Maximising Tropical Forestry Project

Linking communities and cutting-edge technology





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Executive summary

Overview & Background

The **Maximising Tropical Forestry Project** was a landmark collaboration between Tiwi people (Tiwi Plantations Corporation), commercial forestry partners (Plantation Management Partners, Port Melville Pty Ltd, Midway Limited), research institutions (University of Melbourne, Charles Darwin University), Forest & Wood Products Australia, and the Northern Territory Government. The project has directly informed an $80 million investment that will underpin the next 35 years of plantation activity on the Tiwi Islands.

Utilizing trees to support culture and livelihoods has been central to Tiwi life for thousands of years. The commercial plantation estate spans over 30,000 hectares. The first rotation of *Acacia mangium*—which generated over 1 million tonnes of woodchips exported to Asian markets via Port Melville—the industry is transitioning to a second rotation of ***Eucalyptus pellita***. *E. pellita* is rapidly emerging across tropical regions as a superior species due to its high wood density, versatile product potential (pulpwood, sawlogs, engineered wood products), and resistance to pests and diseases.

Program 1: Tropical Hardwood Plantation Productivity

Program 1 evaluated fundamental silvicultural, edaphic, and climatic dynamics to maximize *E. pellita* growth, nutrient retention, and long-term site sustainability:

Harvest Residue Management

Leaving harvest residues (leaves, bark, twigs, branches) on-site after logging retains an estimated 35 tonnes per hectare of organic matter. Residue mineralization supplies up to 75 kg/ha of Nitrogen (N) and 73 kg/ha of Calcium (Ca) over the first six months, effectively fulfilling annual tree nutrient demands, preserving soil moisture, suppressing weed growth (including *Acacia mangium* wildings), and reducing synthetic fertilizer costs.

Soil Texture & Site Stratification

Tree survival, basal area, and Mean Annual Increment (MAI) strongly scale with topsoil clay content. *E. pellita* achieved an average MAI of 19.51 m^3/ha/yr—about 150% higher than *Acacia mangium*. Topsoil clay percentage provides a critical decision-support metric for forest managers to adjust stocking rates, lower establishment costs, and prioritize high-yielding planting sites.

Ash-Bed Effects & Fertilizer Regimes

While windrow residue burning creates localized growth boosts ("ash-bed effect"), applying later-age macro + micronutrients to non-ash-bed trees significantly enhanced basal area and stand volume, offering a mechanism to improve uniform stand productivity.

Soil Black Carbon

Pyrogenic carbon plays a vital role in long-term carbon sequestration and nutrient/water holding capacity across nutrient-poor tropical sandy soils.

Program 2: Higher Value Products & Future Plantings

Program 2 evaluated the standing *E. pellita* resource at both genomic and phenotypic levels to guide breeding programs and product diversification:

Genomics & Genomic Selection (GS):

Hybrid Correction

High-density single nucleotide polymorphism (SNP) genotyping (5,528 markers) revealed and corrected historical documentation errors in existing trial plots, successfully categorizing trees into pure *E. pellita*, *E. pellita* × *E. brassiana*, and *E. pellita* × *E. urophylla* hybrids across 10 distinct subpopulations (P1–P10).

Breeding Value Optimization

Using Genomic Best Linear Unbiased Prediction (GBLUP) and Machine Learning models (Random Forest), researchers identified the top-ranked 100 parent trees based on a target index of 60% volume, 30% wood density, and 10% Kraft Pulp Yield (KPY).

Pollen Flow Dynamics

Paternity analysis established that 87.3% of effective pollination occurs within 80 meters of the mother tree, providing key baseline design criteria for establishing open-pollinated (OP) seed orchards and managing pollen contamination risks.

Phenotyping & Non-Destructive Testing (NDT):

Advanced non-destructive tools (SilviScan, NIRS, IML-Resistograph) demonstrated that breast-height core sampling accurately predicts whole-tree wood properties (R^2=0.67-0.88).

Juvenile-to-Mature Wood Transition

Microfibril angle (MFA) stabilization indicated that xylem maturation occurs at approximately 6 to 7 years of age in dominant trees. Solid wood rotations should extend beyond 7 years to maximize mature wood formation, while 5 to 7-year rotations are optimal for pulpwood.

Wood Processing & Structural Engineering:

Sawn Timber & Veneer Yields

E. pellita × *E. brassiana* backcross hybrids exhibited superior wood density, bending strength (MOR), and stiffness (MOE), with 10-year-old trees meeting Australian structural stress grades F14 to F17 (and up to F34 in specific traits).

Laminated Veneer Lumber (LVL)

Rotary peeling trials achieved net veneer recoveries up to 70% on high-productivity sites. 5-ply LVL panels manufactured using hybrid core veneers bonded with mature *E. pellita* face veneers passed rigorous structural bending and bond-line shear quality tests.

Program 3: First Nations Participation & Industry Growth Model

Program 3 established practical pathways for Tiwi self-determination, economic participation, and capability building across the northern Australian forestry industry:

National Workforce Training Strategy

Insights from the Tiwi Islands Forestry Workforce Profile directly informed a submission to the Australian Government's Forestry Workforce Training Program. All key Northern Australian recommendations were adopted nationally, securing $780,000 in dedicated funding.

Workforce & Skill Development Benchmarks (to 2026)

In the first year 55 Tiwi people were involved in employment at the plantation. This varied from single days through to full-time employment. Over $1.4 million was paid in wages to Tiwi people with more than 33,000 hours of paid work completed.

Intercultural Workspace & Governance

Ongoing PhD research at Charles Darwin University utilizes Participatory Narrative Inquiry (PNI), Sen's Capability Approach, and Bourdieu's Theory of Practice to co-design an intercultural workspace aligned with Tiwi cultural obligations, commercial goals, and long-term community aspirations.

Micro-Business Development

Published strategy reports identified viable local enterprise opportunities (nursery management, transport/logistics, equipment maintenance, biosecurity, and local milling) designed to build local private enterprise beyond standard direct employment.

Summary of Key Recommendations for the Second Rotation

Retain Harvest Residues

Preserve on-site residues to maintain soil organic matter, reduce synthetic fertilizer expenditure, retain moisture, and control weed invasion.

Stratify Sites by Topsoil Clay %

Map soil clay profiles to rank site productivity, optimize tree stocking density, and lower establishment costs.

Deploy Targeted Genotypes

Deploy *E. pellita* × *E. brassiana* backcrosses on structural timber sites (higher density/stiffness) and *E. urophylla* hybrids or pure E. pellita (subpopulation P3) for pulpwood objectives on lighter soils.

Establish Seed Orchards & Clonal Deployment

Convert high-performing trial stands and top 100 GBLUP-ranked trees into elite seed orchards, applying 20–80 m spatial buffer zones to optimize outcrossing and minimize foreign pollen contamination.

Tailor Rotation Lengths

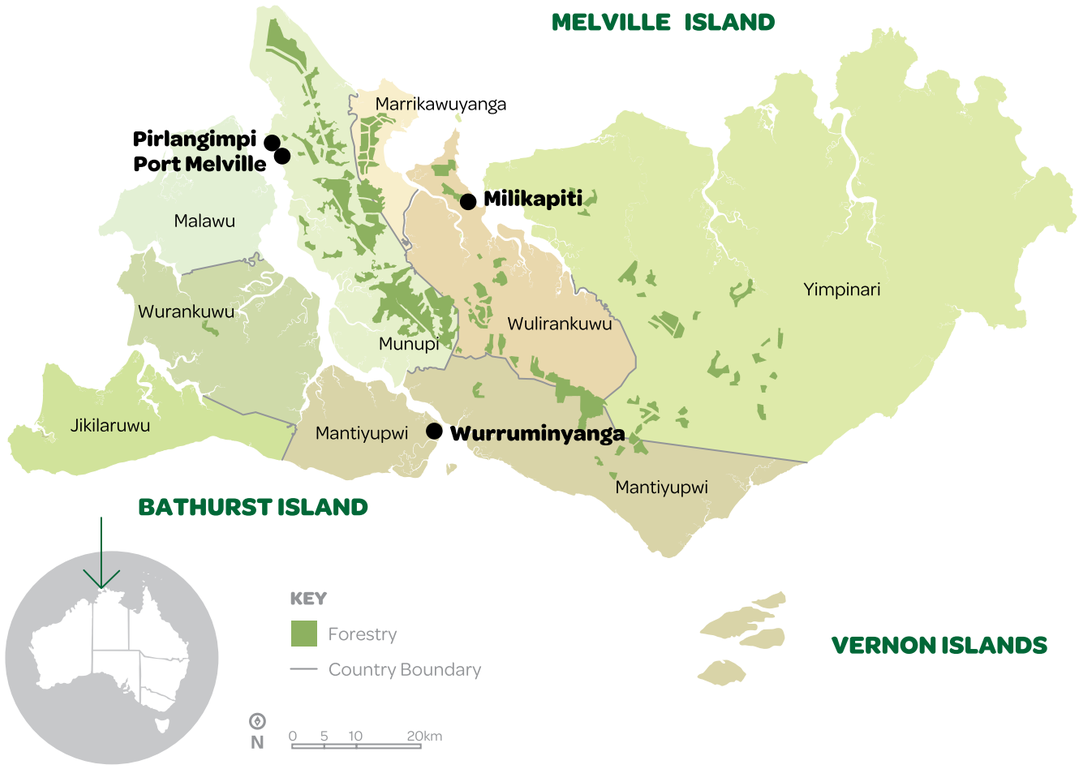
Maintain short 5–7-year rotations for pulpwood efficiency, but extend solid wood and veneer rotations beyond 7 years to capture high-value mature wood properties.

Sustain First Nations Training & Mentorship

Expand intercultural workforce training, local mentoring, and micro-business incubation to ensure sustainable, long-term Tiwi ownership and economic self-determination.

Introduction

The Maximising Tropical Forestry Project has answered key research questions that have helped to de-risk investment in a *Eucalyptus pellita* plantation on the Tiwi Islands. The collaboration between Tiwi people, research organisations and industry has identified how to increase productivity, deliver higher value timber products and grow Indigenous employment.



TPC is the project leader with the other partners being Plantation Management Partners, Port Melville Pty Ltd, University of Melbourne, Forest and Wood Products Australia, Charles Darwin University and Northern Territory Government. The total cash investment is $1.95m with around half from partners. The total budget, including in-kind is $4.68m for the life of the project.

Three complimentary research programs were conducted in the project which was co-funded by the CRC from 2020-2024. The programs were:

Program 1

Tropical hardwood plantation productivity

Existing trials of eucalypt species, provenances and hybrids will be assessed for growth and used to establish new planting trials. The most promising material will be used in spacing and fertiliser factorial trials to determine optimal productivity and profitability. Potential invasiveness will be determined from performance on-site and published literature.

Program 2

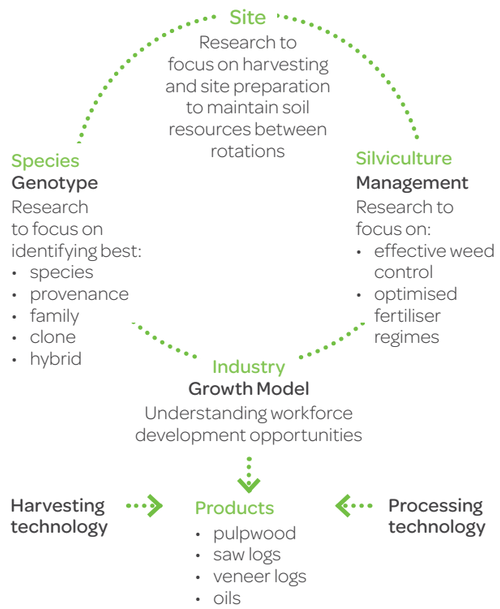
Higher value products and future plantings

Wood quality and properties of logs will be determined from promising tree material as a basis for determining potential for higher-value products and options for forestry product diversification. Genomic tools and molecular marker technology will be used targeting specific domestication traits including growth rate, quality, yield and potentially disease resistance. Results will help determine potential for genetic improvement through breeding and selection, ultimately leading to higher performing material for establishment of superior tree orchards by Tiwi Plantations Corporation.

Program 3

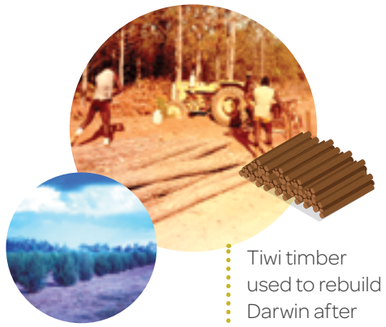
Northern forestry industry growth model

Researchers and community development practitioners will work with Aboriginal and rural communities across northern Australia to document best practice forestry plantation establishment practices and develop a Northern Forestry Industry Growth Model. Community based workshops, key stakeholder interviews, and historic industry analysis will be used identify key forestry industry challenges and devise high level industry development strategies.



Background

Utilising trees to support livelihoods and culture on the Tiwi Islands has been practiced for thousands of years by Tiwi people. From providing food, making hunting tools through to ceremonial poles trees have been a continual part of life.







Tiwi Forestry History

1960

1970

1980 Tiwi timber used to rebuild Darwin after Cyclone Tracy

1990 First *Eucalyptus pellita* trials planted

2000 Tiwi entered into an agreement with Sylvatech and 28,000 hectares of *Acacia mangium* were planted

2005 Sylvatech was bought by Great Southern

2010 Great Southern left. Tiwi Plantation Corporation (TPC) is a Tiwi company that was formed to look after the plantation after Great Southern left

2015 Cypress pine was first planted

2016 A further 2800 hectares were planted

2017 Total of 4935 hectares planted

2018

2019 *Eucalyptus pellita* trials extended





Midway

2015 Harvest of *Acacia* began

2016 First shipment of woodchips exported to Asia

2017 Midway bought Plantation Management Partners (PMP). PMP manage the plantations by agreement with TPC

2018

2019 More than 1,000,000 tonnes of *Acacia* wood chips exported to Asia from Port Melville

2025 Second rotation planting of *Eucalyptus pellita.*

2025 Construction of new Port Melville wharf completed

Program 1 – Tropical hardwood plantation productivity

This research supports improvement of site productivity for the establishment and growth of tropical forestry plantations across northern Australia.

Existing trials of Eucalyptus, located next to the plantings of *Acacia mangium* and native forests were assessed for growth and soil traits to support development establishment silviculture for new plantings. Effects of contrasting soil types/site types, especially in relation to soil texture profile, surface soil organic matter status, and inferred hydrological status were investigated to determine optimal productivity.

This program allows the development of a fundamental understanding of how trees interact with climatic and edaphic factors, for the subsequent development of empirical and mechanistic models to underpin decision support systems. Key steps in the research program include determining impact of harvest residue management on subsequent rotation performance; site specific second rotation fertiliser regimes; application of fertilisers at later age of trees and importance of soil black carbon in retention of soil nutrients.

1. Sustainable management of *Eucalyptus pellita* plantations – a review

We reviewed current knowledge of *Eucalyptus pellita* plantations to identify management practices for optimising productivity and maintaining sustainability in the equatorial and tropical environments where it is grown. A combination of genetic improvement and silvicultural practices have markedly improved *E. pellita* productivity in recent decades. The productivity of *E. pellita* plantations around the world ranges from 9.4 to 34.9 m^3 /ha/year, with a tendency to be more productive in regions that receive higher annual rainfall.

Because responses vary on water-limited sites, site-specific management practices such as the planting of superior hybrids and clones, and stocking management, are important for optimising *E. pellita* growth. We identified several research gaps in *E. pellita* management practices for optimising growth and maintaining plantation sustainability: the impact of *E. pellita* harvest residue management on tree growth, benefits of intercropping *E. pellita* with N-fixing species, the capability and required management of *E. pellita* coppices to develop new rotation, *E. pellita* water use and water requirements and tree spacing. The details of this review are published in an open access article of Forest Ecology and Management https://doi.org/10.1016/j.foreco.2023.120941.



2. *Eucalyptus pellita* harvest residue management

Plantation forestry on sandy and relatively nutrient poor soils in the tropics is a relatively recent development in Australia, where a 30,000-hectare *Acacia mangium* and *Eucalyptus pellita* estate has been established on Melville Island, Northern Australia. Current harvesting of this estate and planned re-establishment with *Eucalyptus pellita* is a challenge for managers because of high harvest residue loads, rapid weedy tree growth on cut sites, and the threat of wildfire during the annual 6-to-8-month dry season.

Despite the known benefits of harvest residue conservation between rotations, there are no studies of harvest residues from plantations established in Australia's monsoon tropics where fire is integral to native forest management. This study aimed to assist plantation managers to develop appropriate inter-rotation harvest residue management for the effective re-establishment and long-term sustainability of *E. pellita* plantations on sandy soils in the tropics.

A 4-hectare experimental trial of *E. pellita*, planted in 2010, was cut with trees processed for woodchips at the coupe edge through May to June 2022 (Fig 2.1). Subsequently the residues from the roadside chipper, including bark, leaves, and twigs, were left on site. These residue treatments were sampled for mass and nutrient content according to residue component. This study discusses implications for plantation long-term sustainability, the maintenance and improvement of plant and soil nutrient status.

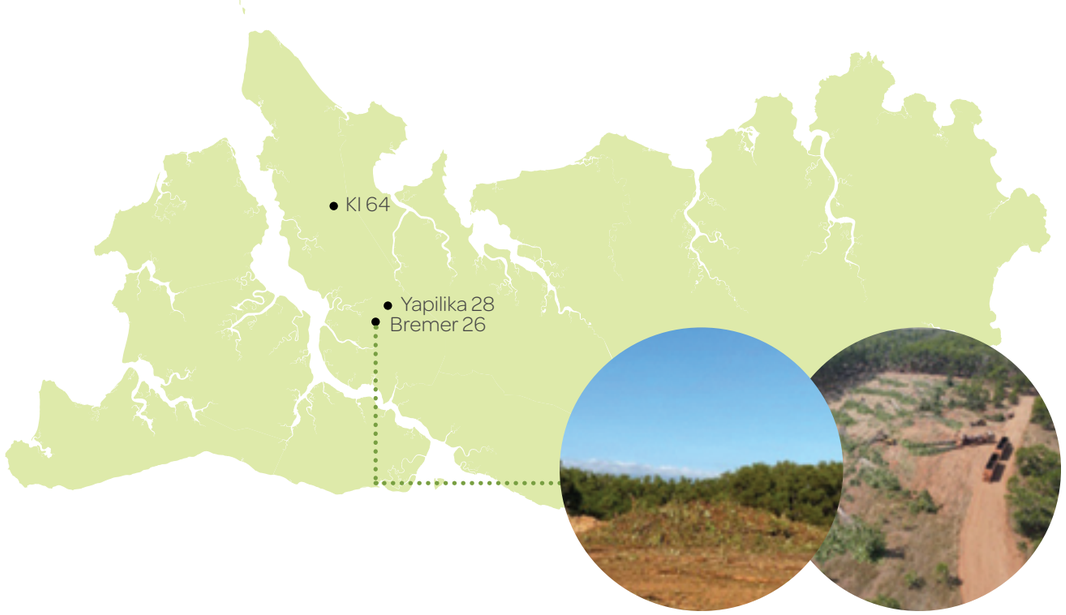


Figure 2.1. Location of *E. pellita* sites across Tiwi Islands with photos of harvest operation in progress

Estimating bark, branch, foliage, and stem loss to harvest revealed that a total of 35 tonnes ha-1 of harvest residues was left on the site (Table 2.1). Bark was the dominant component accounting for 60% (or 24.5 t/ha) of the total residue. Leaf and branch residues tended to contain higher concentrations of N, Ca, Cu, K, Mg, Mn, P, and Zn than other tested materials (Table 2.1).

