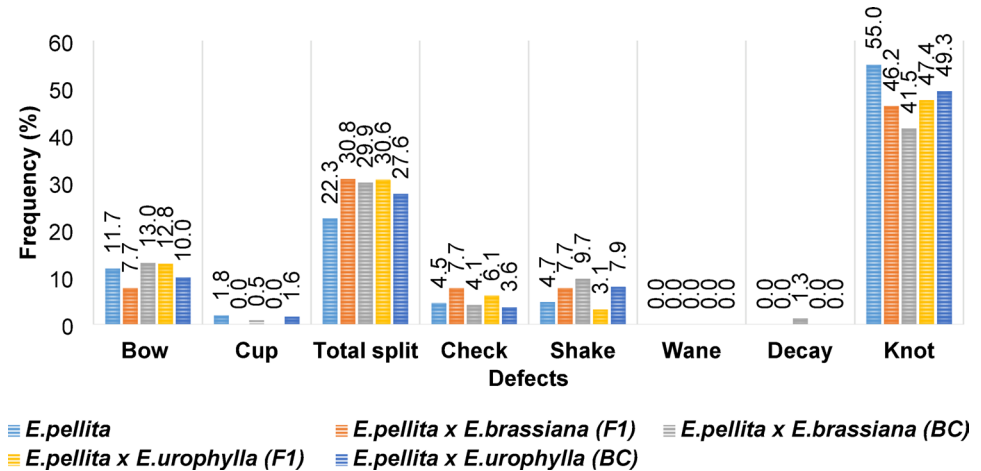
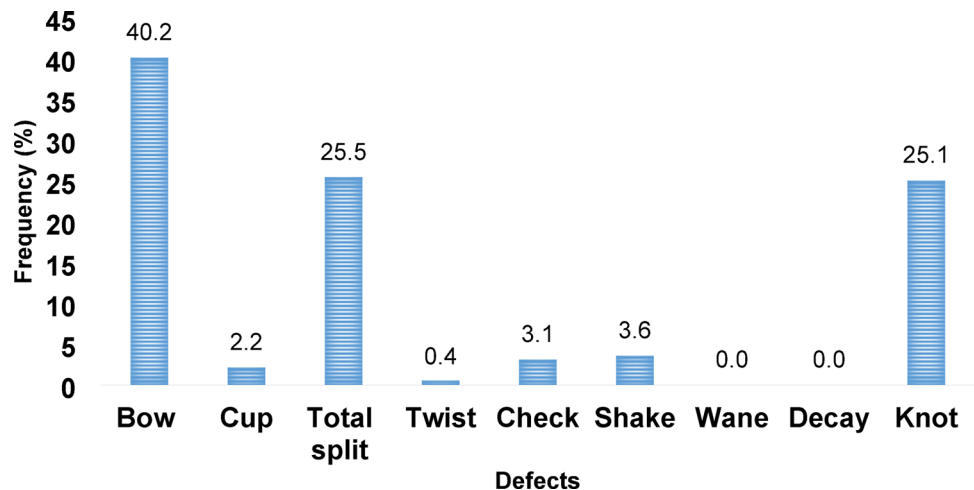


Fig. 5 Sawn board defects observed in logs in Mature *E. pellita* (30 years old) from the Bremer site. A total of 26 boards were assessed



At Yapilika 28, knots remained the most common defect (41.5–55.0%) (Fig. 4). Splits were more prevalent than at Kilu Impini 64, exceeding 30% in *E. pellita* x *E. brassiana* (F1) and *E. pellita* x *E. urophylla* (F1), highlighting a stronger site effect. In contrast, bow was less pronounced (7.7–13.0%), suggesting better dimensional stability. Check and shake occurred at moderate levels, with *E. pellita* x *E. brassiana* (BC) recording the lowest check (3.6%) and *E.*

pellita x *E. urophylla* (F1) the lowest shake (3.1%). Wane and decay were absent.

The mature *E. pellita* trees (Fig. 5) displayed a distinct defect profile. Bow was highest (40.2%), likely due to internal stresses in older wood, and total splits were also relatively high (25.5%). In contrast, knot frequency was lower (25.1%) compared to the hybrids, likely due to self-pruning and slower growth. Other defects, such as check (3.1%) and

shake (3.6%), were minimal, and twists occurred in only 0.4% of boards. No wane or decay was observed.

The observed defect patterns align with previous studies on defects of sawn boards, including splits, knots, bows, shakes, and checks (Cown et al. 2013; McGavin and Leggate 2019; Japarudin et al. 2021a; Balasso et al. 2022). Balasso et al. (2022) reported high knot frequency and internal checking in 21-year-old *E. nitens* logs, particularly under minimal pruning regimes and rapid growth conditions, similar to the trends at Kilu Impini 64 and Yapilika 28. Hii et al. (2017) also recorded a high incidence of knots and end splits in 9-year-old *E. pellita*, consistent with the observations in this study. The high split frequency at Yapilika 28 with moderate productivity reinforces the impact of environmental conditions on sawn wood quality. These results highlight the combined effects of genetic background and site-specific factors on defect formation and overall timber grade outcomes (Kombi Kaviriri et al. 2021). The higher knot and split frequencies observed in hybrids, though associated with fast growth, pose challenges for structural applications and reduce recovery potential. The findings provide insights into how these defect trends vary by genotype and site, offering a basis for breeding programs to better balance growth traits with wood quality. Moreover, site-specific management, such as targeted pruning and optimised drying protocols, could mitigate the impact of defects and improve product yield. For example, the high knot frequency observed in unpruned hybrids highlights the need for early and consistent pruning to reduce branch-related defects. Similarly, the elevated split rates at Yapilika 28 suggested that adjustments to drying schedules, such as slower initial drying or pre-conditioning, may help reduce drying stress and end-splits, consistent with observations on drying

behaviour and defect control in timber reported by Ramage et al. (2017).

To examine how log and stem traits influenced processing efficiency, correlation analysis was performed between recovery metrics and key characteristics (Table 5). Strong positive correlations were observed among SR, SGR, and DDR ($r=0.80$ – 0.99), indicating consistent performance across recovery stages. Log dimensions, particularly SED, SEHD, volume, and DBH, showed moderate to strong correlations with all recovery metrics ($r=0.52$ – 0.61). This highlighted their importance in predicting yield.

Knot diameter was moderately correlated with SR, SGR, and DDR ($r\approx 0.33$ – 0.39), while the number of knots showed no significant correlation. Although knots are known to influence grade recovery, their weak correlations with recovery outcomes likely reflect limited variation in defect severity across logs, as most billets were of comparable quality. Sweep and ovality also showed weak associations with recovery, indicating that dimensional factors, rather than form defects, dominated the overall conversion efficiency. Heartwood proportion had a modest correlation with SR ($r=0.31$), suggesting only a minor influence of internal wood characteristics on yield. Overall, recovery was primarily influenced by log size, with diameter traits being the strongest predictors.

3.3 Rotary peeling and veneer recovery of *E. pellita* and hybrids

Table 6 presents veneer billet characteristics from four hybrids at Kilu Impini 64, one from Yapilika 28, and a mature *E. pellita* log from Bremer site (included for comparison). Hybrid billet volumes ranged from 0.05 to 0.06 m³, while the mature *E. pellita* was larger (0.13 m³). SED were relatively uniform among hybrids (186–201 mm), with similar trends in heartwood diameters. The Bremer billet had the largest average SEHD (287 mm), reflecting its maturity.

Heartwood proportion (HP) across the sampled logs ranged from 65.2% to 75.2%. Knot presence varied among the sampled hybrid logs (7–15 knots; 43.0–59.1 mm diameter), while no knots were observed in the mature log. End splits were minimal in logs sampled from Kilu Impini 64 (0.0–4.72%), higher in the log from Yapilika 28 (19.44%), and moderate in the mature log (5.33%). All sampled logs exhibited low taper and ovality, indicating favourable log form for rotary peeling. Given that only one log was assessed per family, these observations reflect individual-log characteristics rather than family-level differences.

Veneer recovery, assessed at green (GR), dry (DR), and net (NR) stages, varied among the sampled logs from the two plantation sites and the mature *E. pellita* (Table 7). Log sampled from Kilu Impini 64 showed generally high veneer

Table 5 Correlation and significance between log traits and sawn (SR), sawn graded (SGR), and dried dressed (DDR) recoveries

	SR (%)	SGR (%)	DDR (%)
SR	1		
SGR	0.80*	1	
DDR	0.80*	0.99*	1
Number of knots	0.08	0.05	0.04
Knot diameter	0.39*	0.33*	0.33*
Log-sweep	0.22	0.02	0.05
ES	0.01	− 0.07	− 0.03
SED	0.56*	0.54*	0.53*
SEHD	0.61*	0.57*	0.57*
Volume	0.53*	0.52*	0.51*
Taper	0.24	0.13	0.17
Ovality	− 0.03	0.03	0.00
HP	0.31*	0.24	0.24
DBH	0.58*	0.57*	0.57*

SED small-end diameter, SEHD, small-heartwood diameter, HP heartwood proportion, ES end splits, DBH diameter at breast height

* $p < 0.05$

Table 6 Log traits of *E. pellita* and hybrid trees selected for veneer peeling

	<i>E. pellita</i>	<i>E. pellita</i> × <i>E. urophylla</i> (F1)	<i>E. pellita</i> × <i>E. urophylla</i> (BC)	<i>E. pellita</i> × <i>E. brassiana</i> (BC)	<i>E. pellita</i> × <i>E. urophylla</i> (BC)	Mature <i>E. pellita</i>
	KI64	KI64	KI64	KI64	YP28	BREMER
Volume (m ²)	0.06	0.05	0.06	0.06	0.05	0.13
SED (mm)	200	186	197	201	187	324
SEHD (mm)	165	139	164	166	154	287
HP (%)	71.4	66.9	71.5	75.2	65.2	76.3
No of knots	14	15	7	8	6	0
Knot diameter (mm)	55.0	43.0	57.2	59.1	50.3	0.0
ES (%)	2.9	4.72	0.83	0.00	19.44	5.33
Taper	0.00	0.00	0.00	0.00	0.01	0.01
Ovality	0.95	0.99	0.94	0.92	0.94	0.96

Values represent one billet per tree per hybrid, shown as means for descriptive comparison and rounded to appropriate precision. KI64 – Kilo Impini 64; YP28 – Yapilika 28; SED: small-end diameter; SEHD: small-end heartwood diameter; HP: heartwood proportion; ES: end splits; first-generation (F1) and backcross (BC)