Table 2.1. Mass and nutrient content of *E. pellita* harvest residue in kg per ha.

Component	Mass, x 10-3	TN	TC	Ca	Cu	Fe	K	Mg	Mn	P	Zn
Bark	24.5	51.5	12021	21.8	0.05	9.15	29.3	10.6	0.71	5.89	0.14
Stem wood	4.71	6.36	2212	2.13	0.009	1.03	3.36	1.20	0.60	0.82	0.03
Branch	3.24	11.0	1553	8.05	0.027	0.32	12.9	4.96	0.54	2.55	0.05
Foliage	2.54	26.9	1296	5.96	0.012	0.49	8.18	7.75	0.32	1.73	0.03
Total harvest residues	**35.02**	**95.8**	**17082**	**37.9**	**0.098**	**10.9**	**53.9**	**24.5**	**2.16**	**10.14**	**0.25**

The current rate of fertiliser at the establishment stage on Tiwi islands is about 225 g/tree DAP (12% N, 11.2% P,14.1 K and 4.3% S) and 100 g/tree Nitrophoska (12% N, 5.2% P, 14.1% K, 6% S, 4.3% Ca, and 1.2% Mg), which is equivalent to 43 kg N/ha, 34 kg P/ha, and 51 kg K/ha. Through residue mineralisation, Eucalyptus harvest residues may release about 75 kg/ha N, 5 kg/ha P, 11 kg/ha K and 73 kg/ha Ca in the first six months after harvesting operations, depending on the type of harvest residue materials, species, and environments. This evidence clearly shows that the annual demand for nutrients can be met from harvest residue. Moreover, retaining the residues on site would not only reduce the cost of fertiliser application, retain moisture, but also reduce the problem of weeds and *A. mangium* wildling germination that is currently a serious weed problem on the island (Fig. 2.2).



Figure 2.2. *E. pellita* seedling, A) growing in harvest residue and B) among weeds growing on bare soil (no harvest residue).

Compared to other commercial Eucalyptus species used around the world (e.g., *E. globulus*, *E. grandis*), *E. pellita* has stringy and thick bark, and we were not able to find examples of using its bark in site preparation for following rotations. Large amounts of thick and fibrous bark of *E. pellita* can create difficulties in replanting the area, distribution of residue will add to the production cost, it also may increase risk of fire. The C/N ratio of *E. pellita* bark in this study (243) is substantially higher than that of its foliage (49) or bark of other Eucalyptus species, such as *E. grandis* x *E. urophylla* hybrids (113).

For this reason, we have established a decomposition trail at Bremer 26 (Fig. 2.3). Samples of 100 g of foliage and twigs and 100 g of bark were assembled into fine mesh decomposition bags and distributed on site in March 2023 and collected in mid-2024.



Figure 2.3 Setting up the decomposition trial at Bremer 26

Showing a pair of foliage (light green) and bark (brown) bags assembled in four pairs.

Conclusion

The retention of harvest residues is essential to maintain site resources, increase nutrient supply to the subsequent plantation from decomposing residues; reduce the cost of fertiliser application; retain soil moisture, reduce competition from weeds, and to maximise carbon sequestration and prolong release of carbon from fine residues.

This study has been peer-reviewed and published. https://doi.org/10.1016/j.tfp.2024.100611

3. Ash bed effect study – application of fertiliser to older trees

On Tiwi, harvest residues are piled and burnt in the roadside or heaped into line rows and burnt (windrow burning) to provide suitable seedbed conditions, reduce fire hazard, and control disease and insect problems. Fire applications during site preparation may alter soil physical, chemical, and biological properties, such as clay mineralogy, microbial community structure, soil organic matter, and soil nutrient content.

Fires may also enhance tree growth in windrow burning known as "ash-bed effect". One way to minimise the growth difference between ash-bed and non-ash bed areas is fertiliser application. In general, fertiliser application in short rotation Eucalyptus plantations is performed at the establishment and the first year of growth, and rarely applied in the later age, thereby, little is known about later age fertiliser capacity to bring the tree growth in adjacent unburnt areas to that in ash-bed areas.

In this study we were interested if application of late fertiliser (to 8-year-old trees) can improve biomass of non-ash trees. In 2022 we established 45 plots in Ash and Non-Ash treatments in two sites affected by windthrow – Yapilika 28 and KI 64 (Fig. 3.1). Plots were measured for aboveground biomass, sampled for litter and soil (up to 10 cm depth) and hemispherical photos for leaf area index (LAI) were taken predawn. All analyses were repeated just prior to application of fertilisers and one year after the application of fertiliser.



Figure 3.1. Plots position in Kilu Impini 64 (A) and Yapilika 28 (B) (Source: Google Earth).

Later-age fertiliser applied in non-ash bed areas consisted of control, macro nutrients only (N, phosphorous [P], and potassium [K]), and macro + micronutrients (N, P, K, magnesium oxide [MgO], iron [Fe], boron [B], molybdenum [Mo], manganese [Mn], copper [Cu], and zinc [Zn]), with 3 replications. N and P fertiliser were applied in the form of diammonium phosphate (DAP) (400 kg/ha), while K fertiliser was applied in the form of granular potassium sulphate (100 kg/ha). Micronutrient fertiliser was applied in the form of Valagro EDTA mix 5 (10 kg/ha). Fertiliser was applied at the end of the dry season (October 2023). Fertiliser was mixed properly and broadcasted evenly inside the plots – fertilisers were prior weighted and divided into 4 equal bags – broadcasting was conducted in 4 segments of an 8 m radius plot (Fig 3.2)



Figure 3.2. Broadcasting the fertilisers at Non-Ash sites

Basal area and stand volume increased in all treatments 1 year after late fertiliser applications (Fig. 3.3). Two-way ANOVA revealed that later-age fertiliser significantly improved basal area ($p < 0.001$), but site effects were not significant. Treatment effects on basal area increment were more pronounced in macro nutrients only and macro + micronutrients. Basal area in macro nutrients only was slightly higher than that in control, but basal area in macro + micronutrients was significantly higher than that in control. Late fertiliser did not have significant effects on stand volume, but interactions between late fertiliser and site were significant ($p <0.005$) where stand volume increment was slightly higher in macro nutrients only in KI 64 and significantly higher in macro + micronutrients in KI 64.

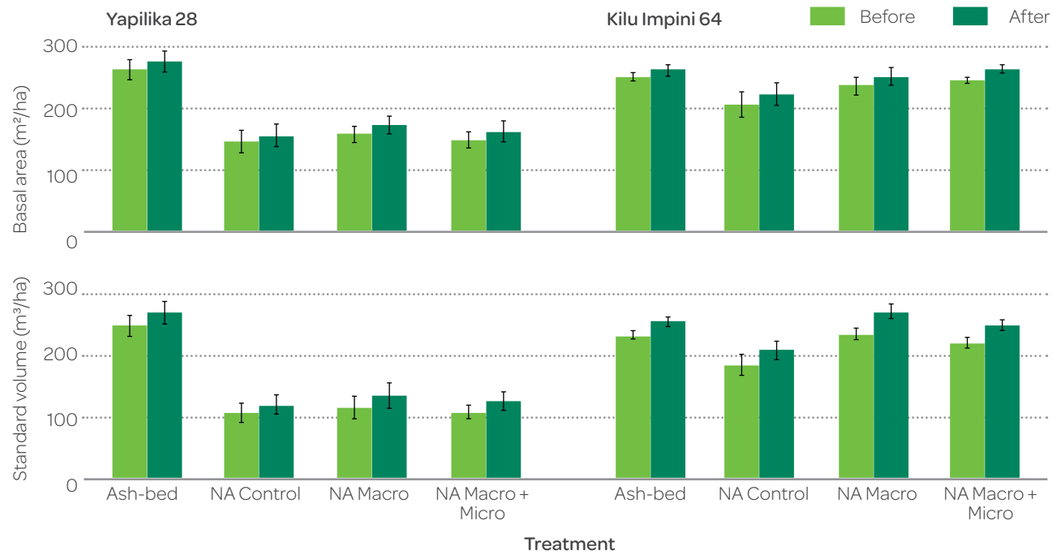


Figure 3.3. Later-age fertiliser impacts on basal area and stand volume in different treatments and sites.

Different capital letters indicate significant differences between sites in each treatment, and different lowercase letters indicate significant differences between treatments in each site at $p<0.05$.

Conclusion

Our study observed that late fertiliser enhanced basal area in non-ash bed trees (when compared to control and ash-bed areas), and it was more pronounced in macro + micronutrients treatment. Although treatment effects were not statistically significant, stand volume in macro + micronutrients treatment tended to be higher than that in control, but lower than that in ash-bed areas. It should be noted, however, that late fertiliser effects on tree growth reported in this study was studied one-year after fertiliser applications. More temporal observations are required to understand the full effect of application of later-age fertiliser on tree growth and its economic benefit for short rotation plantations. This study has been peer-reviewed and published. https://doi.org/10.1016/j.foreco.2025.122502

4. Comparison of growth of *Eucalyptus pellita*, *Acacia mangium* and native forests across soil and rainfall gradients

This study compares the growth of routine plantings of *A. mangium* with trial plantings of *E. pellita* and nearby native forests across six broadly distributed locations on Melville Island, northern Australia (Figs 4.1-4.2).



Figure 4.1. Location of study sites across Melville Island



Figure 4.2. The general pictures of 3 land uses: *E. pellita* plantation (A), *A. mangium* plantation (B), and native forests in study sites (C).

Tree biomass was assessed as the average of 3 circular plots (8 m radius) per land-use per site, established on a 50 m transect installed randomly. *E. pellita* standing biomass was assessed in several permanent sampling plots (PSPs), depending on the number of PSPs in different sites. Within each plot in each land use, all trees with DBH ≥5 cm were measured for diameter and 5 trees were measured for height using a Vertex III hypsometer (Haglöf Sweden AB, Långsele, Sweden). Litter (leaves, bark, twigs with d<2.5 cm, flowers, fruits, and other plant material) and soil were sampled every 12.5 m along a 50 m transect. Litter and soil were analysed for total carbon (TC), total nitrogen (TN), total phosphorus (TP), total calcium (TCa), total copper (TCu), total potassium (TK), total magnesium (TMg), total manganese (TMn), total zinc (TZn), and total sodium (TNa) at the facilities of the University of Melbourne.

Stocking did not differ significantly among 3 land-uses, but it was positively related to clay content (p = 0.003). Average DBH of *E. pellita* (18.44 ± 0.67 cm) was 4 cm to 4.66 cm higher than DBH of *A. mangium* and native forests (p = 0.035). Although DBH tended to increase with clay content, this effect was not significant (p = 0.252). *E. pellita* was also taller than *A. mangium* and native forests trees. *E. pellita* tree height (18.70 ± 0.46 m) was about 4.15 m to 5.77 m taller than *A. mangium* and native forests (p < 0.001), with tree height increasing with increasing clay content (p = 0.018), (Fig. 4.3)

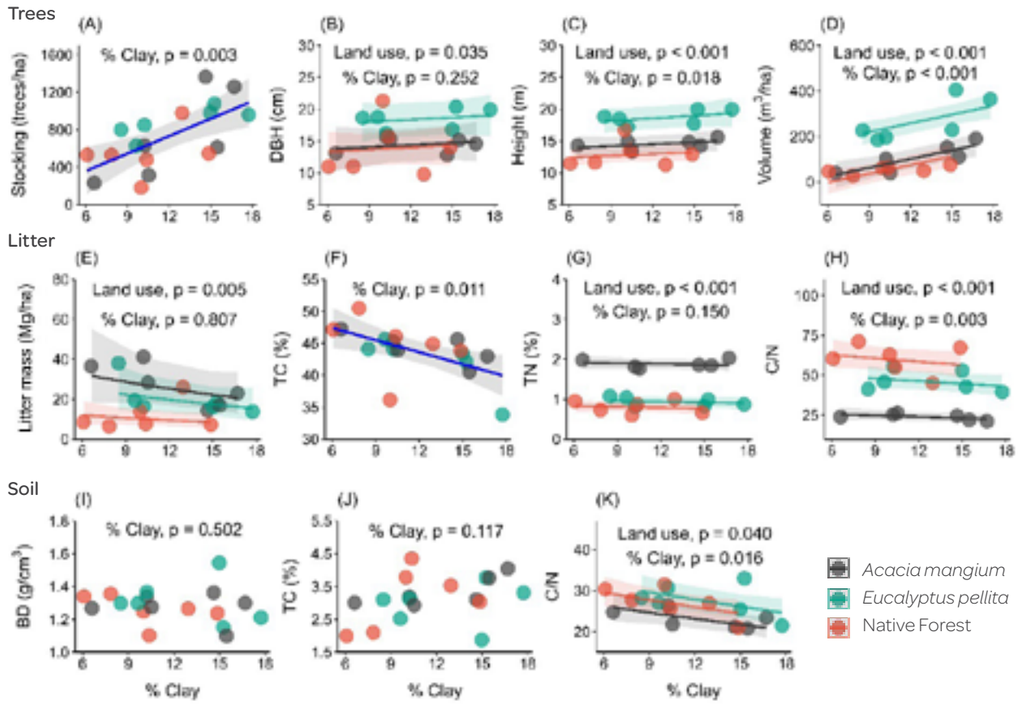


Figure 4.3. Tree growth, litter properties, and soil properties at 10 cm depth in different land uses and clay content.

Stocking (A), DBH (B), height (C), volume (D), litter mass (E), litter TC (F), litter TN (G), litter C/N (H), soil BD (I), soil TC (J), and soil C/N (K). EU represents *E. pellita*, AC represents *A. mangium*, and NF represents native forests. P values indicate the significance of explanatory variables (land use and clay) on response variables. The mean annual increment (MAI) of *E. pellita* and *A. mangium* was positively correlated with clay content (p = 0.005, Fig. 4.4).

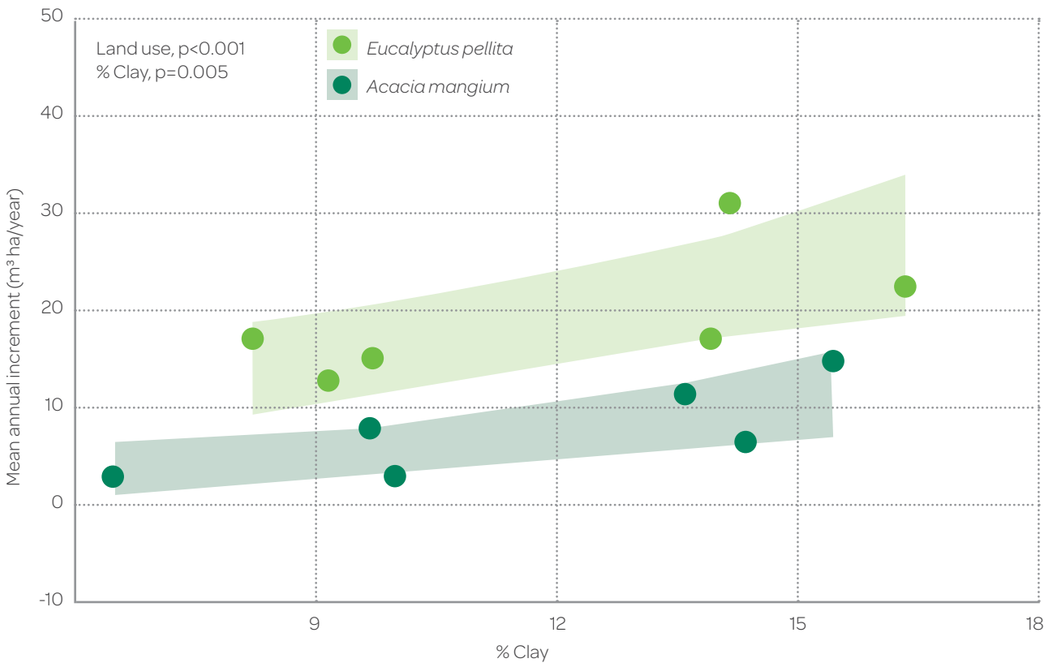


Figure 4.4. The mean annual increment (MAI) of forest plantations in different clay content.

Where EU = *E. pellita* and AC = *A. mangium*. P values indicate the significance of explanatory variables (land use and clay content) on response variables.

Stepwise regression showed that annual rainfall and soil bulk density (BD) explained 68.2% of the variation in *E. pellita* DBH. Together, annual rainfall, sand content, and BD explained 76.6% of the variation in *E. pellita* tree height. Annual rainfall, BD, and electrical conductivity (EC) explained 31.7% of the variation in *A. mangium* DBH, while clay content explained about 2.10% of the variation in *A. mangium* tree height.

The diameter, height, and volume of *E. pellita* was almost 30% higher than *A. mangium* which recorded similar diameter and height to native forest stands. On average, the MAI of *E. pellita* was about 19.51 m³/ha/yr, which is about 150% higher than that of *A. mangium*.

Conclusion

Tree growth, litter properties and many key soil nutrient parameters scaled with clay content, indicating the positive impacts of soil clay particles on soil nutrient holding capacity. For the plantation sites, all of which were planted with around 1100 trees per hectare, tree survival to around 16 years correlated positively with clay content, suggesting that tree mortality declined with increasing clay content.

The relationship between topsoil clay % and tree growth provides forest managers with a clear guide to adjusting stocking rate to reduce establishment costs and optimise biomass production and decide which sites to be planted with *E. pellita*.

This study has been peer-reviewed and published. https://doi.org/10.1016/j.foreco.2024.121930

5. Soil black carbon for nutrient retention

Black Carbon (BC) referred as char, charcoal, and pyrogenic carbon, is formed through incomplete combustions of biomass and fossil fuels, and it can be found in soils, ice, sediment, and the atmosphere, with most BC in soils stored in the form of microscopic and macroscopic charcoal particles. Soil BC is resistant to decomposition and can persist on site between 1160 and 5040 years.

Soil BC has critical role in various biogeochemical processes, including water and nutrient retention, providing suitable habitat for soil microorganisms, acting as C pool for climate change mitigation and tracer of fire history. However, soil BC availability and dynamics is poorly understood, and there is a growing interest in quantifying soil BC and to understand the dynamics and interactions between BC, soils, and plants in different land-uses.

Fire is used during site preparation on Tiwi Islands, and surrounding native forests are frequently prescribed burnt to reduce the risk of wild forest fires. Land-use change and fire applications during land management are expected to influence soil BC, though these impacts in Melville environments are not fully understood.

This study is aimed to quantify soil BC in different land-uses (native forests, *A. mangium*, and *E. pellita* plantations) and observe the capability of MIRS (mid-infrared spectroscopy [MIRS] - a simple analytical technique combined with partial least-squares regression [PLSR]) and nitric acid-hydrogen peroxide digestion methods in estimating soil BC. This study will contribute to our understanding of the role of BC in retaining soil nutrients for improved plantation management.

Soil to 1 meter depth was collected during the rainy season in 2023 (Fig 5.1), at 3 land-uses (native forests, *E. pellita*, and *A. mangium*), in the sub-set of sites discussed in the previous chapter (namely KI 14, Yapilika 48, Picker 3 and Andar 3B).



Figure 5.1. Collecting soil at *Eucalyptus pellita* plantation, *Acacia mangium* and native forest.