Table 7 Green (GR), dry (DR), net (NR) recoveries and veneer grades from *E. pellita* and hybrids at Kilo impini 64 (KI64) and Yapilika 28 (YP28)

Hybrid	Site	DBH (mm)	Veneer recovery (%)			Veneer grade proportion (%)					
			GR	DR	NR	A	S	B	C	D	Rejects
<i>E. pellita</i>	KI64	200.0	76.0	65.3	55.5	0.0	0.0	0.0	0.0	46.6	53.4
<i>E. pellita</i> × <i>E. urophylla</i> (F1)	KI64	190.0	80.1	74.7	63.5	0.0	0.0	0.0	0.0	100.0	0.0
<i>E. pellita</i> × <i>E. urophylla</i> (BC)	KI64	200.0	82.2	78.3	66.6	0.0	0.0	0.0	0.0	73.4	26.6
<i>E. pellita</i> × <i>E. brassiana</i> (BC)	KI64	190.0	83.6	83.1	70.7	0.0	0.0	0.0	0.0	77.5	22.5
<i>E. pellita</i> × <i>E. urophylla</i> (BC)	YP28	180.0	53.5	43.5	37.0	0.0	0.0	0.0	0.0	0.0	100.0
Mature <i>E. pellita</i> tree	Bremer	360.0	79.3	64.4	54.8	67.1	18.2	0.0	8.9	0.0	5.8

Each value represents one billet (one tree) per hybrid used for veneer peeling; KI64 - Kilo Impini 64; YP28 - Yapilika 28; DBH - Diameter at breast height; First-generation (F1) and backcross (BC) hybrids

recovery across all stages, with GR ranging up to 83.6%, DR up to 83.1%, and NR up to 70.7%. Net recovery among the sampled logs at this site ranged from 55.5% to 70.7%. Overall recovery values obtained in this study exceed those reported in previous studies, for example, net recoveries of 41.1% for *E. pellita* and 40.0% for *E. camaldulensis* (Belleville et al. 2018), and 54.5% green recovery for *E. globoides* (Guo and Altaner 2018). Similarly, the lower total recovery of 65.8% reported for *E. urophylla* × *E. grandis* (Peng et al. 2014) contrasts with the higher green recovery observed in this study's hybrids, reflecting differences in plantation conditions, log size, and resource characteristics.

Despite the high recoveries observed, all veneer sheets produced from logs sampled at Kilo Impini 64 hybrids were classified as D-grade. This aligns with previous studies on *Eucalyptus* and other plantation-grown hardwood species, such as African mahogany and rubberwood, where veneer sheets were similarly limited to D-grade. This is largely due to juvenile wood properties, growth stresses, defects, and processing outcomes common to fast-grown plantation hardwoods (Valencia et al. 2011; Peng et al. 2014; Khoo et al. 2018; McGavin et al. 2021). Variation in rejection rates was observed among sampled logs. For example, *E. pellita* × *E. urophylla* (F1) yielded 100% D-grade with no rejects, while *E. pellita* had only 46.6% D-grade and a rejection

rate of 53.4%, indicating greater susceptibility to grading defects. At Yapilika 28, veneer recovery from the sampled *E. pellita* × *E. urophylla* (BC) showed the lowest recovery at all stages (GR: 53.5%, DR: 43.5%, NR: 37.0%) and was fully rejected. The higher rejection rate corresponded with frequent end splits, suggesting that factors, such as growth stress, may have adversely affected veneer quality and processing performance (Japarudin et al. 2021a).

In contrast, the mature *E. pellita* tree from Bremer showed moderate net recovery (54.8%) but produced a higher proportion of appearance-grade veneer (67.1% A-grade and 18.2% S-grade), with a low rejection rate (5.8%). This outcome is consistent with its larger diameter and absence of knots, which reduce veneer curvature and defect frequency, resulting in more uniform veneer thickness, fewer grade-limiting defects, and improved veneer grading performance (Japarudin et al. 2021a). These observations illustrate the trade-off between veneer yield and product quality in plantation hardwood processing and highlight the importance of aligning resource characteristics with intended end-use requirements.

To explore factors influencing veneer grade allocation, key downgrading defects were examined in the sampled material (Fig. 6). As only one billet per hybrid per site was analysed, the results are presented as descriptive

observations rather than comparative assessments. The most frequently observed defects included splits, knots, stains, and decay. Splits were commonly associated with logs exhibiting pronounced growth stress during peeling, consistent with the presence of tension wood in fast-grown eucalypts (Leggate et al. 2017). Knot-related defects were associated with branch inclusions, reflecting limited self-pruning and reduced visual quality (Ramage et al. 2017). Stain was more frequent in the mature *E. pellita* (70%) than in *E. pellita* × *E. urophylla* (BC) at Yapilika 28 (10%). Stain and occasional decay were also observed in some samples, likely influenced by extractive content, microbial activity, or storage conditions. Even at low incidence, these defects substantially affect veneer grading by reducing strength, durability, and appearance quality (Leggate et al. 2017; Ramage et al. 2017).

The defects observed in this study align with previous findings. Belleville et al. (2020) reported knots, splits, discoloration, and decay as common downgrading defects in plantation-grown rubberwood. Similarly, knots and splits were major defects in *E. urophylla* × *E. grandis* (Peng et al. 2014). Guo and Altaner (2018) noted severe splitting in *E. globoidea* veneer. In this study, variability in defect occurrence was observed among sampled hybrid logs across sites. As these results are based on descriptive observations from limited number of samples, they indicate potential

influences of log form and site-related factors on veneer quality.

To explore factors affecting recovery, correlations were assessed between recovery metrics and log traits (Table 8). Green (GR), dry (DR), and net (NR) recoveries were strongly correlated ($r \geq 0.98$), showing consistency across processing. Veneer recoveries showed positive but non-significant associations with DBH ($r = 0.71$ – 0.76), heartwood proportion (HP, $r = 0.73$ – 0.74), small-end diameter (SED, $r = 0.53$). Although these relationships were not statistically significant, the observed trends align with previous reports that logs with larger diameters and more uniform geometry tend to improve recovery and reduce rounding losses (McGavin and Leggate 2019; Tyron et al. 2020). Taper showed a strong negative correlation with recovery ($r = -0.92$ to -0.93), indicating that highly tapered logs reduce veneer yield due to unstable rotation and greater losses (Peng et al. 2014; Hamilton et al. 2015). End-split (ES) showed a very strong negative correlation with recovery ($r = -0.94$ to -0.98), as splits can interrupt continuous peeling and cause sheet breakage (Lutz 1971; Peng et al. 2014; Guo and Altaner 2018). Knot traits (number and diameter), and ovality showed weak, non-significant correlations with recovery ($r \leq 0.37$). These findings highlight observed variation in log geometry among hybrids.

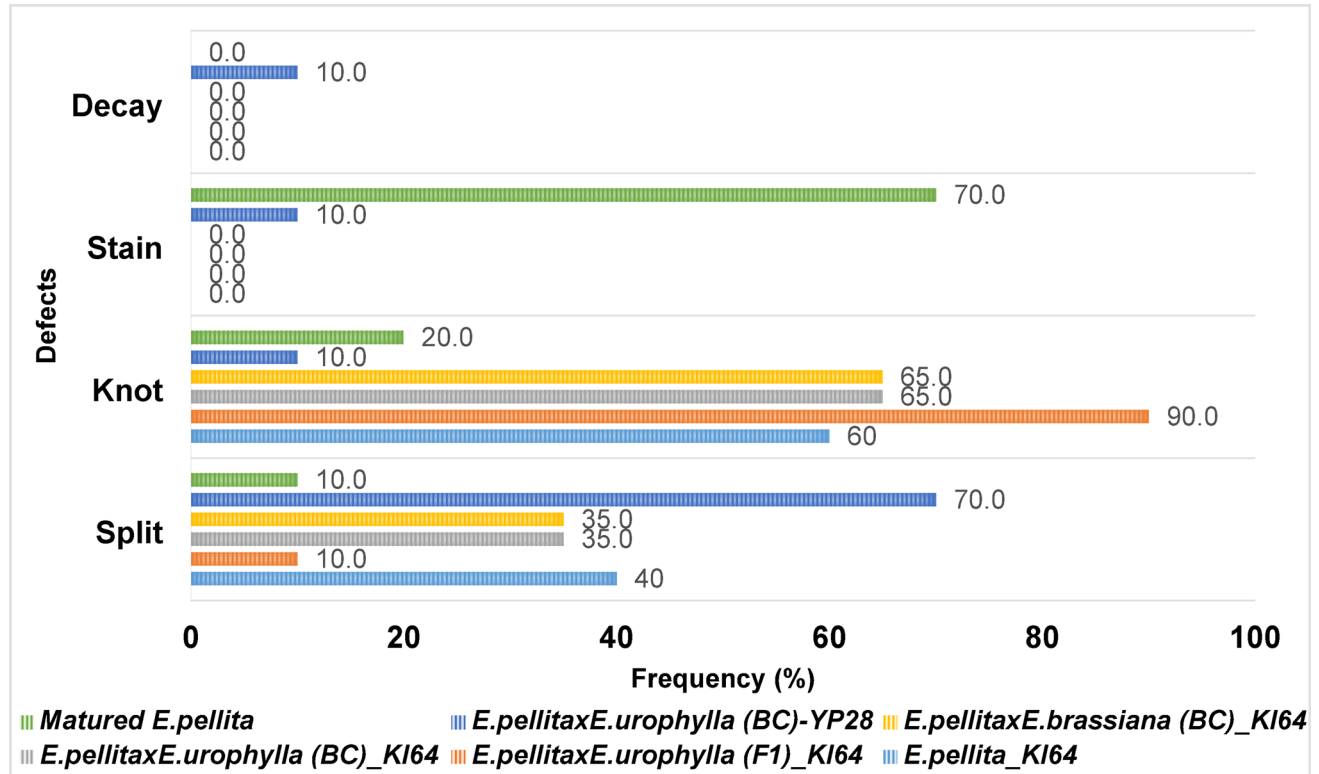


Fig. 6 Downgrading defects observed in veneer sheets recovered from *E. pellita* and its hybrids, including first-generation (F1) and backcross (BC) types, at Kilu Impini 64 (KI64) and Yapilika 28 (YP28)

Table 8 Pearson correlation coefficients between veneer green (GR), dry (DR), and net (NR) recovery and log traits