Soil BC was determined using 3 different methods: nitric acid-hydrogen peroxide digestion, MIRS, and Hypy. Soil BC determination with MIRS and Hypy were performed in 4 depths (0-10, 10-30, 30-50, and 50-100 cm), while nitric acid-hydrogen peroxide digestion was only performed in the first 3 depths due to limited resources. Before analysis, the fizz test was performed using 1M hydrochloric acid (HCl) to test the calcium carbonate in soils, and the result was negative, indicating that soil samples were noncalcareous.

Total Organic Carbon (TOC) was not affected by land use but by soil depth ($p < 0.001$). TOC in all land uses decreased with increasing soil depth (Fig. 5.2). On average, TOC under native forests ranged between 4.63% (top 10 cm) and 0.76% (deeper soil layer). TOC under *A. mangium* ranged between 4.61% (top 10 cm) and 0.42% (deeper soil layer). TOC under *E. pellita* ranged between 3.29% (top 10 cm) and 0.38% (50-100 cm). A rapid decline in TOC was observed at depth 10-30 cm, where TOC declined by more than 60% (when compared to the top 10 cm).

Total Nitrogen (TN) was significantly affected by land use ($p < 0.01$) and soil depth ($p < 0.001$). TN under *A. mangium* was higher than those under native forests and *E. pellita* (Fig. 5.2). On average, TN under *A. mangium* ranged between 0.01% (deeper soil layer) and 0.16% (surface soil layer). TN under native forests ranged between 0.01% (deeper soil layer) and 0.14% (top 10 cm soil layer). TN under *E. pellita* ranged from 0.01% to 0.10% in deeper soil layer and surface soil, respectively. TN content declined rapidly at depth 10-30 cm, where TN declined over 67% when compared to TN content in the top surface.

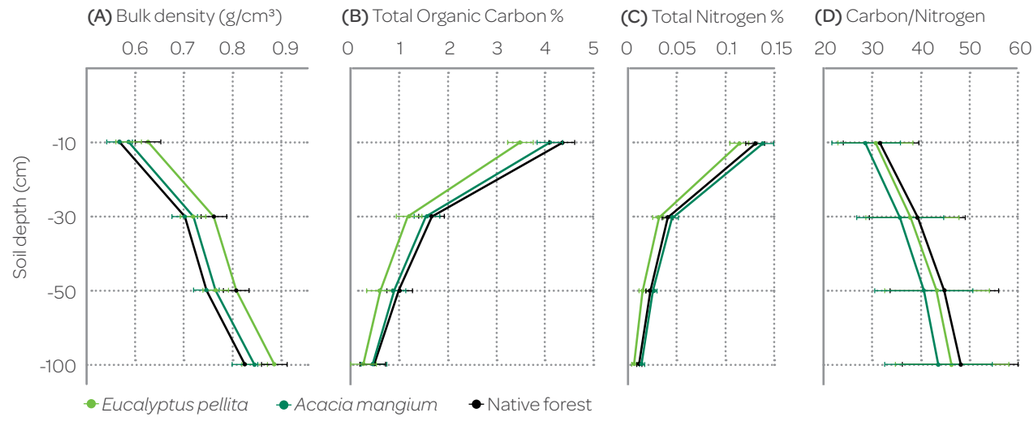


Figure 5.2. Soil BD, TC, TN, and C/N in different land-uses and depth.

Soil TN was positively correlated with TOC (Fig. 5.3).

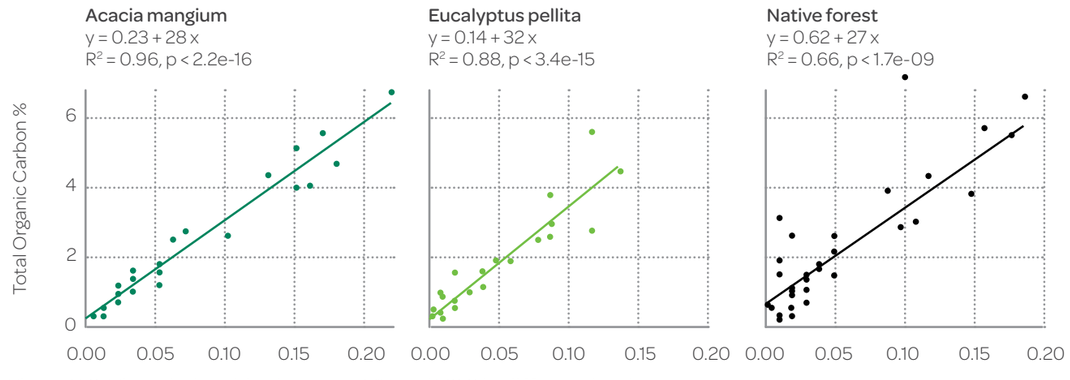


Figure 5.3. The relationships between TN and TOC in different land uses.

The amount of TOC stocks to 1 m depth observed in this study was lower than those reported under native forests and Eucalyptus plantations of Brazilian Cerrado (savanna) which was ranged between 167 Mg/ha and 174 Mg/ha, Eucalypt open forests of Australia (229 Mg/ha), and Eucalyptus (102.66 Mg/ha) and Acacia plantations (132.70 Mg/ha). TOC stocks under *A. mangium* and native forests were consistently higher than under *E. pellita* at different soil depths, which indicate that *E. pellita* establishment decreases SOC stocks.

This study has been peer-reviewed and published. 10.1016/j.catena.2025.109784

Lessons for the 2nd rotation

To summarise our report, we suggest for the second rotation to be a success, following will be required:

The retention of harvest residues to:

- Maintain site resources including soil organic matter and soil moisture.
- Increase nutrient supply to the subsequent rotation of trees.
- Reduce the cost of fertiliser application for the subsequent rotation.
- Reduce competition from weeds; and,
- Maximise carbon sequestration on site.

The application of fertiliser is recommended for earlier stages of plantation establishment (say year 1 [mainly phosphorus amendments, to include calcium] and up to year 4 [nitrogen is recommended for addition post year 2 and before year 5]).

The stratification of available planting sites according to surface soil clay content: this will enable adjustments to planting density to reduce losses to mortality and it provides a means to rank sites according to water and nutrient retention properties. This will lead to reduced establishment costs and the overall ability to predict volume production from the estate.

Research gaps

We also identify the following research gaps and unknown impact of new species establishment:

- Research into seasonal water use by *E. pellita* and potential impact on ground water supply; with site stratification according to topsoil clay content and landscape position, this could be linked to stocking management to optimise plantation productivity.
- Potential of *E. pellita* to become a weed species, over competing local species.
- Research into the best use of *Acacia mangium* residues for the subsequent *E. pellita* plantation establishment.
- Impact of different planting spacing densities in sandier soils or dryer areas.
- Remeasurement of ash bed sites to determine the value of later-age application of fertiliser for improving the sub-optimal growth of non-ashbed trees to a commercially viable outcome.



Program 2 – Higher value products and future plantings

Beata Skiba, Antanas Spokevicius, Benoit Belleville, Gerd Bossinger, Barbara Ozarska,
Listya Mustika Dewi, Umar Ibrahim, Oluwatosin Falade

General overview and introduction

In south-east Asia, *Eucalyptus pellita* is fast emerging as the preferred species to replace *Acacia mangium* in large commercial tropical plantations mainly due to its resistance to pests and diseases. *Eucalyptus pellita* also displays high wood density and can be used both to produce pulp and paper as well as for solid wood or Engineered Wood Products (EWP) in general (bridges, poles, beams, flooring, panels, etc.) and furniture production.

In this program, we have characterised and assessed the quality and properties of the existing Tiwi *E. pellita* plantation resource, that will assist in determining its potential for higher-value products, and options for forest product diversification. We have assessed wood recovery and quality through sawing and veneer peeling trials. Resulting wood processing methods and wood product options will be determined according to the characterised wood properties and grade quality volumes providing guidance for plantation improvement strategies.

The *E. pellita* material already trialled on the islands is at a very early stage of selection. We have investigated its genetic diversity and population structure in order to gain a better understanding of the existing resource at the genomic level. This program captured its inherent improvement potential by exploring opportunities for genomic selection aiming to identify to ranking trees, for targeted specific domestication traits, that can be utilised for improvement of this species for second rotation plantings.

Genomic selection presents concrete opportunities for significantly accelerating the progress of forest tree breeding cycles by shortening progeny field testing periods, increasing selection intensity, increasing accuracy of breeding values and therefore by increasing genetic gains per year. Results from this work can help determine potential for genetic improvement through breeding and selection, ultimately leading to higher performing material for establishment of superior tree orchards by Tiwi Plantations Corporation.

Trial sites and existing *E. pellita* resource

Five *E. pellita* trial sites were selected for this study, which formed part of the Tiwi Plantations Corporations (TPC) *E. pellita* research program, on the Tiwi Islands, Northern Territory, Australia (Table 1). Sites Yapilika 28 (Y28) and Kilu Impini 64 (KI64) were planted in 2012 in a randomised complete block design with four complete replicates, 25 trees per replicate. Trees grown at these sites were reported to be from ten bulked seed sources from six known origins including Dendros, Ingham, Queensland, PNG, Vietnam, and Melville (Table 2). A total of 1000 trees were planted at each site.

The *E. pellita* trees at sites and Yapilika 48 (Y48), Andranangoo3b (A3b) and Imalu 18 (I18)) were planted in 2006, 2007 and 2008 respectively, using seedlings from seedlot 20760, originating from Danbulla SSO. Trees were planted in a randomised block design with three complete replicates, with 32 to 36 trees per replicate, resulting in a total of approximately 100 trees at each site.

Table 1. Research trial sites studied on Tiwi.

Site	Coordinates	No. of seedlots	Year planted	No. trees planted	No. living trees/ sampled (2022/23)	Soil	Rainfall
Kilu Impini 64 (KI64)	11°25'6.00"S 130°30'0.00"E	10	2012	1000	763	Red sandy soils and grey to yellow sandy soil >2m	1200-1400
Yapilika 28 (Y28)	11°33'45.00"S 130°34'39.00"E	10	2012	1000	666	Moonkinu Member sandstone >3m	1200-1400
Andranangoo 3b (A3b)	11°41'44.7"S 131°03'04.1"E	1	2007	108	62	Van Diemen sandstown >2m	1400-1600
Imalu 18 (I18)	11°12'45.8"S 130°24'14.1"E	1	2008	96	62	Red sandy soils and grey to yellow sandy soil >3m	1200-1400
Yapilika 48 (Y48)	11°34'26.2"S 130°35'35.7"E	1	2006	96	76	Moonkinu Member sandstone >3m	1200-1400

Table 2. Origins of individual tree seedlots at KI64 and Y28.

Trial Entry	Seedlot	Source	Origin	Parents	Species
1	688	PMP	Dendros		*E. pellita* x *E. brassiana*
2		ATSC	Ingham	2ep6 163 (x6198)	*E. pellita*
				2ep6 171 (x6204)	*E. pellita*
				2ep6 170 (x6203)	*E. pellita*
				2ep6 166 (x6200)	*E. pellita*
				2ep6 159 (x6197)	*E. pellita*
				2ep6 157 (x6195)	*E. pellita*
3	7EP46A (20946)	PMP		47	*E. pellita* x *E. urophylla*
4	7EP4SC (20945)	PMP		10	*E. pellita* x *E. urophylla*
6	21175	ATSC	Ingham	52	*E. pellita*
	18598	ATSC	Qld	15	*E. pellita*
	18596	ATSC	Qld	7	*E. pellita*
	18597	ATSC	Qld	23	*E. pellita*
7	21217	ATSC	Vietnam	117	*E. pellita*
8	18602	ATSC	Melville	10	*E. pellita*
9	PMP2	PMP		Unknown	*E. pellita* x *E. urophylla*
10	18197 + 18198	ATSC	PNG	50 +	*E. pellita*

1. Characterisation of standing trees by genotype

1a. Hybrid identification of trees at KI64 and Y28

Objectives

To identify and validate the hybrid population in the Tiwi research trials and categorise the population based on genomic proportions with the available high-density SNP markers.

Methods and results

DNA was extracted from stem cambium scrapings collected from all living trees at KI64 and Y28, as described in Tibbits et al. (2006). SNP genotyping was performed at Gondwana Genomics Pty Ltd, Canberra Australia, using their custom *E. pellita* marker panel, comprising of SNP markers and small biallelic insertion deletions (INDEL) markers from 2000 candidate genes. The markers included in the marker panel were distributed across the 11 chromosomes and preselected for potential association with various traits (Thavamanikumar et al., 2020). 5550 markers were genotypes across all trees. SNPs were then filtered for quality, with SNPs exhibiting <90% call rate and a minor allele frequency (MAF) <0.1 removed. In total, 5528 markers were genotyped in each and used in all subsequent analyses.

Hybrid identification and confirmation of trees at KI64 and Y48 was carried out utilising the SNP dataset with R package LEA (Landscape and Ecological Association Studies; Frichot et al., 2015).

The hybrid analysis revealed that the documented provenance details based on seedlot information and hybrid identities are unreliable. The individuals in the entire dataset were assigned to different population clusters based on reference samples using hierarchical clustering. According to individual ancestry proportions based on reference samples with a subset of two selected populations, LEA genetic structure analysis assigned the individual trees from 10 seedlots in the KI64 and Y28 to various clusters. From LEA analysis, we can confirm the identity of putative hybrids *E. pellita* x *E. urophylla* and putative *E. pellita* x *E brassiana* hybrids in our population as in the reported documented data. This reaffirms that the population under study is composed of two types of hybrid crosses: *E. pellita* × *E. brassiana* (Fig. 1a.1) and *E. pellita* × *E. urophylla* (Fig. 1a.2) in the research trial. PCA helped to visualise the hybrid clusters based on the reference samples (Fig. 1a.3 & 1a.4). The LEA & PCA output revealed that most of the individuals from seedlot hybrid *E. pellita* x *E. brassiana* is of pure *E. pellita* origin whereas seedlot hybrid *E. pellita* x *E. urophylla* also had admixed individuals of *E. pellita*. We found admixture of hybrids and pure *E. pellita* in all the remaining seedlots based on our confirmation of the identity of the hybrid individuals.

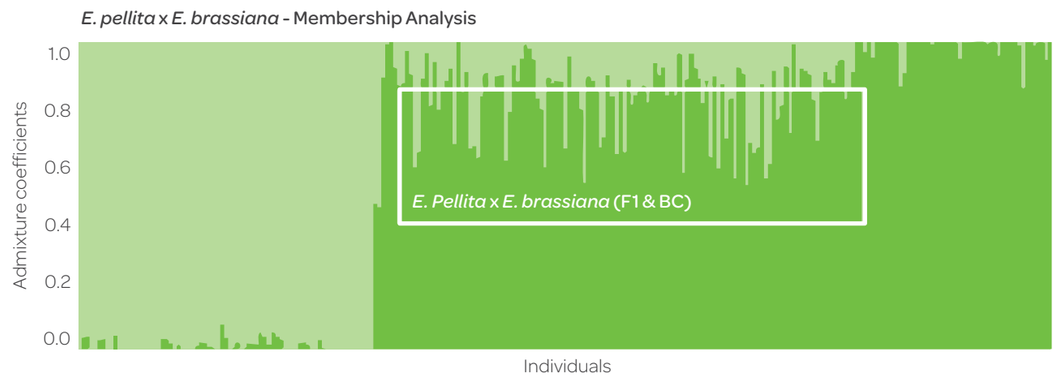


Figure 1a.1. Bayesian assignment analysis was conducted using LEA (R package designed for Landscape and Ecological Association Studies). The analysis utilised 5528 genome-wide SNP data obtained from samples of *E. pellita*, *E. brassiana* and reference individuals. The genomes of *E. brassiana* are assigned in ■, and genomes of *E. pellita* are assigned in ■. Individuals exhibiting multiple colours are of admixed (hybrid) ancestry.

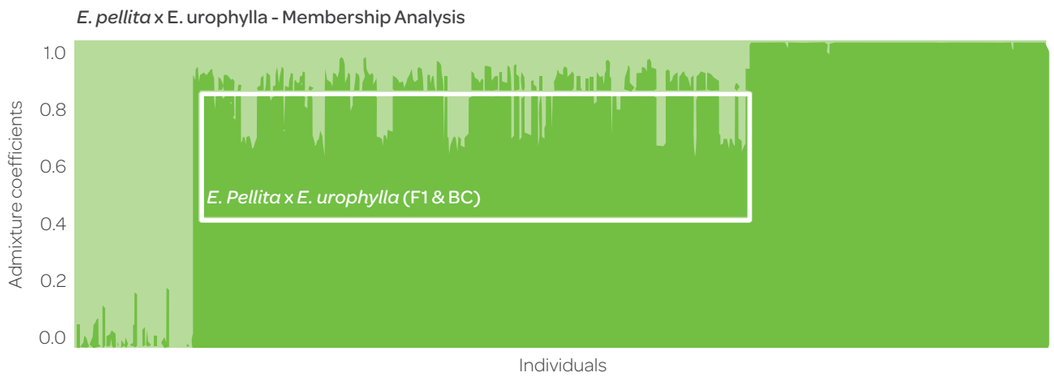


Figure 1a.2. Bayesian assignment analysis was conducted using LEA (R package designed for Landscape and Ecological Association Studies). The analysis utilised 5528 genome-wide SNP data obtained from samples of *E. pellita, E. urophylla* and reference individuals. The genomes of *E. urophylla* are assigned in ■, and genomes of *E. pellita* are assigned in ■. Individuals exhibiting multiple colours are of admixed (hybrid) ancestry.

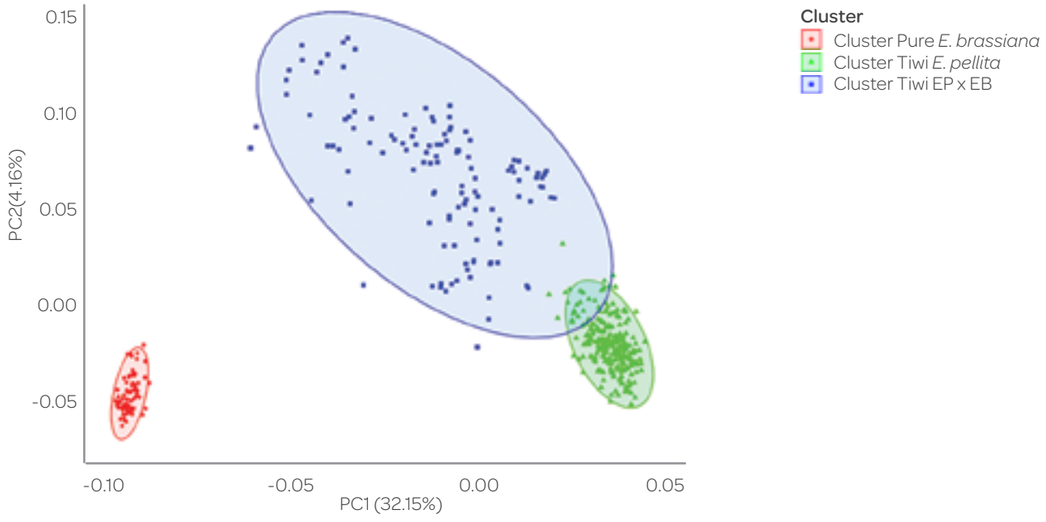


Figure 1a.3. SNP genome-wide data (based on 5528 SNP markers) from the subset of *E. pellita* and *E. brassiana* cluster were analysed using principal component analysis (PCA). The circles function as a visual aid to emphasise the clustering of individuals: the red circle represents the cluster of pure *E. brassiana*, the green circle represents pure *E. pellita* and the clue circle represents individuals of hybrid origin, specifically *E. pellita* and *E. brassiana*.