	GR	DR	NR
GR	1		
DR	0.98*	1	
NR	0.98*	1*	1
Number of knots	0.37	0.23	0.23
Knot diameter	0.28	0.32	0.32
ES	-0.98*	-0.94*	-0.94*
SED	0.55	0.53	0.53
SEHD	0.19	0.19	0.19
Volume	0.11	0.07	0.07
Taper	-0.92*	-0.93*	-0.93*
Ovality	0.15	0.07	0.07
HP	0.73	0.74	0.74
DBH	0.76	0.71	0.71

Pearson correlation coefficients (r) were calculated using data from six billets ($n=6$)

SED small-end diameter, SEHD small-end heartwood diameter, HP heartwood proportion, ES end splits, DBH diameter at breast height

* $p<0.05$

Table 9 Density, modulus of elasticity (MOE) and modulus of rupture (MOR) of laminated veneer lumber (LVL) produced from *E. pellita* and hybrids

LVL combination	Density (kg/m ³)	MOE (GPa)	MOR (MPa)
Layup 1	703 (31.77)	14.4 (0.40)	122 (8.43)
Layup 2	788 (2.90)	15.8 (2.41)	124 (22.87)
Layup 3	791 (18.45)	18.8 (2.35)	139 (8.83)
Layup 4	815 (14.44)	14.9 (5.18)	123 (33.68)
Layup 5	774 (33.23)	16.3 (2.54)	132 (12.48)
Layup 6	732 (50.34)	15.4 (4.37)	127 (23.85)
Layup 7	736 (24.69)	14.5 (0.65)	127 (5.62)
Layup 8	756 (13.59)	16.6 (1.06)	138 (11.80)

One LVL panel was manufactured per layup. Values are means (standard deviation in parentheses) of specimens cut from the same panel; results are descriptive only

3.4 Properties of laminated veneer lumber (LVL) from *E. pellita* and hybrid veneers

After veneer recovery and grading, LVL panels were fabricated, each representing a different layup combination, using hybrid veneers in the core and mature *E. pellita* veneers for the face and back layers. From these panels, test samples were machined and evaluated for density, MOE, and MOR. Although mean differences were observed among layups, only one LVL panel was produced per layup type; therefore, the results are descriptive and not statistically comparable between hybrids. Mean values of density, MOE, and MOR are presented in Table 9. Density values across the LVL panels ranged from 703 to 815 kg/m³, reflecting variation among the tested layup configurations, including panels with mixed and full hybrid cores.

MOE values across the tested LVL panels ranged from 14.4 GPa to 18.8 GPa and modulus of rupture (MOR) ranged from 122 to 139 MPa across the tested LVL panels. Variation in mechanical performance was observed among layups incorporating different veneer arrangements; however, given the limited replication, these differences are interpreted as descriptive panel-level.

Density varied among the tested LVL panels, while MOE and MOR values were generally comparable across the different layup configurations. Overall, the results demonstrate that LVL panels incorporating hybrid veneers can achieve stiffness and strength values suitable for structural applications.

The mechanical properties observed in this study are consistent with those reported for *Eucalyptus*-based LVL. Aydın et al. (2004) reported MOE values up to 9411 MPa and MOR values up to 94 MPa for *Eucalyptus camaldulensis* from the Tarsus-Karabucak Region, Turkey, which were lower than those observed in this study. Although tree age was not specified, the species was selected for its rapid diameter growth (Aydın et al. 2004). Similarly, Bal (2016) recorded MOE values of up to 10,554 MPa and MOR values of around 100 MPa for LVL from *E. grandis*, depending on the adhesive and pressing conditions used. Although Martins and Dias (2025) recorded higher MOE (up to 22,000 MPa) in *E. globulus*, MOR values were lower than those observed in the present study. The MOE and MOR ranges obtained here fall within the spectrum reported for structural *Eucalyptus* LVL, indicating competitive mechanical performance of the tested panels.

McGavin et al. (2019) reported that veneer layup composition significantly affects LVL strength, particularly when core and outer layers differ in wood type. In this study, layups with multiple hybrid core layers showed comparable mechanical performance to those with single hybrid layers. Compared to LVL from other hardwoods, the strength values in this study exceeded those reported for *Hevea* logs (MOE: 11,189 MPa; MOR: 91.05 MPa) using flatwise testing (Khoo et al. 2021). The mechanical property ranges observed here are consistent with values reported for LVL manufactured from plantation-grown hardwoods. Collectively, these results indicate that the hybrid veneer combinations tested are technically suitable for LVL manufacture and have potential for use in structurally engineered wood products.

Bond quality testing was conducted to evaluate the adhesive performance of LVL panels manufactured using hybrid veneer combinations (Fig. 7). Bond quality scores were consistently high across all tested panels, with mean values ranging from 9.8 to 10.0 on a 1–10 scale. All panels were bonded using phenol formaldehyde (PF) Type A adhesive, and no significant differences were observed among the

Layups. The consistently high bond quality scores indicate effective glue line integrity and adequate adhesive penetration, likely supported by proper veneer surface preparation and moisture conditioning before lamination.

These results align with previous findings that reported excellent bond performance in hardwood-based LVL bonded with phenol-formaldehyde adhesives (Khoo et al. 2019, 2020). In contrast, Guo and Altaner (2018) reported poor bonding quality in *E. globoidea* LVL, which was associated with its high density and bonding difficulty. Similarly, Darmawan et al. (2015) found that lathe check characteristics negatively affected glue bond quality in *Paraserianthes moluccana*. The findings confirm that the hybrid veneer combinations in this study are compatible with PF adhesives and meet Type A bond quality standards under AS/NZS 2098.2. This supports their suitability for structural LVL use.

3.5 Genetic correlation between single nucleotide polymorphisms (SNPs) and selected log traits influencing sawing and peeling recoveries

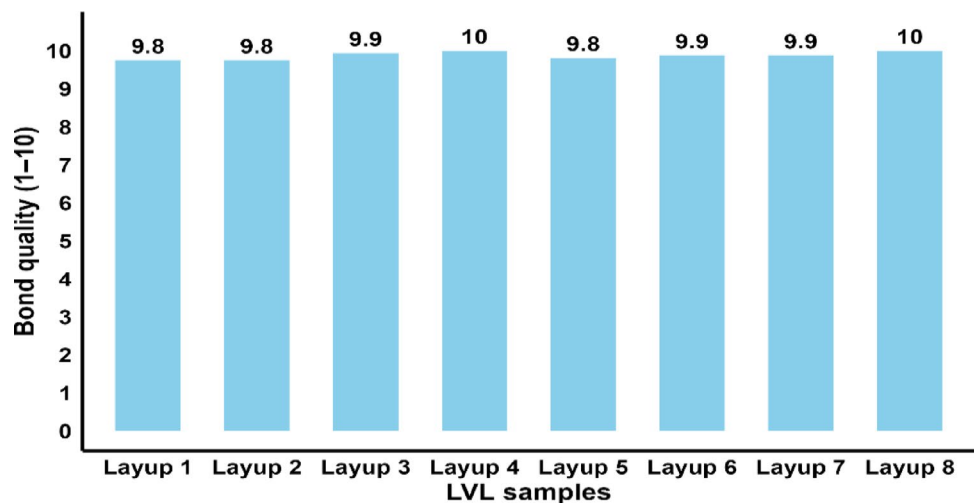
A genetic analysis was conducted using a final set of approximately 3,000 high-quality SNPs (filtered from an initial dataset of ~5500 SNPs provided by Gondwana Genomics for *E. pellita*) to assess associations with small-end diameter (SED), heartwood proportion (HP), knot diameter, and end split, traits that influenced log form, wood quality and processing performance. Figure 8 presents Manhattan and Q–Q plots based on the Blink model in GAPIT. Associations were generally moderate, with most SNPs falling below the suggestive significance threshold ($-\log_{10}(p)=5$). For SED, p-value distributions were uniform, suggesting polygenic control or limited power due to the small population size ($n=50$). In contrast, significant SNPs were detected for HP, knot diameter, and end split, showing elevated $-\log_{10}(p)$ values and Q–Q plot deflections, indicating

potential associations. These may reflect true biological effects or linkage to causative loci not directly captured by the genotyped SNPs. The Q–Q plots showed that most points aligned closely with the expected diagonal ($x=y$), suggesting that the model adequately controlled for population structure and relatedness.

Three top SNPs ($p<0.001$) were identified and are detailed in Table 10. For SNP1358 associated with end split, the allele showed a positive effect (+50.87), indicating an association with increased splitting, an undesirable trait. In contrast, the allele at SNP4964 showed a negative effect (−34.73), suggesting an association with reduced end splitting. For heartwood proportion, the allele at SNP2187 showed a significant negative effect (−10.55), indicating reduced heartwood content, whereas the allele at SNP3547 exhibited a smaller positive effect (+8.59), suggesting a potential association with increased heartwood proportion despite lower statistical significance. For knot diameter, the allele at SNP3201 was associated with a negative effect (−8.86), consistent with a reduction in knot size. For diameter traits, the allele at SNP13 showed a negative association with small-end diameter (SED; −26.36), while SNP3055 also exhibited a negative effect on SED (−38.17), both of which are generally unfavourable for productivity. In contrast, the allele at SNP4505 showed a positive association with SED (+39.62), indicating a potential contribution to increased stem diameter. While these SNP–trait associations are statistically significant, their relevance for breeding depends on breeding objectives and trait priorities.

The current study utilised an SNP panel of approximately 5500 markers in a relatively small population size ($n=55$) and identified significant associations for traits such as end split, heartwood proportion, and knot diameter. However, the limited population size may have constrained the detection of associations of more SNPs, especially in traits like small end diameter (SED). This observation aligns with findings from Müller et al. (2017), who reported that in

Fig. 7 Bond quality scale recorded across laminated veneer lumber (LVL) combinations