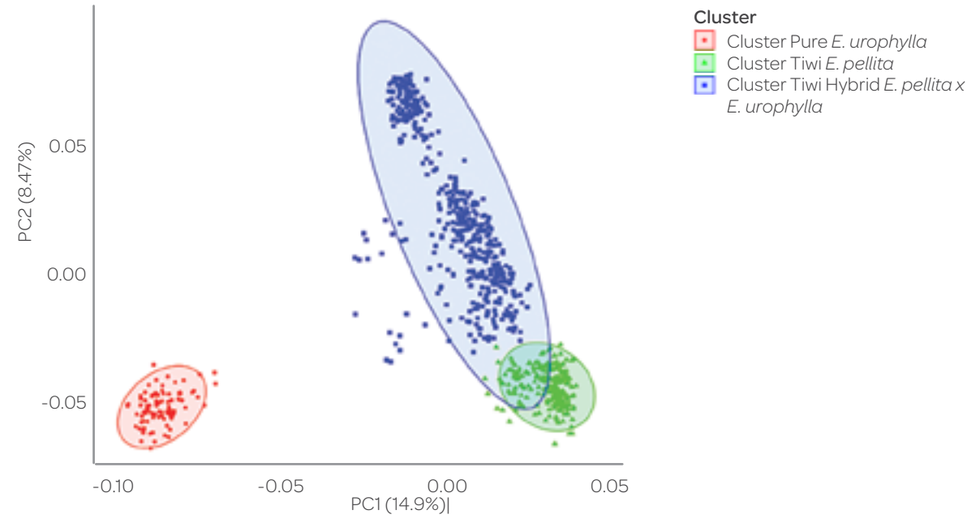


Figure 1a.4. SNP genome-wide data (based on 5528 SNP markers) from the subset of *E. pellita* and *E. urophylla* cluster were analysed using principal component analysis (PCA). The circles function as a visual aid to emphasise the clustering of individuals: the red circle represents the cluster of pure *E. urophylla*, the green circle represents pure *E. pellita* and the clue circle represents individuals of hybrid origin, specifically *E. pellita* and *E. urophylla*.

Key findings

These results have demonstrated the ability of SNP markers to detect and correct errors in the documented identities in trials not designed for genetic gains and without pedigree information.

The species of each tree has been confidently identified, which will assist with subsequent analyses and planning tree improvement strategies utilising the existing resource of *E. pellita* trees and hybrids on Tiwi.

1b. Population structure

Population structure is a common place feature of genetic variation and it has importance in numerous application areas, including evolutionary genetics, conservation genetics. At a broad level, population structure is the existence of differing levels of genetic relatedness among the same subgroups within a sample. Understanding the structure in a sample population is necessary before more sophisticated analyses are undertaken.

As illustrated in section 1a Hybrid Identification, significant errors exist in the genetic and documented identity of the trees at KI64 and Y28. Hierarchical clustering analysis helped to divide the entire population of trees at KI64 and Y28 into pure *E. pellita*, hybrid *E. pellita* x *E. brassiana*, hybrid *E. pellita* x *E. urophylla* clusters based on the reference samples. As it was documented that ten seedlots were originally sourced to establish the stands at KI64 and Y28, it is assumed that this population of trees could be further divided into subpopulations based on their genomic similarity, thereby providing a sound understanding of the population structure of the existing *E. pellita* resource on Tiwi for subsequent analyses.

Objectives

To identify *E. pellita* subpopulations within the Tiwi resource, based on shared genomic proportions.

To look at the diversity and relationship within and between identified subpopulations.

Methods and results

Along with the trees at KI64 and Y28, trees at Andranangoo3b (A3b), Imalu 18 (I18) and Yapilika 48 (Y48) were also genotyped using the same SNP panel from Gondwana Genomics Pty Ltd. The SNP dataset from these three sites were combined with that from KI64 and Y28 and used to determine the genetic population structure of the 1600+ trees from the five sites assessed. This was done using Discriminant analysis of principal components (DAPC) in the R package 'adegenet.' Analysis supported the distribution of the trees into 10 populations, based on their genomic similarities. A visual representation of the genomic proportions estimated from the population structure analysis of the Tiwi dataset is presented in Fig 1b.1. Each colour represents a subpopulation and each individual is represented as a vertical line.

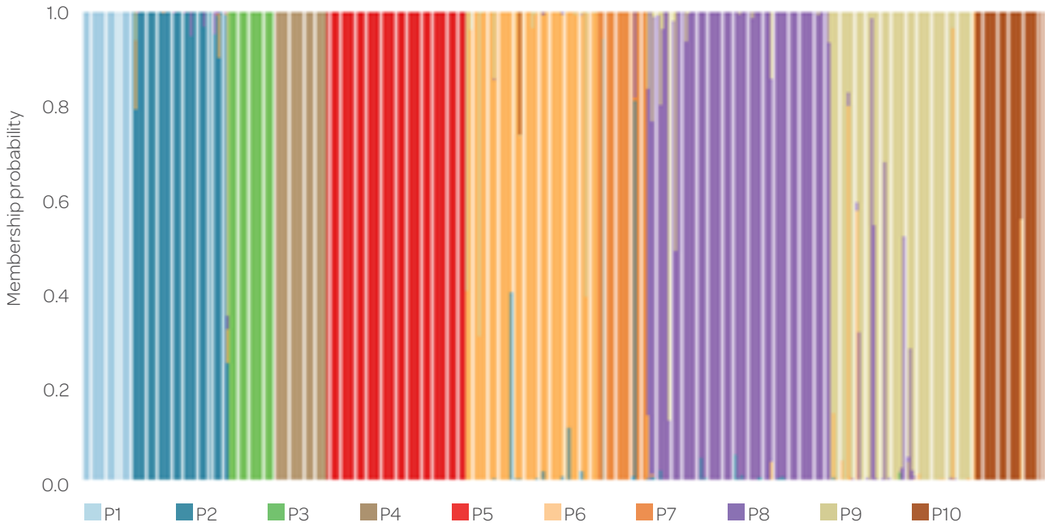


Figure 1b.1. Population structure of the *E. pellita* resource at KI64, Y28, A3b, I18 and Y48. Each vertical line represents an individual tree and each colour a separate population.

The distribution of the ten subpopulations at KI64 and Y28 is shown in Fig 1b.2, and each subpopulation is represented across the two sites.

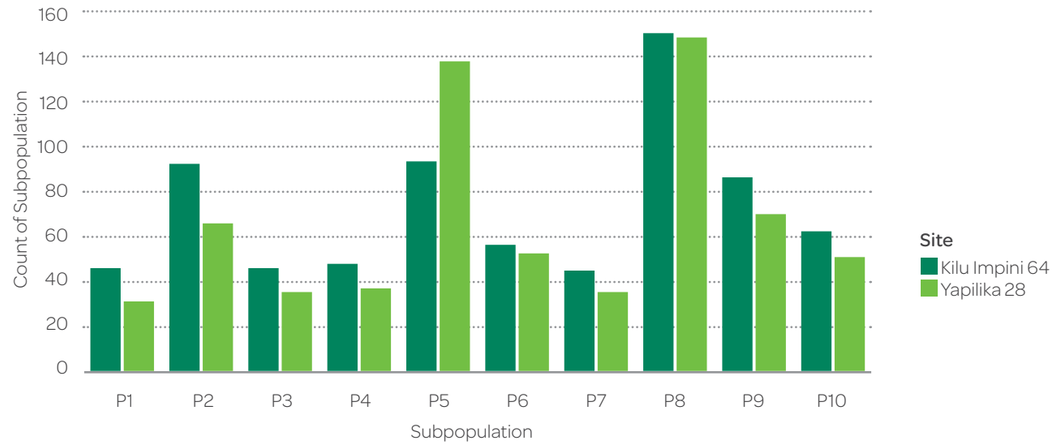


Figure 1b.2. Distribution of trees as KI64 and Y28 based on population structure analysis.

Trees planted at A3b, I18 and Y48 are reported to be from seedlot 20760, originating from Danbulla SSA. The majority of trees at these three sites belong to populations P6 and P9, with a few trees identified to belong to populations P2, P7 and P8 (Fig. 1b.3).

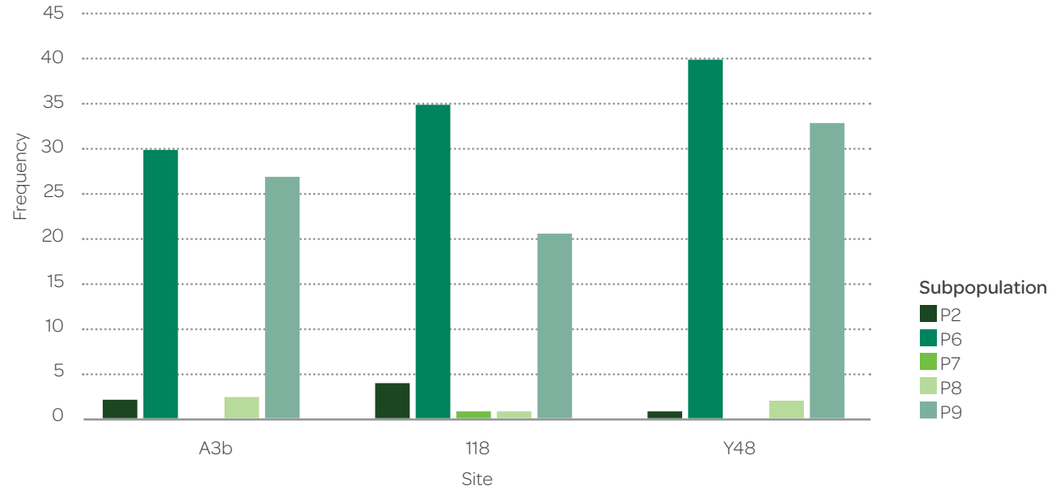


Figure 1b.3. Distribution of trees as A3b, I18 and Y48 based on population structure analysis.

Key findings

Genetic population structure of the 1600+ trees from the five sites assessed, using Discriminant analysis of principal components (DAPC), supported the distribution of the trees into 10 populations, based on their genomic similarities.

Subsequent analysis on the trees at the five assessed Tiwi sites will be performed based on these ten subpopulations.

1c. Genetic diversity

Genetic diversity is the foundation of all biodiversity because it provides the raw material for individuals, populations and species to evolve and adapt especially under abiotic and biotic tress and changing climate and environmental conditions. As such, individuals and populations that have high genetic diversity should have better chances of persistence and adaptation under climate change conditions. Therefore, genetic diversity maintenance is an important consideration in forestry, for the survival, adaptation and evolution of individuals, populations and species, safeguarding against changing environmental conditions.

Genetic diversity analysis is the basis for plant breeding and genetic improvement, as it helps to understand the current status of *E. pellita* biodiversity on Tiwi and this genetic variation is important in plant breeding in order to make progress in breeding successive generations.

Objectives

To examine the genetic diversity of the existing populations of *E. pellita* and hybrids, in order to assess their suitability for any potential future tree breeding efforts, ensuring the risk to inbreeding and its adverse effects are minimised.

Methods and results

The genetic diversity of the ten identified populations was assessed using the same SNP dataset utilised for the genetic structure analysis of the assessed Tiwi trees. The following diversity matrices were calculated using GenAlEx v6.5 (Peakall and Smouse, 2006): Shannon's information Index (I), observed heterozygosity (Ho), expected heterozygosity (He) and Wright's fixation Index/inbreeding coefficient (Fis). These diversity matrices for each population are presented in Table 1c.1.

Table 1c.1. Genetic diversity indices for the ten subpopulations of *E. pellita* trees located at KI64 and Y28 (standard error in parentheses).

Population	No. of trees	I	Ho	He	FIS
P1	76	0.246(0.004)	0.158(0.003)	0.147(0.003)	-0.040(0.002)
P2	156	0.269(0.003)	0.147(0.002)	0.170(0.002)	0.124(0.003)
P3	79	0.194(0.004)	0.131(0.003)	0.123(0.003)	-0.019(0.003)
P4	85	0.345(0.004)	0.233(0.003)	0.226(0.003)	0.008(0.003)
P5	230	0.241(0.004)	0.156(0.003)	0.156(0.003)	0.022(0.003)
P6	108	0.294(0.003)	0.179 (0.003)	0.185(0.002)	0.045(0.003)
P7	80	0.295(0.004)	0.181(0.003)	0.188(0.003)	0.056(0.003)
P8	295	0.285(0.003)	0.167(0.002)	0.180(0.003)	0.089(0.003)
P9	155	0.285(0.003)	0.172(0.003	0.180(0.003)	0.065(0.003)
P10	110	0.248(0.004)	0.138(0.002)	0.157(0.002)	0.105(0.003)

Heterozygosity is one of the most useful parameters for measuring population genetic variation, and the value of the expected heterozygosity reflects the degree of population genetic diversity. It is based on the probability that two alleles chosen randomly from the population will be different. The mean expected heterozygosity (He) for the whole population of assessed trees was 0.171, suggesting moderate genetic diversity. This is further supported by the Shannon's information index result (I = 0.270). Observed heterozygosity (Ho) in the whole population was slightly lower (Ho = 0.166) than He, indicating some heterozygosity deficits and excesses of homozygotes for the whole population of assessed trees. The average of Wright's fixation index for the Tiwi population was 0.047, suggesting the trees are slightly inbred.

Of the ten subpopulations of trees, P2 appears to be the most inbreed, presenting a FIS value of 0.124, and Ho was lower than He (0.147 and 0.170 respectively) also indicating a heterozygotic deficit in this subpopulation.

The subpopulation with the highest level of genetic diversity was seen in P4 (He = 0.226, I = 0.345). Observed heterozygosity (Ho = 0.233) was slightly higher than He, therefore suggesting a small heterozygote excess. However, Wright's inbreeding coefficient (Fis) for this subpopulation was close to zero (FIS = 0.008), suggesting that there is little inbreeding in this population. Other subpopulations that also show little inbreeding are P1 and P3, based on calculated Ho and He values for these populations.

Despite the differences between observed and expected heterozygosity for all subpopulations, these were determined not to be statistically significant following chi-square testing, indicating that the allele frequencies and population genotypes tended to follow the Hardy-Weinberg Equilibrium.... i.e. frequencies of alleles and genotypes in the populations are not changing from generation to generation, because of mutations, selections migration of genetic drift. **Therefore, a seed orchard consisting of these trees can be expected to maintain its genetic structure in the next generation, through open pollination and thereby support genetic resource conservation.**

Key findings and recommendation

Genetic diversity within the population of trees assessed at KI64 and Y28 was determined to be moderate, indicating that there is a reasonable degree of genetic variation among individual trees within the Tiwi *E. pellita* population. No significant differences were detected between observed and expected heterozygosity in all subpopulations, therefore a seed orchard consisting of these trees can be expected to maintain its genetic structure in the next generation. While suitable for short-term breeding, this level of genetic variation constrains long-term selection potential and adaptive capacity. Genetic improvement would benefit from the introduction of additional genetic material and management strategies aimed at maintaining effective population size and minimising inbreeding.

2. Characterisation of standing trees by phenotype

2a. Non-destructive characterisation of *Eucalyptus pellita*: influence of genotype and site on wood properties and growth

Understanding how wood properties vary among individual trees within a plantation is essential for optimising the value of plantation resources and supporting breeding decisions. Traditional methods for assessing wood quality are time-consuming and destructive, requiring trees to be felled and samples processed in laboratories. This limits the amount of information that can be gathered from standing trees and increases costs for plantation managers and breeders. Recent advances in non-destructive testing (NDT) technologies—such as micro-drilling resistance tools and near-infrared spectroscopy—now enable rapid assessment of wood properties without harvesting trees. These tools can measure density, stiffness, fibre characteristics, and chemical composition from small samples collected at breast height (1.3 m above ground). However, for *E. pellita*, there is limited knowledge of how wood properties vary across a population, or how different genotypes and environmental conditions influence wood quality. Understanding this variation is crucial for identifying superior trees for breeding, determining the suitability of plantation resources for specific end-uses such as pulpwood or solid wood production, and supporting management decisions. This section characterises wood properties across a large population of *E. pellita* trees at breast height using multiple non-destructive testing methods. By quantifying the range and distribution of wood quality traits, and identifying which genotypes and sites produce the most desirable properties, we provide practical information to support plantation improvement strategies and targeted breeding for higher-value products.

Objectives

To evaluate growth traits and selected wood properties of *E. pellita* genotypes across two plantation sites using non-destructive testing (NDT) methods, and to understand how site conditions and genetic background influence wood quality characteristics important for both pulp and solid wood applications.

Methods and Results

Study sites and sampling

Diameter and height measurements were taken, and wood chip samples were collected non-destructively from 1,502 living *E. pellita* trees at two trial sites: Kilu Impini 64 (KI64) and Yapilika 28 (Y28). The sites differ in soil type: KI64 has red sandy soils with good drainage and moisture retention, whilst Y28 is characterised by sandstone soils with lower water retention, however, may suffer periodic waterlogging. Both sites experience similar annual rainfall (1,883 mm/year) and temperature regimes.

Wood properties were assessed using three complementary non-destructive techniques:

- SilviScan: Measured anatomical properties including cell wall thickness, fibre diameter, microfibril angle (MFA), and air-dry density from wood chips
- Near-Infrared Spectroscopy (NIRS): Predicted chemical composition including kraft pulp yield (KPY), lignin content, cellulose, and basic density
- IML-Resistograph (Resi): Estimated wood density and mechanical properties (modulus of elasticity and acoustic wave velocity) in standing trees

Population structure analysis using 5,528 SNP markers classified trees into 10 genetically distinct subpopulations (P1–P10) based on their genomic similarity.

Site effects on growth and wood properties

Trees at KI64 (red sandy soils) demonstrated significantly superior growth compared to Y28 (sandstone soils), with greater mean diameter at breast height (DBH: 15.6 vs 13.7 cm), height (16.9 vs 15.6 m), and volume (0.13 vs 0.09 m^3) (Table 2a.1). Trees at KI64 also exhibited higher microfibril angle (8.1° vs 7.7°), larger fibre diameter (16.8 vs 16.7 µm), and higher cellulose content (42.6% vs 42.0%).

In contrast, trees at Y28 produced denser wood with significantly higher air-dry density (737.1 vs 722.4 kg/m^3), greater stiffness (17.2 vs 16.8 GPa), higher basic density (524.8 vs 512.9 kg/m^3), and elevated klason lignin (25.8% vs 25.4%) and extractives (6.2% vs 5.9%). These differences reflect the influence of soil water availability: trees on sandstone soils with lower water retention developed denser, stiffer wood as an adaptive response to water stress, whilst trees on red sandy soils had faster relative growth due to better access to water.