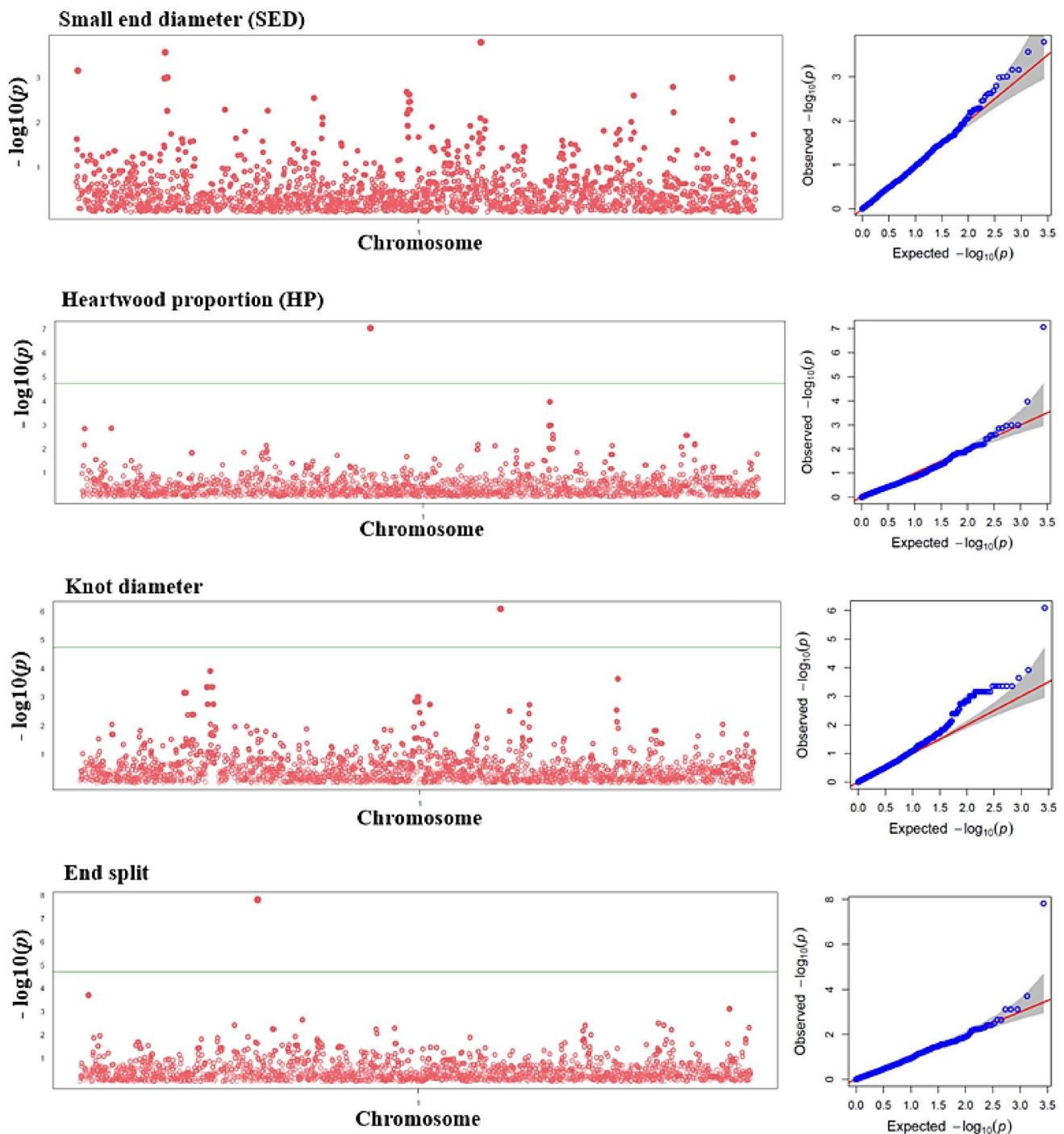


Fig. 8 Manhattan and Q–Q plots showing single nucleotide polymorphisms (SNPs)–trait associations for log traits in *Eucalyptus pellita* hybrids using the Blink model. The Manhattan plot displays SNPs mapped to Chromosome 1, reflecting the genomic scope of the tar-

geted SNP panel used in this study. In the Q–Q plot, the red line represents the expected distribution of p values under the null hypothesis, indicating no marker–trait association

breeding populations of *Eucalyptus benthamii* (505 individuals) and *E. pellita* (732 individuals), GWAS identified only a few significant associations, whereas genomic prediction methods captured a larger proportion of heritable variation for growth traits. Similarly, Valenzuela et al.

(2021) conducted a GWAS on *Eucalyptus cladocalyx* (480 individuals) under arid conditions and found 87 SNPs and 3 haplotype blocks significantly associated with growth and wood quality traits, including 11 loci with pleiotropic effects on wood hardness, height, and diameter. These studies

Table 10 Identified single nucleotide polymorphisms (SNPs) associated with end split (ES), Heartwood proportion (HP), knot diameter, small-end diameter (SED), and the annotated gene information. All SNPs are located on chromosome 1

Marker name	Traits	Alleles	Pos	P value	MAF	Allelic effect	Nearest gene
SNP1358	End split	A/G	1358	0.000**	0.045	50.867	<i>Eucgr.A00211</i>
SNP66		T/A	66	0.000**	0.091	22.785	
SNP4964		A/T	4964	0.001*	0.076	− 34.726	
SNP2187	HP	T/A	2187	0.000**	0.283	− 10.549	
SNP3547		G/A	3547	0.000**	0.321	8.591	
SNP3544		C/T	3544	0.001*	0.123	− 8.574	
SNP3201	Knot diameter	T/C	3201	0.000**	0.228	− 8.863	
SNP991		A/G	991	0.000**	0.370	− 5.069	
SNP4093		T/C	4093	0.000**	0.402	5.410	
SNP3055	SED	C/T	3055	0.000**	0.151	− 38.175	
SNP672		T/G	672	0.000**	0.179	− 27.566	
SNP13		T/A	13	0.001*	0.236	− 26.356	