Trait	KI64 site		YP28 site		Whole population (both sites)				Unit
	Mean	SD	Mean	SD	Mean	SD	Minimum	Maximum	
DBH	**15.6***	4.79	13.7	3.81	14.7	4.4	3.2	28.2	cm
Height	**16.9***	3.55	15.6	2.93	16.3	3.3	1.1	23.6	m
Volume	**0.13***	0.08	0.09	0.06	0.1	0.1	0.0	0.5	m^3
ADD	722.4	84.6	**737.1***	76.4	729.7	81	276.1	1091.5	kg/m^3
CWT	2.44	0.36	**2.46**	0.329	2.4	0.3	0.9	5	µm
MFA	**8.1***	2.64	7.7	2.53	7.9	2.6	1.6	0.5	°
S_MOE	16.8	2.99	**17.2***	2.95	17	3	4.1	25.1	GPa
RFD	**16.8***	1.13	16.7	1.11	16.8	1.1	9.1	21.6	µm
TFD	17.3	1.10	17.3	0.95	17.3	1	9.6	21.6	µm
CRS	214	33.6	**215**	32.9	214.5	33.3	78.7	463.7	µg/m
NBD	512.9	34.6	**524.8***	29.6	518.8	32.8	414.9	786.5	kg/m^3
KPY	**47.2**	2.95	47.0	3.07	47.1	3.0	33.3	58.7	%
TL	32.3	1.48	32.3	1.32	32.3	1.4	27.8	36.9	%
KL	25.4	1.74	**25.8***	1.64	25.6	1.7	18.5	33.2	%
Extractive	5.9	1.63	**6.2***	1.54	6.1	1.6	2.7	26.3	%
Cellulose	**42.6***	1.89	42	1.96	42.3	2.0	32.6	47.8	%
AWV	**4.27**	0.316	4.26	0.314	4.3	0.3	2.1	5.7	km/sec
R_MOE	**21.2**	4.89	21.1	4.74	21.1	4.8	3	50.4	GPa
RED	560.1	53.4	**564.8**	49.4	562.4	51.5	286.5	797.6	kg/m^3
RCD	569.9	48.4	**570.8**	45.6	570.3	47.0	397.1	771.8	kg/m^3
RDD	**590.44**	52.04	587.57	48.97	589.0	50.6	339	809.8	kg/m^3

Table 2a.1. Summary statistics of *E. pellita* growth and wood properties across two plantation sites (KI64 and Y28). Values show mean and standard deviation for key traits measured using SilviScan, NIRS, and IML-Resi methods. Asterisks indicate statistically significant differences between sites at $p < 0.05$. DBH: Diameter at breast height; ADD: air-dry density; CWT: cell wall thickness; MFA: microfibril angle; S_MOE: SilviScan modulus of elasticity; RFD: radial fibre diameter; TFD: tangential fibre diameter; CRS: fibre coarseness; NBD: NIRS basic density; KPY: kraft pulp yield; TL: total lignin; KL: klason lignin; AWV: acoustic wave velocity; R_MOE: Resi modulus of elasticity; RED: Resi entry density; RCD: Resi core density; RDD: Resi disc density. Asterisks indicate statistically significant differences between sites ($p < 0.05$).

Genotype effects on wood properties

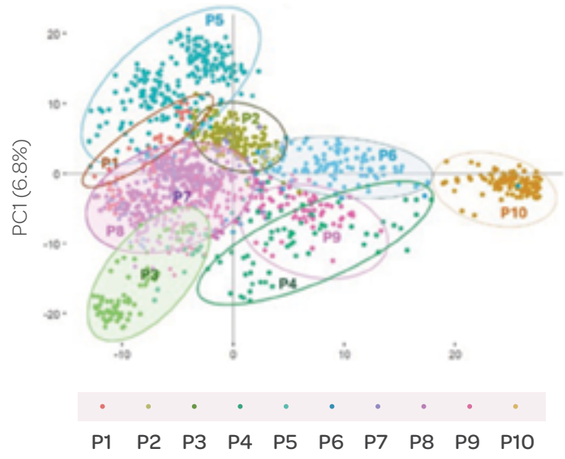
Significant variation in wood properties was observed among the 10 subpopulations (Table 2a.2). Subpopulation P4 exhibited the highest wood density (766.8 kg/m³ air-dry density) and mechanical properties (acoustic wave velocity 4.5 km/sec, modulus of elasticity 24.7 GPa), with thicker cell walls (2.7 µm) and larger fibre dimensions. These properties make P4 particularly suitable for solid wood applications. Subpopulation P3 demonstrated superior pulpwood characteristics with the highest kraft pulp yield (48.4%) and cellulose content (43%), combined with relatively low fibre coarseness. Subpopulation P10 was distinct for having the highest total lignin (32.6%) and klason lignin (26.3%), highest microfibril angle (10.3°), but lowest cellulose content (41%) and kraft pulp yield (44.6%), making it less suitable for either application.

Trait	Subpopulations										
	P1	P2	P3	P4	P5	P6	P7	P8	P9	P10	Unit
DBH	14.84	14.54	14.68	14.73	14.23	15.52	15.76	15.68	**16.48**	11.91	cm
ADD	704.8	742.3	703	**766.8**	720.4	746.1	737.1	737	712.7	734.2	kg/m³
CWT	2.3	2.5	2.3	**2.7**	2.4	2.5	2.5	2.5	2.4	2.5	µm
MFA	8.5	7.1	7.7	7.6	8.4	8.3	7	7.1	7.5	**10.3**	°
S_MOE	16.4	**17.8**	16.7	17.6	16.6	16.6	17.7	17.7	17	15.1	GPa
RFD	16.6	16.7	16.7	**17.4**	16.6	16.8	16.8	16.7	16.8	17.1	µm
TFD	17.1	17.4	17	**17.8**	17.2	17.3	17.3	17.3	17.4	17.6	µm
CRS	200.6	219.3	205.1	**239.5**	206.3	220	214.9	215	210	224.2	µg/m
NBD	496.3	522.1	511.5	**540.4***	514.2	525.2	513.7	518.8	514.7	535.2	kg/m³
KPY	46.6	47.3	**48.4***	46.8	46.9	46.5	47.5	47.6	47.8	44.6	%
TL	32.3	32.2	32.3	32.4	32	32.2	32.5	32.4	32.3	**32.6**	%
KL	26.1	25.4	25.2	25.3	25.4	25.8	26	25.6	25.5	**26.3***	%
Extractive	**6.7***	6.2	5.5	5.4	6.2	6.1	6.4	5.9	5.8	6.5	%
Cellulose	42	42.4	**43***	42.4	41.8	42	42.4	42.7	42.8	41	%
AWV	4.1	4.3	4.3	**4.5**	4.1	4.3	4.3	4.3	4.3	4.2	km/sec
R_MOE	18.1	22.2	21.8	**24.7**	18.9	20.8	22	21.8	21.8	20.1	GPa
RED	530.3	570.6	570.4	**588.7**	542.8	560.6	565.5	568.9	570.8	553.9	kg/m³
RDD	556.9	598.7	585	**620.6**	571	586.2	600.9	595.9	596.6	577.5	kg/m³
RCD	537.7	579.9	576.8	**607.3**	548.6	567.4	580.1	576	577.3	560.2	kg/m³

Table 2a.2. Summary statistics of *E. pellita* wood properties across 10 genetically distinct subpopulations (P1–P10). Values represent mean measurements for key traits assessed using SilviScan, NIRS, and IML-Resi methods. Bold values indicate the highest mean for each trait; underlined values indicate the lowest. Subpopulation P4 shows superior density and mechanical properties suitable for solid wood applications, whilst P3 demonstrates optimal pulpwood characteristics. Abbreviations as in Table 2c.1.

Genetic relatedness analysis revealed that more closely related subpopulations exhibited greater phenotypic similarity in wood properties. For example, subpopulations P1 and P3, which clustered together genetically (Fig2a.1a and 2a.1b), showed no significant differences in traits including total lignin, basic density, air-dry density, fibre diameter, cell wall thickness, microfibril angle, and stiffness. Similarly, subpopulations P3 and P8, which are closely related genetically, demonstrated high phenotypic similarity across of measured traits. In contrast, genetically distant subpopulations such as P1 and P6 showed significant differences in wood traits including basic density, air-dry density, fibre coarseness, cell wall thickness, and Resi-derived density and stiffness. This pattern suggests that genetic background is a primary driver of wood property variation, and that genomic information can be used to predict phenotypic similarity among genotypes.

(a) PCA of 10 subpopulations



(b) Phylogram of 10 subpopulations

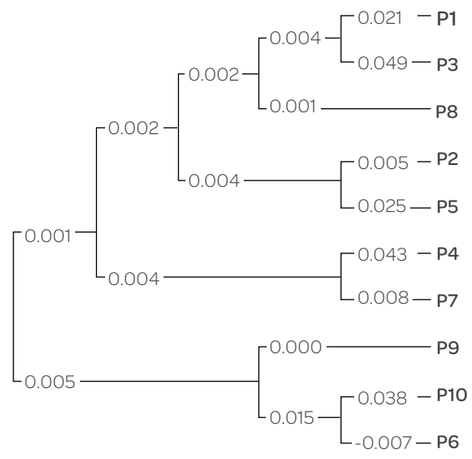


Figure 2a.1. Genetic distance and clustering among 10 *E. pellita* subpopulations. (a) Principal component analysis (PCA) plot showing the distribution of subpopulations P1–P10 in two-dimensional space defined by the first two principal components (PC1 and PC2), which together explain 11.8% of total genetic variation. Ellipses enclose each subpopulation cluster. (b) Unrooted neighbour-joining phylogram based on pairwise FST values showing genetic relationships among subpopulations. Bootstrap values (1,000 replicates) are shown at branch nodes. Four main clustering patterns are evident: Cluster 1 (P1, P3, P8), Cluster 2 (P2, P5), Cluster 3 (P4, P7), and Cluster 4 (P6, P9, P10). Genetically related subpopulations tend to exhibit more similar wood properties.

Relationship between growth and wood properties

Correlation analysis revealed consistent patterns across both sites (Fig 2a.2). Microfibril angle showed strong negative correlation with modulus of elasticity ($r = -0.68$, $p < 0.001$), acoustic wave velocity ($r = -0.54$, $p < 0.001$), kraft pulp yield ($r = -0.42$, $p < 0.001$), and cellulose content ($r = -0.38$, $p < 0.001$), but positive correlation with total lignin ($r = 0.31$, $p < 0.001$), klason lignin ($r = 0.28$, $p < 0.001$), and extractives ($r = 0.25$, $p < 0.001$). Cell wall thickness was positively correlated with wood density ($r = 0.52$, $p < 0.001$) and stiffness ($r = 0.48$, $p < 0.001$). Kraft pulp yield was positively correlated with cellulose ($r = 0.61$, $p < 0.001$) and negatively correlated with total lignin ($r = -0.58$, $p < 0.001$) and extractives ($r = -0.35$, $p < 0.001$). These relationships are consistent with established understandings and were maintained across both sites, indicating that the fundamental relationships among wood properties are robust and site independent.

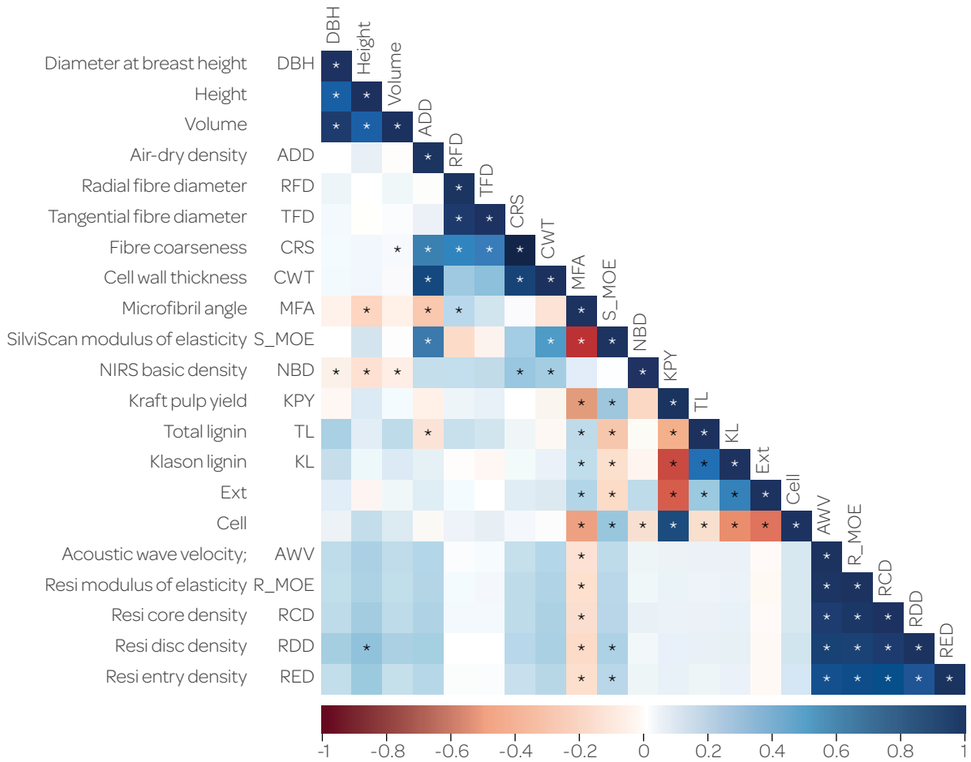


Figure 2a.2. Correlation matrix of wood properties for the entire *E. pellita* population across both sites. Colour gradient indicates correlation strength and direction: blue represents positive correlations, red represents negative correlations. Asterisks denote statistically significant correlations at $p < 0.05$ (95% confidence interval).

Diameter growth exhibited trade-offs with several wood properties (Table 2a.3). As DBH increased, kraft pulp yield decreased by approximately 0.08 percentage points per 1 cm increase in diameter ($p < 0.001$). Conversely, increasing diameter was associated with higher total lignin (0.17% per cm DBH, $p < 0.001$), klason lignin (0.13% per cm, $p < 0.001$), extractives (0.07% per cm, $p < 0.001$), and mechanical properties including modulus of elasticity (0.03 GPa per cm, $p < 0.001$) and acoustic wave velocity (0.02 km/sec per cm, $p < 0.001$). However, no significant relationships were detected between DBH and basic density, cellulose content, microfibril angle, or air-dry density. These trade-offs reflect the physiological constraints on resource allocation: as trees grow larger, they invest proportionally more in structural support (lignin, mechanical properties) at the expense of pulping efficiency (kraft pulp yield). This indicates that diameter measurements may be useful in predicting some wood properties.

Wood properties	Coefficient	Equation
KPY	-0.08***	KPY = 48.18 – (0.08X) ± 0.02
Total lignin	0.17***	TL = 30.59 + (0.17X) ± 0.01
NIR Basic density	-0.01	NBD = 519.8 - (0.01X) ± 0.2
Klason lignin	0.13***	KL = 23.70 + (0.13X) ± 0.01
Extractives	0.06***	Ext = 5.07 + (0.07X) ± 0.01
Cellulose	0.01	Cell = 42.21 + (0.001X) ± 0.01
AWV	0.02***	AWV = 4.04 + (0.02X) ± 0.002
Resi MOE	0.30***	MOE = 17.24 + (0.03X) ± 0.03
Resi core density	3.31***	RCD = 527.57 + (2.95X) ± 0.29
Resi disc density	4.36***	RDD = 528.89 + (5.06X) ± 0.30
Resi entry density	3.44***	RED = 515.79 + (3.16X) ± 0.32
MFA	-0.02	MFA = 8.017 - (0.01X) ±1.56
Cell wall thickness	0.05*	CWT = 2.39+(0.005X) ± 0.002
Fibre coarseness	0.59**	CRS = 206.79+(0.59X) ± 0.21
Air-dry density	0.53	ADD =720.21+(0.53X) ±1.56
Tangential fibre diameter	0.02*	TFD = 17.12+(0.02X) ± 0.01
Radial fibre diameter	0.03***	RFD = 16.44+(0.03X) ± 0.01

Table 2a.3. Linear regression coefficients for predicting wood properties from diameter at breast height (DBH). Equations show the estimated change in each wood property per 1 cm increase in DBH, with standard errors and significance levels. Significance levels: ***p < 0.001; **p < 0.01; *p < 0.05; ns = not significant.

Model comparison analysis indicated that the relationship between diameter growth and wood properties was influenced by both site and genotype factors (data not shown). For traits including total lignin, klason lignin, extractives, and Resi entry density, the interaction between site and genotype was the primary driver of variation. For other traits such as fibre diameter, fibre coarseness, cell wall thickness, and mechanical properties, genotype alone was the dominant factor. This indicates that whilst genotype consistently influences wood property development, the expression of some traits (particularly chemical composition) is modulated by site-specific environmental conditions. Such genotype × environment interactions have important implications for breeding and deployment strategies, as they suggest that optimal genotypes may differ between sites.

Implications for plantation management and product selection

Solid wood production: Trees at Y28 (sandstone soils) produced wood with superior mechanical properties (higher density, stiffness, and thicker cell walls with lower microfibril angle), making this site more suitable for solid wood applications. Subpopulation P4 is particularly recommended for solid wood production, as it consistently demonstrated the highest density, stiffness, and cell wall thickness across both sites. The modulus of elasticity values (21–25 GPa) also meet the requirements for F17 stress grade classification under Australian standards (AS 1720.1:2010), commonly used for structural applications.

Pulpwood production: Trees at KI64 (red sandy soils) demonstrated superior pulpwood characteristics with higher kraft pulp yield and cellulose content. Subpopulation P3 is recommended for pulpwood applications, with kraft pulp yield of 48.4% and cellulose content of 43%. However, the kraft pulp yield (47.1% across both sites) is comparable to but not markedly superior to other pulpwood-focused species such as Acacia hybrids (52.5%) or some eucalypt species (47.3–57.6%), suggesting that pulp production should be considered a secondary utilisation pathway for *E. pellita* on Tiwi Islands.

Trade-offs and site-genotype interactions: The significant interaction between site and genotype for several wood properties indicates that genotype performance varies across environments. This emphasises the importance of matching specific genotypes to target sites and end-use applications to optimise both growth and wood quality. These findings support the development of site-specific deployment strategies that account for both genetic potential and environmental suitability (see section 2e for more detail).

Key Findings

Non-destructive testing methods (SilviScan, NIRS, IML-Resi) successfully characterised wood properties across a large population (1,502 trees), demonstrating the feasibility of rapid, comprehensive wood quality assessment for breeding applications.

Soil type significantly influences both growth and wood properties: red sandy soils (KI64) favour faster growth and pulpwood characteristics, whilst sandstone soils (Y28) produce denser, stiffer wood suitable for solid wood applications. Ground water relations may also be a factor based on anecdotal evidence where periodic waterlogging and drying at YP may have had a significant effect on growth and wood properties.

Genetic background is a primary driver of wood property variation: genetically related subpopulations exhibit greater phenotypic similarity, and subpopulation P4 and P3 are recommended for solid wood and pulpwood applications, respectively.

Consistent trait correlations across sites indicate that fundamental wood structure relationships are robust and site independent.

Site-genotype interactions for some wood properties (total lignin, klason lignin, extractives) indicate that optimal genotypes may differ between sites, supporting the development of site-specific deployment strategies.