** $p < 0.001$, * $p < 0.01$, Pos: SNP position in the population structure; MAF: minor allele frequency; Allelic effects represent changes in the original units of each trait (e.g., mm for SED and knot diameter, % for HP and ES) for each allelic effect estimated by the BLINK model in GAPIT

underscore the importance of larger population sizes and higher marker densities to uncover the genetic architecture of complex traits in *Eucalyptus*. Rocha et al. (2022) performed single- and multi-trait GWAS in an open-pollinated *E. grandis* population (1772 trees) and identified numerous QTLs associated with growth and wood traits. Their findings highlight the potential of multi-trait GWAS approaches to detect pleiotropic loci that may be missed in single-trait analysis. These studies support the relevance of our findings and place them within the broader context of genetic research on *E. pellita* wood traits. Although based on a limited sample size, this study contributes to existing knowledge and highlights the need for larger, replicated datasets to improve the detection power and reliability of genetic associations in *E. pellita* and its hybrids.

All SNPs significantly associated with log traits (SED, HP, knot diameter, and end splits), were located within the same intergenic region upstream of *Eucgr.A00211* on Chromosome 1 (Table 10), which encodes a lipase-containing protein related to the CGI-141 family. Although the function of this gene in *Eucalyptus* remains uncharacterised, lipase-like proteins are generally involved in lipid metabolism, membrane remodelling, and stress-related signalling pathways. The variants identified in this region were annotated with MODIFIER impact, suggesting they do not alter the protein sequence but may influence gene expression. Lipid-mediated processes play important roles in cambial activity, xylem development, and heartwood formation, all of which contribute to variation in stem form and wood structure (Herrera-Ramírez et al. 2021; Xie et al. 2021). The clustering of significant SNPs within a single genomic region was not unexpected, given the small population size, which may have restricted the detection of additional loci. These findings provide preliminary evidence that *Eucgr.A00211* may play a regulatory role in wood formation and quality

traits and represents a promising candidate for further investigation and for marker-assisted selection in *E. pellita* improvement.

While the sample size in this study is limited, previous research has shown that meaningful SNP-trait associations can be identified in forest trees using similarly sized populations. For example, González-Martínez et al. (2007) detected significant associations between SNPs and wood property traits in loblolly pine using a candidate gene approach. Likewise, Zhou et al. (2022) identified genetic loci for growth and wood traits in *Picea crassifolia* despite working with a moderate sample size. These studies highlight the potential of well-designed association analyses with accurate phenotyping to yield valid results, even under sample size constraints. Based on the reviewed literature, this study is the first to explore SNP-trait correlations for operational log traits directly influencing sawing and peeling recoveries in *Eucalyptus* hybrids. Large-scale phenotyping of such traits remains challenging due to destructive sampling and intensive measurement requirements. Nevertheless, despite the smaller sample size, the findings presented here provide novel insights into the genetic basis of log quality traits relevant to *Eucalyptus* breeding. While the results are promising, limited statistical power may affect generalisability. Future studies with larger and more diverse populations, supported by advanced non-destructive phenotyping methods for log traits, will be crucial to validate these associations and enable their application in breeding programs.

In addition to sample size constraints, the genomic scope of the present SNP-based association analysis was limited to markers mapped to Chromosome 1, reflecting the design of the targeted SNP panel used. As a result, loci influencing log traits that reside on other chromosomes could not be detected, and additional genetic variation contributing

to these traits may exist elsewhere in the genome. Future studies incorporating genome-wide marker coverage will be important to validate the associations identified in this study and to capture the full genetic architecture underlying operational log traits in *Eucalyptus*.

4 Conclusion

This study provides new insights into the genetic and processing performance of *Eucalyptus pellita* hybrids grown in dry tropical plantations, demonstrating their potential for sustainable structural timber production. By evaluating log traits, recovery and product performance, the study highlights how genetic and site factors influence the utilisation potential of plantation-grown hardwoods. Hybrids generally outperformed pure *E. pellita* in log form and recovery, particularly at the more productive site, reflecting the combined effects of genetic improvement and environmental adaptability. Several hybrids showed reduced severity, contributing to improved product outcomes and suitability for higher-grade applications. The LVL panels fabricated from hybrid veneers showed consistent mechanical and bond performance, confirming their structural suitability. Preliminary SNP–trait associations for heartwood proportion, knot diameter, and end split provide a starting point for integrating molecular tools into breeding programs aimed at improving wood quality and processing efficiency. These findings demonstrate that *E. pellita* hybrids can support the diversification of tropical plantation forestry by enabling the production of higher-value engineered wood products. The study underscores the untapped potential of dry tropical regions for sustainable timber production and offers a scalable model for improving wood quality through genetic and silvicultural strategies.

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Author contributions O.E.F. was responsible for conceptualisation, methodology, software, formal analysis, investigation, data curation, visualisation, original draft preparation, and project administration. B.B. contributed to conceptualisation, methodology, validation, supervision, project administration, review and editing, and funding acquisition. B.O. contributed to conceptualisation, validation, supervision,

resources, review and editing, project administration, and funding acquisition. G.B. was involved in conceptualisation, validation, supervision, resources, review and editing, project administration, and funding acquisition. A.S. contributed to conceptualisation, validation, supervision, review and editing, project administration, and funding acquisition. J.F., U.I., and B.T. contributed to data curation.

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Data availability Dataset available on request from the authors.

Declarations

Conflict of interest The authors declare no conflicts of interest.

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