2b. Radial wood properties and xylem maturation of *Eucalyptus pellita* planted in dry tropical monsoon climate

Wood quality in plantation trees changes dramatically as trees grow, reflecting the transition from juvenile to mature wood. Juvenile wood, formed during early tree development, typically has lower density, weaker mechanical properties, and different fibre characteristics compared to mature wood. Understanding when this transition occurs is critical for determining optimal harvest ages and predicting the proportion of high-quality wood in harvested logs. However, the timing of xylem maturation varies among tree species, growth rates, and environmental conditions, and this variation is poorly understood in tropical species like *E. pellita*. Additionally, trees growing at different rates within the same plantation (dominant, codominant, and suppressed trees) may mature at different ages, yet this has rarely been investigated. Lastly, seasonal variations in water availability—particularly important in tropical dry monsoon climates—may influence wood formation and the rate of maturation. This section investigates radial wood property variation and xylem maturation across different growth classes and sites, using high-resolution wood property measurements from pith to bark. By identifying when mature wood formation occurs and how this timing varies among a population of trees, we can provide practical guidance for determining minimum harvest rotation ages and predicting wood quality in standing trees. This knowledge supports more informed management decisions to balance growth productivity with wood quality objectives.

Objectives

To evaluate the effect of growth rates on radial wood property variation and xylem maturation of *E. pellita* across different growth classes and sites, and to understand how seasonal water availability influences wood formation during juvenile and mature wood development.

Methods and Results

Study sites and sampling

Increment core samples were collected from 105 *E. pellita* trees at two plantation sites on Melville Island: Kilu Impini 64 (KI64, higher productivity site) and Yapilika 28 (Y28, lower productivity site). Trees were classified into three growth classes based on diameter at breast height (DBH). These growth classes broadly represent suppressed, codominant, and dominant trees within the plantation stand, respectively.

Wood cores were analysed using SilviScan to measure radial variation in air-dry density (ADD), cell wall thickness (CWT), microfibril angle (MFA), modulus of elasticity (MOE), radial and tangential fibre diameter (RFD, TFD), fibre coarseness (CRS), and specific surface area (SS) at 25 µm resolution from pith to bark.

Effect of growth class on wood properties

Variance component analysis revealed that growth class significantly influenced wood property variation, but the magnitude of this effect differed between sites (Table 2b.1). At the higher productivity site (KI64), growth class explained substantial proportions of variability in most wood traits, with air-dry density showing the highest variance component ratio (21.9%), followed by modulus of elasticity (19.6%), microfibril angle (17.5%), and cell wall thickness (6.9%). Medium-sized trees at KI64 exhibited the highest values for ADD (641.2 kg/m^3), CRS (193.8 µg/m), MOE (12.9 GPa), and CWT (2.4 µm).

In contrast, at the lower productivity site (Y28), growth class-related variation was observed only for microfibril angle (16.6% variance explained) and modulus of elasticity (3.9%), suggesting that wood properties were generally more uniform among growth classes under less favourable growing conditions. Small trees at Y28 exhibited the lowest MFA (10.5°) and highest MOE (12.9 GPa), indicating that slower-growing trees may produce stiffer wood with more favourable fibre characteristics.

	Trait	Fixed-effect parameter (μ)			Random-effect parameter (D)			VCR (%)
		Estimate	SE	p-value	Small	Medium	Large	
Higher productivity site	ADD	622.9	17.1	<0.01	9.7	**18.3**	-28.1	21.9
	RFD	16.0	0.1	<0.001	-0.01	-0.01	**0.02**	0.4
	TFD	16.3	3.1	<0.001	0	0	0	0
	CRS	191.5	3.1	<0.001	-2.0	**2.3**	-0.3	3.6
	MFA	13.7	1.3	<0.05	-1.1	-0.9	**2.0**	17.5
	MOE	12.3	0.8	<0.01	0.6	**0.7**	-1.3	19.6
	CWT	2.3	0.04	<0.001	-0.03	**0.05**	-0.02	6.9
	SS	348.2	5.2	<0.001	**3.4**	-5.0	1.7	5.1
Lower productivity site	ADD	627.9	10.9	<0.001	0	0	0	0
	RFD	15.9	0.1	<0.001	0	0	0	0
	TFD	16.4	0.1	<0.001	0	0	0	0
	CRS	197.1	3.2	<0.001	0	0	0	0
	MFA	11.7	0.9	<0.05	-1.2	0.1	**1.1**	16.6
	MOE	12.7	0.5	<0.05	**0.2**	0.1	-0.3	3.9
	CWT	2.4	0.1	<0.001	0	0	0	0
	SS	338.2	5.6	<0.001	0	0	0	0

Table 2b.1. Estimated values of fixed- and random-effect parameters and variance component ratio (VCR) of wood properties across growth classes and sites. Fixed-effect parameter (μ) represents the mean value across all trees; random-effect parameters (D) show deviations from the mean for each growth class; VCR indicates the percentage of total variance explained by growth class differences. Higher VCR values indicate stronger influence of growth class on wood property variation. Bold values indicate the highest wood property values within each site. Zero values indicate no variation across growth classes. Abbreviations: ADD, air-dry density (kg/m³); RFD, radial fibre diameter (μm); TFD, tangential fibre diameter (μm); CRS, fibre coarseness (μg/m); MFA, microfibril angle (°); MOE, modulus of elasticity (GPa); CWT, cell wall thickness (μm); SS, specific surface area (m²/kg); SE, standard error.

These findings reflect the interaction between site resource availability and competitive dynamics within forest stands. At the higher productivity site with better resource availability, competitive interactions among growth classes are more pronounced, leading to differentiation in wood properties. Faster-growing dominant trees allocate resources to height growth rather than wood structural development, resulting in lower wood density. In contrast, suppressed trees with limited light access develop denser wood as a survival strategy.

Radial variation in wood properties across growth classes and sites

Radial traces of wood properties from pith to bark revealed consistent patterns across both sites and growth classes (Fig. 2b.1). Air-dry density, cell wall thickness, modulus of elasticity, and fibre coarseness exhibited an initial decline from the pith, followed by a gradual increase towards the middle of the growing period, before either stabilising or showing only minor decline in the outer wood. This pattern reflects the transition from juvenile to mature wood, where initial rapid growth produces lower-density wood with thinner cell walls, followed by the development of denser, more structurally robust mature wood.

In contrast, microfibril angle, tangential fibre diameter, radial fibre diameter, and specific surface area generally declined from pith to bark and remained relatively stable thereafter. The decreasing microfibril angle from pith (approximately 20°) to bark (approximately 6°) is particularly significant, as MFA is a primary determinant of wood stiffness, with lower angles producing stiffer. At the higher productivity site, tangential and radial fibre diameter remained stable in large trees, whereas values in small and medium trees increased slightly towards the outer wood, suggesting that growth class influences the timing and magnitude of fibre diameter stabilisation.

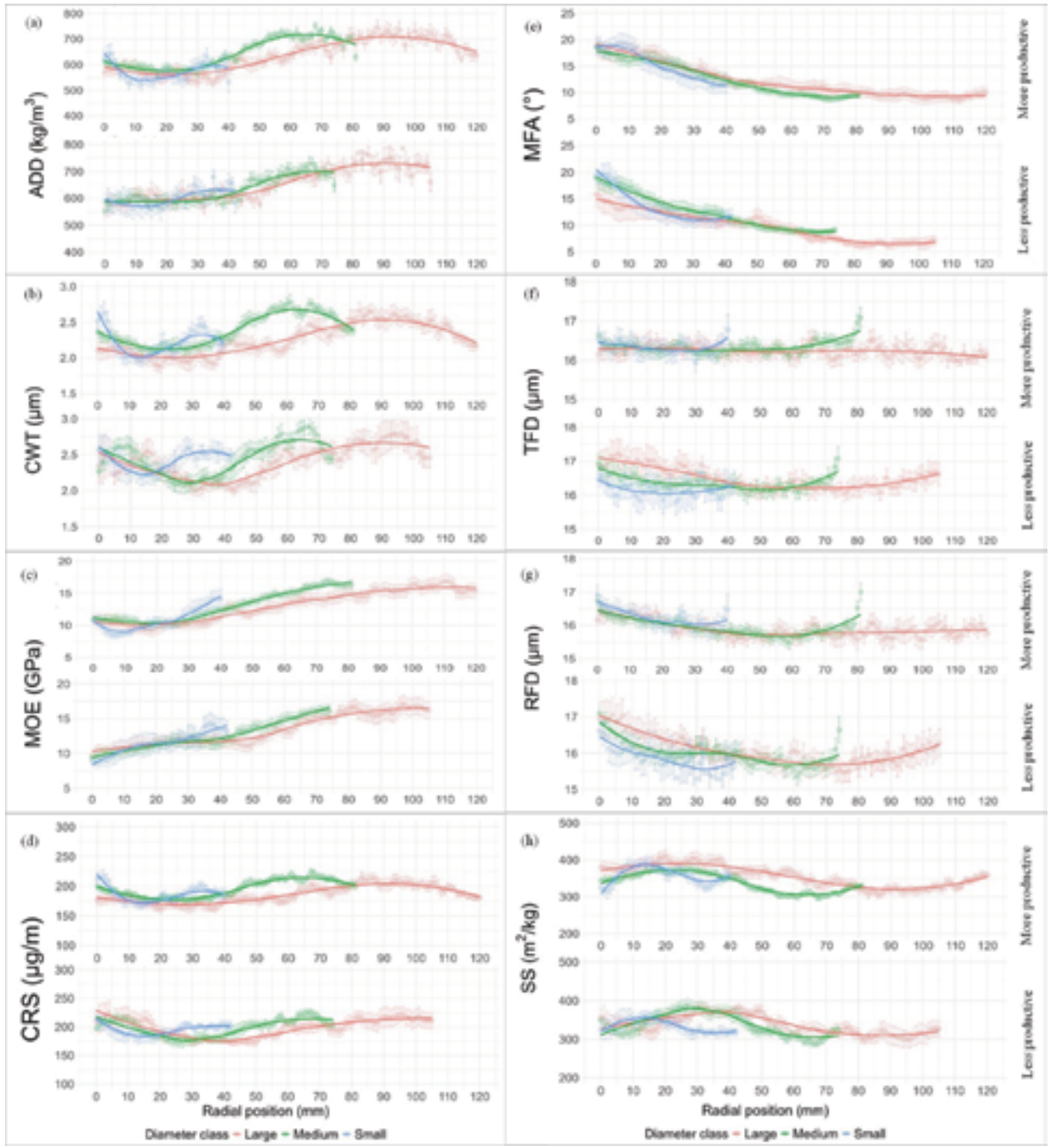


Figure 2b.1. Radial wood properties in relation to distance from pith at higher productivity (KI64) and lower productivity (Y28) sites. Plots show (a) air-dry density (ADD), (b) cell wall thickness (CWT), (c) modulus of elasticity (MOE), (d) fibre coarseness (CRS), (e) microfibril angle (MFA), (f) radial fibre diameter (RFD), (g) tangential fibre diameter (TFD), and (h) specific surface area (SS). Lines represent LOESS (locally estimated scatterplot smoothing) function of mean wood properties for each growth class (small, medium, large). Shaded regions indicate the range of variation. At both sites, ADD, CWT, MOE, and CRS show initial decline followed by increase and stabilisation, whilst MFA, TFD, RFD, and SS show gradual decline and subsequent stabilisation. Growth class influences the magnitude and timing of these transitions, particularly at the higher productivity site.

Juvenile-mature wood transition and xylem maturation

To identify the transition from juvenile to mature wood, quadratic regression models with plateau were fitted to radial wood property data for each growth class and site (Table 2b.2). Microfibril angle and modulus of elasticity provided the most reliable indicators of xylem maturation, with coefficient of determination values ≥ 0.9. Greater emphasis is placed on MFA-derived transition ages for subsequent analysis as MFA represents a directly measured property rather than a derived estimate.

At the higher productivity site, the average distance from pith to the juvenile-mature wood boundary based on MFA was 29 mm for small trees, 58 mm for medium trees, and 80 mm for large trees. When converted to cambial age (years since tree establishment), large trees transitioned to mature wood at approximately 6.5 years, whilst medium and small trees matured at 6 years. At the lower productivity site, the boundary occurred at 27 mm (small trees, 5.8 years), 62 mm (medium trees, 7.5 years), and 81 mm (large trees, 6.9 years). Notably, the timing of xylem maturation differed between growth classes, with small trees at the lower productivity site maturing earlier (5.8 years) than large trees (6.9 years), contrary to the pattern observed at the higher productivity site. This suggests that site productivity and competitive interactions influence the rate of wood maturation. At the higher productivity site, dominant trees with greater resource access maintain prolonged juvenile wood formation, whilst suppressed trees transition to mature wood more rapidly. At the lower productivity site, resource limitations may slow down maturation in large and medium growth classes, but accelerate this in smaller trees.

Trait	Parameter	Higher productivity site			Lower productivity site		
		Small	Medium	Large	Small	Medium	Large
ADD (kg/m^3)	x_0	21	53	69	29	60	81
	p	581.7	706.3	692.9	629.9	700.6	730.8
	CA	4.7	5.9	5.2	6.2	7.2	6.9
	R^2	0.58	0.88	0.86	0.70	**0.90**	0.88
MFA (°)	x_0	29	58	80	27	62	81
	p	11.9	9.3	9.5	11.2	8.9	6.6
	CA	6.5	6.5	6.0	5.8	7.5	6.9
	R^2	**0.94**	**0.98**	**0.97**	**0.98**	**0.98**	**0.97**
CWT (µm)	x_0	22	52	72	27	57	69
	p	2.3	2.6	2.5	2.5	2.7	2.6
	CA	4.8	5.8	5.4	5.8	6.9	5.9
	R^2	0.73	0.84	0.79	0.93	0.74	0.82
MOE (GPa)	x_0	38	66	81	39	71	80
	p	14.9	16.3	15.6	13.5	16.2	16.6
	CA	8.6	7.4	6.1	8.3	8.6	6.9
	R^2	0.94	0.98	0.93	0.90	0.96	0.94
RFD (µm)	x0	20	37	84	34	24	56
	p	16.1	15.8	15.8	15.6	15.9	15.8
	CA	4.5	4.1	6.3	7.3	2.9	4.8
	R^2	0.71	0.51	0.64	0.64	0.65	0.82
TFD (µm)	x_0	14	14	40	23	20	56
	p	16.3	16.3	16.2	16.1	16.3	15.8
	CA	3.1	1.6	2.9	5.0	2.4	4.8
	R^2	0.14	0.03	0.23	0.21	0.44	0.82
CRS (µg/m)	x_0	23	53	71	28	57	71
	p	188.3	210.7	198.9	201.0	214.7	210.3
	CA	5.1	5.8	5.4	5.9	6.9	6.1
	R^2	0.79	0.87	0.77	0.93	0.80	0.80
SS (m^2/kg)	x_0	23	51	69	28	57	68
	p	349.65	317.16	328.98	318.35	304.41	316.89
	CA	5.2	5.6	5.2	5.9	6.9	5.8
	R^2	0.73	0.59	0.84	0.94	0.80	0.79

Table 2b.2. Estimated boundary between juvenile and mature wood based on quadratic regression model with plateau. Parameters include x_0 (distance from pith in mm representing the juvenile-mature wood boundary), *p* (plateau value representing wood property value at transition), CA (cambial age in years), and R^2 (coefficient of determination).

The difference between MFA-derived and MOE-derived transition ages is noteworthy for some growth classes. At the higher productivity site, MFA transition occurred 1–3 years earlier than MOE transition for medium and small trees, respectively. This suggests that microfibril orientation stabilises before the full development of mechanical stiffness, which is influenced by multiple factors including MFA, wood density, and cell wall thickness. The delayed MOE transition may reflect the time required for complete lignification and cell wall thickening to develop full mechanical properties.

Effect of seasonal water availability on wood properties

To understand how seasonal and annual water availability influences wood formation, radial wood properties were overlaid with drought index (SPEI-6, Standardised Precipitation-Evapotranspiration Index at 6-month timescale) for 10 large trees from the higher productivity site. Visual observation revealed that fluctuations in wood properties were generally greater during early growth (0–6 years) and became less pronounced towards the end of the growing period (6–10 years), regardless of interannual variation in drought conditions (Fig. 2b.2). Impacts of annual water availability on wood properties did not show any significant impacts, however due to large changes during juvenile wood development and insufficient mature wood to determine trends this was hard to confirm.

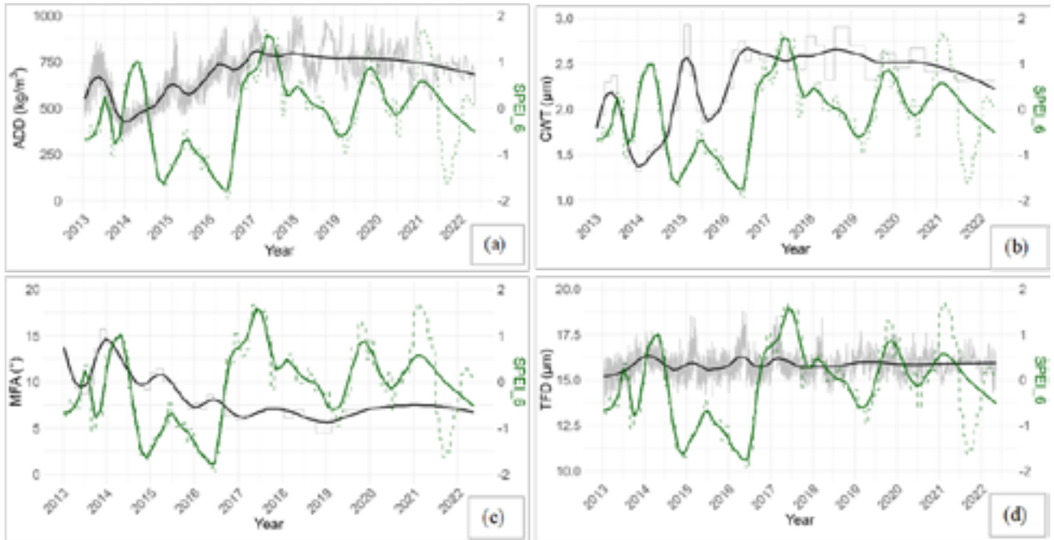


Figure 2b.2. Relationship between radial wood properties and 6-month timescale drought index (SPEI-6) for an individual large tree from the higher productivity site (KI64). Grey and black lines represent wood property values and LOESS regression trends. Dashed and solid green lines represent SPEI-6 records and trends. Plots show (a) air-dry density (ADD), (b) cell wall thickness (CWT), (c) microfibril angle (MFA), and (d) tangential fibre diameter (TFD).

Analysis of seasonal differences in wood properties revealed that the proportion of variation explained by seasonal climate (wet vs. dry season) varied across years, with the highest variance proportions observed in early years (2014–2016) indicating a modest impact of seasonal water availability on trait determination. Air-dry density and cell wall thickness in 2014 showed the greatest explained variance (approximately 95%), whilst tangential fibre diameter (90.6%) and microfibril angle (95.8%) showed maximum variance in 2015 and 2016, respectively. When averaged across the juvenile phase (0–6 years) and mature phase (6–10 years), all selected wood properties showed higher average variance during juvenile wood development (Fig. 2b.3).

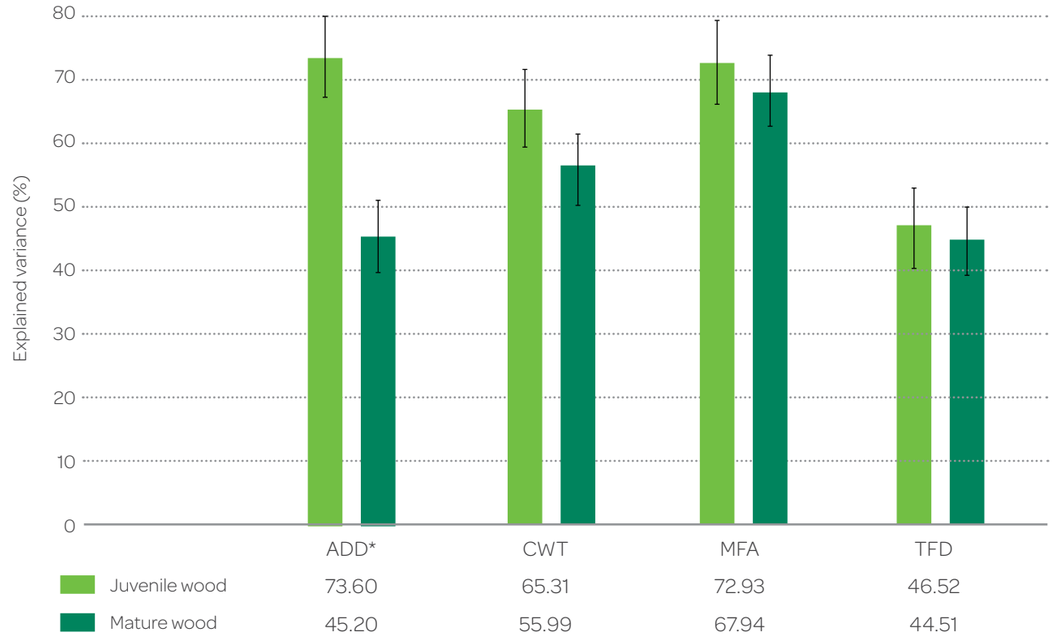


Figure 2b.3. The percentage of variance explained between juvenile and mature wood phase. ADD: air-dry density (kg/m³), CWT: cell wall thickness (µm), MFA: microfibril angle (°), TFD: tangential fibre diameter (µm). *Significantly different ($p<0.05$).

Importantly, air-dry density was the only trait showing statistically significant difference in seasonal variance between juvenile and mature wood phases ($p < 0.05$), with juvenile wood exhibiting 73.6% variance explained by seasonal climate compared to 45.2% in mature wood. This indicates that wood density is particularly sensitive to seasonal water availability during early development, reflecting the greater developmental plasticity of juvenile wood. In contrast, microfibril angle, cell wall thickness, and tangential fibre diameter showed relatively small differences between juvenile and mature phases, suggesting these anatomical traits are more developmentally constrained.

Key Findings

Growth class effects on wood properties: At the higher productivity site, growth class significantly influenced wood properties, particularly air-dry density, modulus of elasticity, and microfibril angle. At the lower productivity site, growth class effects were minimal, suggesting that resource limitations reduce competitive differentiation among growth classes. This is different to what was observed in the analysis across the whole population, as noted in the section 2a.

Consistent radial patterns across all growth classes: Air-dry density, cell wall thickness, modulus of elasticity, and fibre coarseness showed initial decline followed by increase and stabilisation, reflecting juvenile-to-mature wood transition. Microfibril angle, fibre diameter, and specific surface area showed gradual decline and subsequent stabilisation.

Xylem maturation timing: Large trees transitioned to mature wood at approximately 6–7 years based on microfibril angle, whilst small and medium trees generally matured slower. Xylem maturation was influenced by both site productivity and growth class, with competitive interactions affecting the rate of wood development.

Seasonal water sensitivity: Wood density exhibited significantly greater seasonal variability during the juvenile phase compared to mature phase, indicating higher sensitivity to seasonal water availability during early wood development. Annual rainfall overall showed a minimal impact on trait determination, however this was difficult to determine due to limited mature wood production.

Implications for harvest timing: The identified juvenile-mature wood transition at 6–7 years provides a practical basis for determining minimum harvest rotation thresholds. For solid wood production, longer rotations beyond this transition are recommended to increase the proportion of mature wood with superior mechanical properties. For pulpwood production, shorter rotations may remain acceptable due to favourable pulping properties of juvenile wood.

Recommendations for Plantation Management

Harvest rotation strategies: For solid wood applications, rotations should extend beyond 7 years to ensure adequate mature wood formation and superior mechanical properties. For pulpwood production, rotations of 5–7 years align with the juvenile-mature wood transition and may optimise the balance between growth productivity and pulping efficiency.

Site-specific management: At higher productivity sites, competitive thinning may be beneficial to reduce differentiation in wood properties among growth classes and promote more uniform wood quality. At lower productivity sites, wood properties are already relatively uniform, and management should focus on maximising growth rates.

2c. Whole-tree mapping of selected wood anatomical, physical and chemical properties for *Eucalyptus pellita* and its hybrids

Predicting wood quality from measurements at a single point on the tree (such as breast height) requires understanding how wood properties vary throughout the stem—both from the centre outward (radially) and from bottom to top (longitudinally). Previous studies on temperate tree species have shown that whole-tree maps of wood properties can reveal important patterns in wood quality variation and support the development of predictive models. However, such comprehensive mapping has rarely been applied to tropical hardwoods like *E. pellita*, and it is unclear whether methods developed for temperate species are equally effective for tropical trees. Additionally, there is limited information on whether different genotypes of *E. pellita* (pure species and hybrids) show similar patterns of wood property variation, or whether genotype-specific maps are needed. Understanding within-tree variation is important for processors who need to allocate logs to different end-uses based on expected wood quality, and for breeders seeking to identify superior genotypes for specific applications. This section develops whole-tree maps of key wood properties for *E. pellita* and its hybrids using multiple-height sampling and advanced spatial interpolation methods. By visualising how wood properties vary throughout the tree, we can identify optimal sampling strategies, develop predictive models for rapid quality assessment, and provide guidance for matching plantation resources to specific end-use applications

Objectives

To map whole-tree wood properties of *E. pellita* and its hybrids using multiple-height sampling and non-destructive testing methods, to understand radial and longitudinal variation in wood properties, and to develop predictive models for estimating whole-tree wood quality from breast-height measurements.

Methods and Results

Study design and sample collection

Thirty 10-year-old trees representing five genotypes (*E. pellita*, *E. pellita* × *E. brassiana* F1 and backcross, *E. pellita* × *E. urophylla* F1 and backcross) were harvested from plantation trial sites on Melville Island. Trees were selected with diameter at breast height (DBH) greater than 15 cm. Multiple-height sampling was undertaken at three longitudinal positions: bottom (0 m), middle (5.4 m), and top (9.3 m) of the stem. Disc samples (5 cm thickness) were collected at each height and analysed for air-dry density (ADD), cell wall thickness (CWT), microfibril angle (MFA), kraft pulp yield (KPY), and Klason lignin (KL) using SilviScan, near-infrared spectroscopy (NIRS), and IML-Resistograph (Resi) measurements. Additional Resi measurements were also taken at other points along the tree stem. Whole-tree maps were generated using Akima's interpolation method, a computational approach that effectively handles non-linear and irregularly spaced data.

Radial and longitudinal patterns of wood properties

Radial wood property profiles revealed consistent patterns across all genotypes (Fig. 2c.1). Longitudinally, more uniform radial patterns were observed between the bottom and middle stem than between middle and top stem. At the bottom and middle stem (0–5.4 m), Resi basic density increased gradually from pith and plateaued towards the bark. However, in the upper stem (7.8–9.3 m), density first increased and then decreased, suggesting that biomechanical demands for wind resistance in the upper stem influence wood formation differently than in the lower stem. Mean radial ADD and KPY values increased longitudinally from bottom to middle stem while cell wall thickness increased from bottom to top stem in early years but was more similar in later years. In contrast, MFA and KL decreased markedly from bottom to middle stem. The upper stem exhibits wood that is more elastic, possibly driven by the need for flexibility to withstand wind forces in the cyclone-prone environment where this species is found naturally.

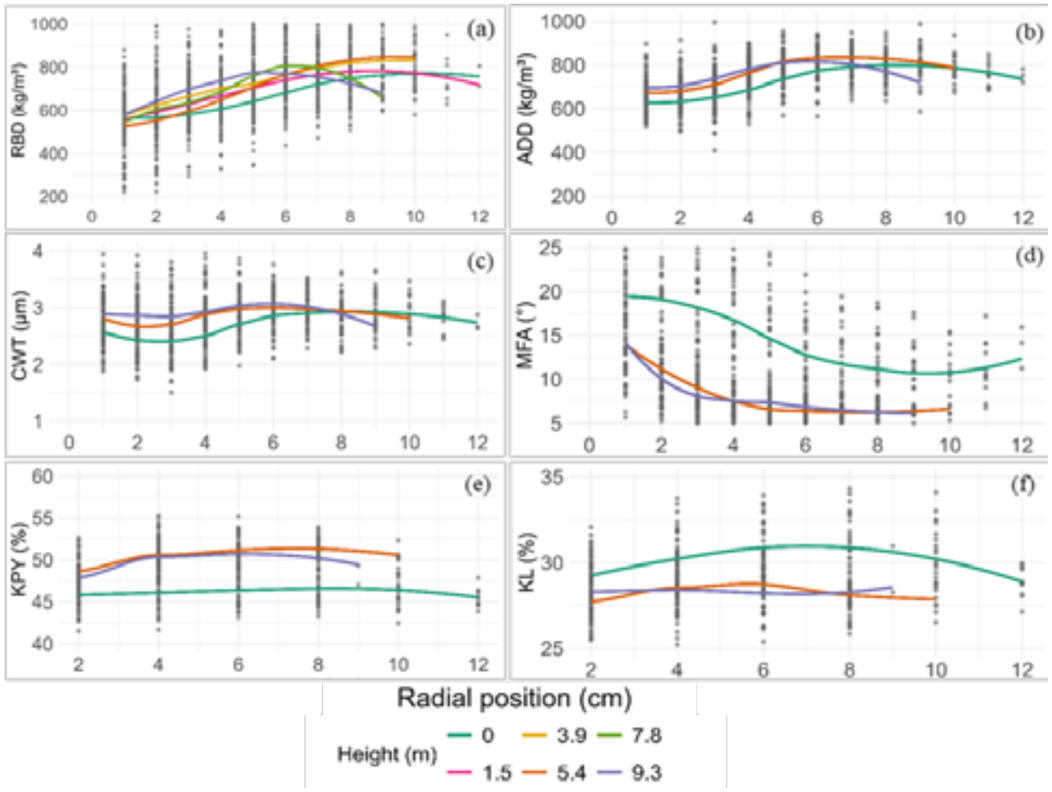


Figure 2c.1. Radial patterns of selected wood properties at different longitudinal positions in *E. pellita* and its hybrids. Plots show (a) Resi basic density (RBD), (b) air-dry density (ADD), (c) cell wall thickness (CWT), (d) microfibril angle (MFA), (e) kraft pulp yield (KPY), and (f) Klason lignin (KL). Lines represent LOESS (locally estimated scatterplot smoothing) function of mean values at different sampling heights from bottom (0 m) to top (9.3 m) stem.

Validation of whole-tree mapping approach

Two validation steps were undertaken to assess the accuracy of Akima's interpolation method for mapping whole-tree Resi basic density – this is the model used to estimate whole tree wood properties and required validation to determine it suitability in this context. Validation step 1 compared maps generated using different numbers of sampling heights along the stem (3, 4, 5, and 6 heights). Results showed no significant improvement in accuracy when more than three sampling heights were used, with mean absolute percentage error (MAPE) values consistently below 10% and root mean squared error (RMSE) values ranging from 33.04 to 54.97 kg/m^3 (Table 2c.1). Three sampling heights (bottom, middle, top) provided the highest accuracy with RMSE of 33.04 kg/m^3 and MAPE of 4.45%, indicating that this sampling intensity is sufficient for accurate whole-tree property mapping.

Parameter	6 sampling heights	5 sampling heights		4 sampling heights		3 sampling heights	
Actual	753.24	753.24	757.68	753.24	748.96	753.24	743.1
Predicted	702.71	702.71		712.99		710.06	
RMSE	50.53	50.53	54.97	40.25	35.97	43.18	33.04
MAPE	6.71	6.71	7.25	5.34	4.8	5.73	4.45

Table 2c.1. Validation accuracy of Resi basic density (RBD) maps generated using different numbers of sampling heights. Predicted values were calculated from the RBD maps that built using training set. Actual values were estimated based on weighted actual whole-tree density from targeted heights using testing set (kg/m^3). Underlined values indicate weighted actual whole-tree density of testing set from 5, 4, and 3 points of height (kg/m^3). RMSE: Root mean squared error (kg/m^3). MAPE: mean absolute percentage error (%).

Validation step 2 evaluated fine-scale accuracy at unsampled positions (breast-height at 1.1 m and mid-upper stem at 7.8 m). Prediction accuracy varied with position within the stem, with MAPE values ranging from 0.1% to 24% and RMSE from 0.52 to 159 kg/m^3 (Table 2c.2). Accuracy was consistently higher at breast-height (1.1 m) than at the upper stem (7.8 m), with MAPE values below 10% for pith-to-bark measurements at both heights. These results support the use of breast-height sampling for developing predictive models of whole-tree wood properties.

Accuracy parameter	Cluster 1				Cluster 2			
	Actual	Predicted	RMSE	MAPE	Actual	Predicted	RMSE	MAPE
Whole tree	725.06	724.54	0.52	0.07	702.71	691.43	11.28	1.63
1.1 m	721.55	701.58	19.97	2.85	678.74	651.87	26.87	4.12
7.8 m	713.03	767.94	54.91	7.15	705.26	761.75	56.49	7.42
RP at 1.1 m of height								
2	565.35	610.07	44.72	7.33	526.83	565.35	38.52	7.31
3	615.84	598.50	17.34	2.90	548.17	615.84	67.67	12.35
4	650.86	614.00	36.86	6.00	585	650.86	65.86	11.26
5	703.51	666.07	37.44	5.62	594.33	703.51	109.18	18.37
6	748.51	702.14	46.37	6.60	626	748.51	122.51	19.57
7	771.27	702.07	69.20	9.86	654.33	771.27	116.94	17.87
8	821.68	703.21	118.47	16.85	662.5	821.68	159.18	24.03
9	814.91	688.83	126.08	18.30	676.17	814.91	138.74	20.52
10	816.88	682.13	134.75	19.75	661.83	816.88	155.05	23.43
RP at 7.8 m of height								
2	533.21	559.82	60.68	9.78	620.5	559.82	60.68	9.78
3	592.57	637.91	10.41	1.66	627.5	637.91	10.41	1.66
4	704.36	693.83	2.34	0.34	696.17	693.83	2.34	0.34
5	796.57	781.24	47.41	6.46	733.83	781.24	47.41	6.46
6	893	811.13	27.37	3.26	838.5	811.13	27.37	3.26
7	896	728.06	83.27	10.26	811.33	728.06	83.27	10.26
8	700.75	748.07	63.27	9.24	684.8	748.07	63.27	9.24

Table 2c.2. Validation accuracy of Resi basic density (RBD) maps at unsampled positions. Predicted value is the average of Resi basic density (RBD) values calculated from the map developed using training dataset (kg/m³). Actual Resi basic density of whole tree was estimated based on weighted tree property using actual data of selected heights (kg/m³). Actual Resi basic density of 1.1 and 7.8 m were estimated based on weighted disc property at these heights (kg/m³). RMSE: Root mean squared error (kg/m³). MAPE: mean absolute percentage error (%). Coloured scales indicate the magnitude of values for each parameter assessed. Different colours represent unit differences: blue is for scaling the RBD values in kg/m³ and green is for scaling percentage (%).RP: Radial position from the pith (cm).

Whole-tree maps of selected wood properties

Whole-tree maps were successfully generated for air-dry density, cell wall thickness, microfibril angle, kraft pulp yield, and Klason lignin across all genotypes (Figs. 2c.2–2c.6). Air-dry density maps showed consistent increase from pith to bark along the entire stem in all genotypes, with *E. pellita* × *E. brassiana* (backcross) exhibiting the highest whole-tree average (789 kg/m³) and *E. pellita* × *E. urophylla* (backcross) the lowest (726.5 kg/m³). More than 74% of whole-tree ADD values across all genotypes fell within the range of 600–900 kg/m³, indicating relatively consistent wood density across genotypes.

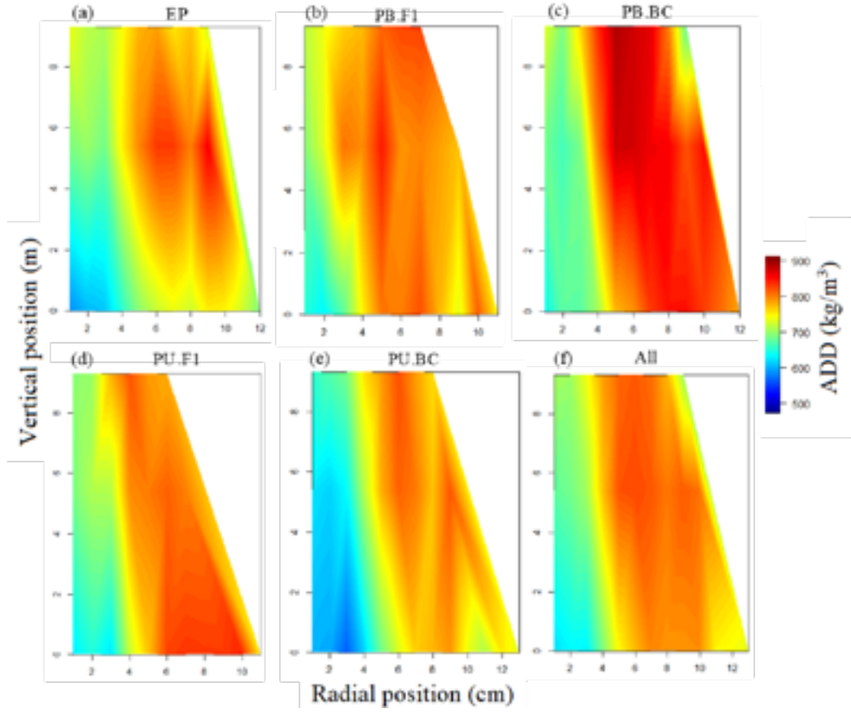


Figure 2c.2. Air-dry density (ADD) maps of *E. pellita* and its hybrids. Maps show (a) pure *E. pellita* (EP), (b) *E. pellita* × *E. brassiana* (F1), (c) *E. pellita* × *E. brassiana* (backcross), (d) *E. pellita* × *E. urophylla* (F1), (e) *E. pellita* × *E. urophylla* (backcross), and (f) all genotypes combined. Colour gradient indicates density values (kg/m³), with blue representing lower densities and red representing higher densities.

Cell wall thickness maps showed general increase from pith to bark with relatively small longitudinal variation (Fig. 2c.3). Thickest cell walls were typically observed in the upper stem at 5 m height, with whole-tree averages ranging from 2.6 to 3.0 µm across genotypes. Microfibril angle maps consistently showed decreasing values from pith to bark along the entire stem, with high MFA values (15–25°) observed at the lower stem close to the pith and low values (5–10°) near the bark (Fig. 2c.4). Pure *E. pellita* and *E. pellita* × *E. brassiana* (backcross) exhibited the narrowest whole-tree average MFA (9.3°), whilst *E. pellita* × *E. urophylla* (F1) showed the highest (11.9°).

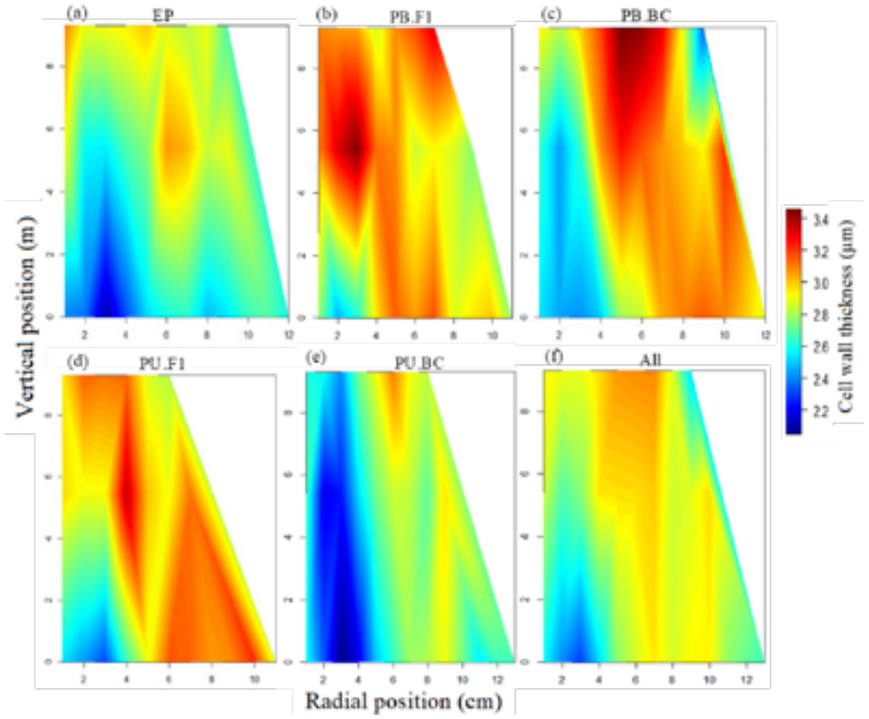


Figure 2c.3. Cell wall thickness (CWT) maps of *E. pellita* and its hybrids. Maps show (a) pure *E. pellita*, (b) *E. pellita* × *E. brassiana* (F1), (c) *E. pellita* × *E. brassiana* (backcross), (d) *E. pellita* × *E. urophylla* (F1), (e) *E. pellita* × *E. urophylla* (backcross), and (f) all genotypes combined. Colour gradient indicates cell wall thickness (µm), with blue representing thinner walls and red representing thicker walls. Thickest cell walls occur in upper stem regions, with relatively uniform patterns across genotypes.

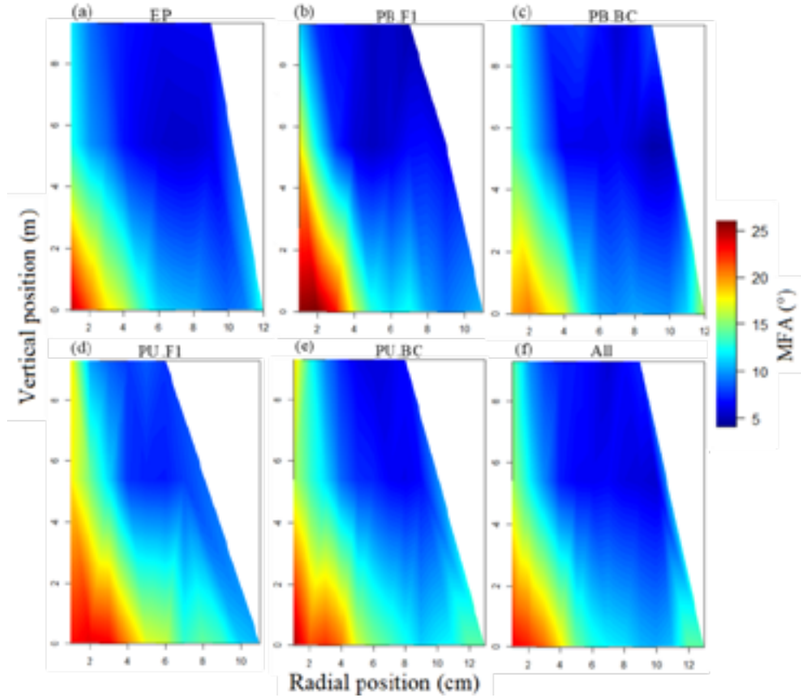


Figure 2c.4. Microfibril angle (MFA) maps of *E. pellita* and its hybrids. Maps show (a) pure *E. pellita*, (b) *E. pellita* × *E. brassiana* (F1), (c) *E. pellita* × *E. brassiana* (backcross), (d) *E. pellita* × *E. urophylla* (F1), (e) *E. pellita* × *E. urophylla* (backcross), and (f) all genotypes combined. Colour gradient indicates MFA (°), with blue representing lower angles and red representing higher angles. Consistent decrease from pith to bark is evident across all genotypes, with highest values at lower stem near pith.

Kraft pulp yield maps showed an increase in KPY from pith to bark along with tree height in most genotypes, with highest values observed at the upper stem starting at 4.5 m height (Fig. 2c.5). Whole-tree KPY ranged from 47.9% to 49.4% across genotypes. Klason lignin maps showed the highest lignin concentration at the lower stem (up to 2 m height), with *E. pellita* × *E. brassiana* (F1) exhibiting the lowest whole-tree KL values (27.1%) compared to other genotypes (Fig. 2c.6). Whole-tree KL content ranged between 27.1% and 29.8% across genotypes.

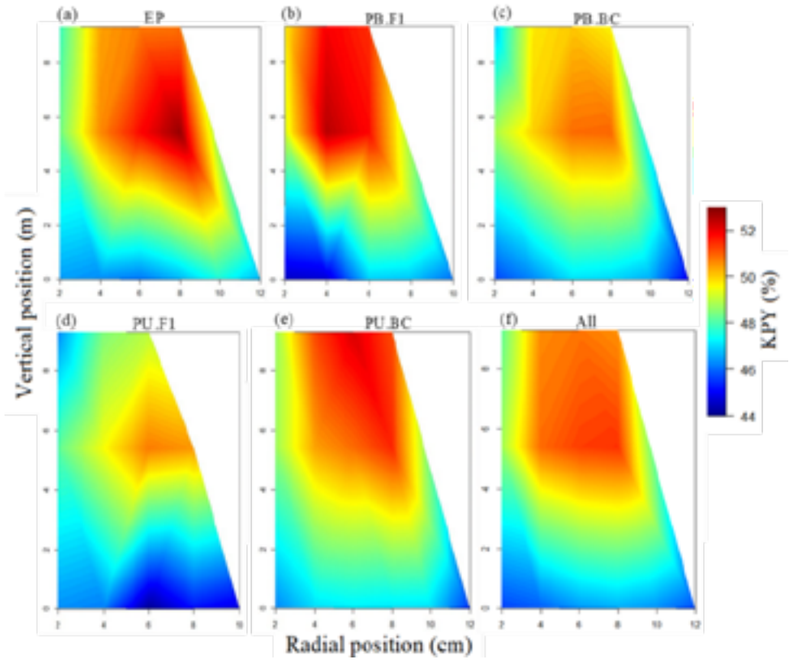


Figure 2c.5. Kraft pulp yield (KPY) maps of *E. pellita* and its hybrids. Maps show (a) pure *E. pellita*, (b) *E. pellita* × *E. brassiana* (F1), (c) *E. pellita* × *E. brassiana* (backcross), (d) *E. pellita* × *E. urophylla* (F1), (e) *E. pellita* × *E. urophylla* (backcross), and (f) all genotypes combined. Colour gradient indicates KPY (%), with blue representing lower yields and red representing higher yields. KPY increases from pith to bark and with increasing stem height, with highest values in upper stem regions.

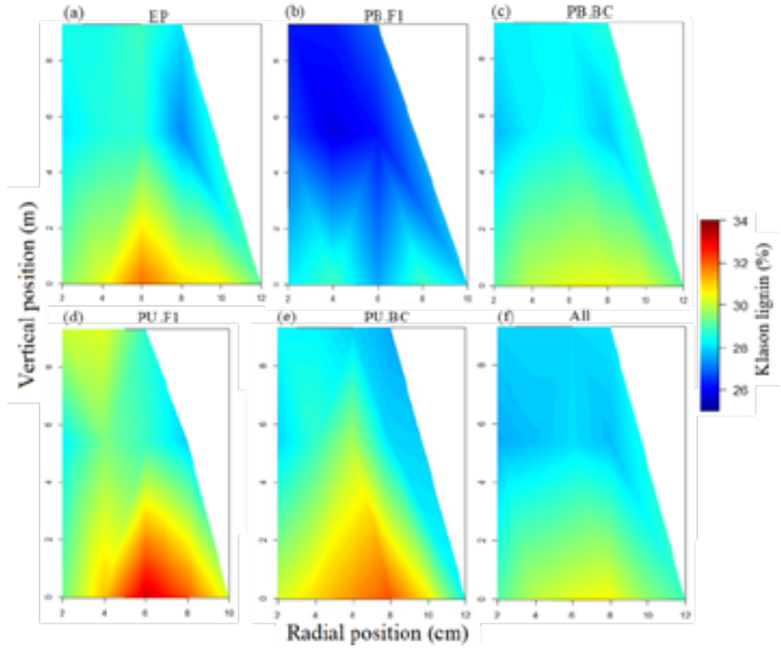


Figure 2c.6. Klason lignin (KL) maps of *E. pellita* and its hybrids. Maps show (a) pure *E. pellita*, (b) *E. pellita* × *E. brassiana* (F1), (c) *E. pellita* × *E. brassiana* (backcross), (d) *E. pellita* × *E. urophylla* (F1), (e) *E. pellita* × *E. urophylla* (backcross), and (f) all genotypes combined. Colour gradient indicates KL (%), with blue representing lower lignin content and red representing higher lignin content. Highest lignin concentrations occur at lower stem regions, with relatively uniform patterns across genotypes.

Prediction accuracy for all traits using maps developed for the combined dataset was consistently high, with MAPE values below 9% at whole-tree and sampling height positions (Table 2c.3). Air-dry density showed slightly higher error values at whole-tree level (RMSE 70.7 kg/m^3), whilst other traits showed minimal deviation between predicted and observed values.

Parameter	Predicted	Actual	RMSE	MAPE
ADD (kg/m³)				
Whole tree	759.4	830.09	70.7	8.52
Top (9.3 m)	764.1	770	5.95	8.52
Middle (5.4 m)	774.3	799.19	24.94	3.12
Bottom (0 m)	739.4	754.38	15	1.99
CWT (µm)				
Whole tree	2.8	2.84	0.01	0.32
Top (9.3 m)	2.9	2.89	0.24	0.82
Middle (5.4 m)	2.9	2.92	0.04	1.53
Bottom (0 m)	2.7	2.77	0.05	1.82
MFA (°)				
Whole tree	10.1	10.89	0.82	7.53
Top (9.3 m)	7.3	7.99	0.66	8.26
Middle (5.4 m)	7.8	8.08	0.27	3.34
Bottom (0 m)	14.3	15.07	0.75	4.98
KPY (%)				
Whole tree	49.1	48.32	0.74	1.54
Top (9.3 m)	50	50.47	0.45	0.88
Middle (5.4 m)	50.6	51.10	0.53	1.04
Bottom (0 m)	46.3	46.13	0.13	0.28
KL (%)				
Whole tree	28.56	28.86	0.3	1.5
Top (9.3 m)	27.99	28.01	0.02	0.08
Middle (5.4 m)	27.87	27.82	0.05	0.18
Bottom (0 m)	30.0636	29.71	0.35	1.19

Table 2c.3. Prediction accuracy of whole-tree wood properties for all *E. pellita* genotypes at different tree levels. Predicted values were calculated from whole-tree maps. Actual values represent weighted tree properties from measured data. RMSE: root mean squared error; MAPE: mean absolute percentage error (%).

Predicting whole-tree properties from breast-height measurements

Linear regression models were developed to predict whole-tree wood properties from breast-height measurements, providing a practical approach for non-destructive assessment of standing trees. Models predicting whole-tree Klason lignin, microfibril angle, and cell wall thickness achieved the highest predictive strength (R^2 = 0.88, 0.87, and 0.85, respectively), whilst kraft pulp yield (R^2 = 0.76) and Resi basic density (R^2 = 0.67) showed comparatively lower but still acceptable predictive accuracy (Fig. 2c.7). These relationships demonstrate that breast-height pith-to-bark measurements can reliably predict whole-tree averages, supporting the feasibility of using breast-height sampling for rapid wood quality assessment in standing trees.

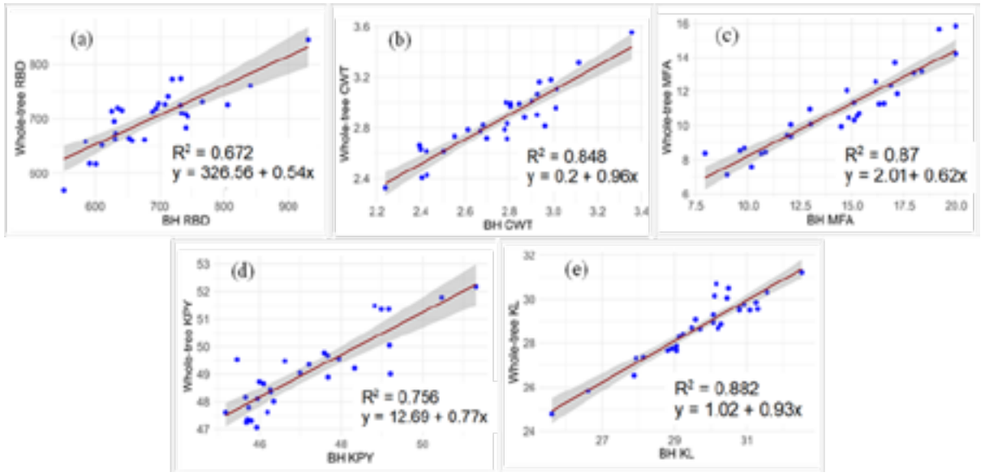


Figure 2c.7. Prediction of whole-tree wood properties from breast-height measurements. Scatter plots with linear regression lines show relationships between breast-height (BH) and whole-tree properties for (a) Resi basic density (RBD, R^2 = 0.67), (b) cell wall thickness (CWT, R^2 = 0.85), (c) microfibril angle (MFA, R^2 = 0.87), (d) kraft pulp yield (KPY, R^2 = 0.76), and (e) Klason lignin (KL, R^2 = 0.88). Blue dots represent individual tree measurements; red lines show linear regression fits with 95% confidence intervals (shaded grey areas).

Interrelationships among wood properties

Correlation analysis revealed significant relationships among wood properties that reflect shared developmental and functional controls (Fig. 2c.8). Resi basic density and air-dry density showed consistent strong positive correlation across all stem positions ($p \leq 0.001$ for whole-tree and bottom/middle stem; $p \leq 0.01$ for top stem). Resi basic density and kraft pulp yield exhibited positive correlations, with significance at whole-tree ($p \leq 0.05$) and middle stem ($p \leq 0.001$) levels. Kraft pulp yield and microfibril angle displayed significant negative correlation in most categories ($p \leq 0.001$), indicating that lower microfibril angles (stiffer wood) are associated with higher pulp yields. Klason lignin showed significant positive correlation with microfibril angle at whole-tree level ($p \leq 0.001$) and negative correlation with both kraft pulp yield ($p \leq 0.001$ for whole-tree; $p \leq 0.01$ for top stem) and cell wall thickness at whole-tree level ($p \leq 0.05$). Cell wall thickness showed consistent significant positive correlation with Resi basic density and air-dry density across all categories. Negative correlations between microfibril angle and mechanical properties, and between kraft pulp yield and lignin content, reflect functional trade-offs in wood formation.

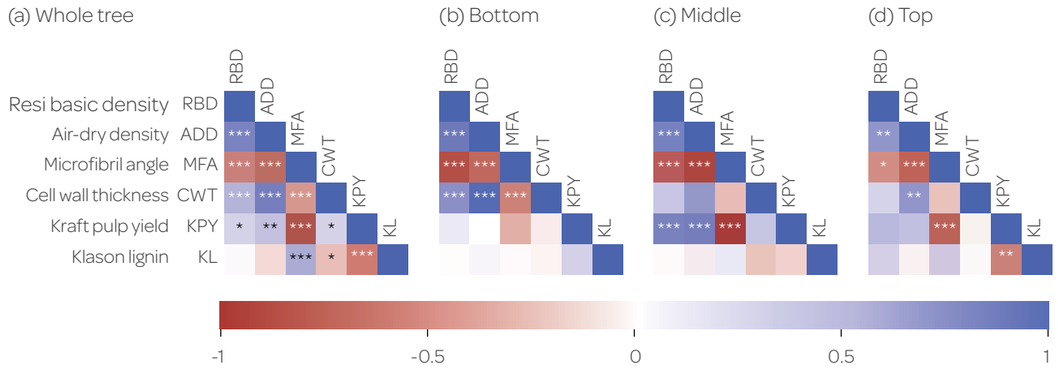


Figure 2c.8. Correlation matrices among selected wood properties at (a) whole-tree, (b) bottom stem, (c) middle stem, and (d) top stem levels. Colour gradient indicates correlation strength and direction: blue represents positive correlations, red represents negative correlations. Asterisks denote significance levels: ***p ≤ 0.001; **p ≤ 0.01; *p ≤ 0.05.

Multiple-trait predictive models

Multiple-trait predictive models were developed to estimate chemical properties (Klason lignin and kraft pulp yield) from field-based non-destructive measurements (Resi basic density and DBH). For predicting whole-tree Klason lignin, the best-performing model incorporated Resi basic density and DBH as predictors, explaining 40.5% of variation with RMSE of 1.1% (Table 2c.4). Including additional anatomical traits (cell wall thickness and microfibril angle) improved model fit to 45.3% variance explained, but the improvement was modest, suggesting that Resi basic density and DBH remain the most influential predictors.

Model	Predictor	Equation	R2	RMSE	AIC
LM_KL1	RBD	WH KL = 25.609 + (0.005*BH RBD)	0.065	1.385	110.88
LM_KL2	RBD, DBH	WH KL = 22.796 + (0.24*DBH) + (0.002*BH RBD)	0.405	1.104	**99.0**(1)
LM_KL3	RBD, DBH, CWT	WH KL = 21.362 + (0.263* DBH) + 0.464* BH CWT + (0.002* BH RBD)	0.409	1.101	100.91(3)
LM_KL4	RBD, CWT	WH KL = 30.671 + (0.005*BH CWT) + (0.002*BH RBD)	0.185	1.293	108.57
LM_KL5	RBD, DBH, CWT, MFA	WH KL = 20.257 + (0.276*DBH) + (0.188*BH CWT) + (0.097*BH MFA) + (0.002*BH RBD)	0.453	1.059	**100.57**(2)
LM_KPY1	RBD	WH KPY = 53.68 – (0.007*BH RBD)	0.144	1.3	**106.86**(3)
LM_KPY2	RBD, DBH	WH KPY = 54.61 + (0.079*DBH) – (0.006*BH RBD)	0.183	1.27	107.47
LM_KPY3	RBD, DBH, CWT	WH KPY = 61.96 – (0.193*DBH) – (2.379* BH CWT) + (0.004* BH RBD)	0.280	1.192	**105.66**(2)
LM_KPY4	RBD, CWT	WH KPY = 55.12 + (0.006*BH CWT) – (0.004*BH RBD)	0.155	1.292	108.49
LM_KPY5	RBD, DBH CWT, MFA	WH KPY = 63.89 – (0.216*DBH) – (1.895*BH CWT) – (0.17*BH MFA) – (0.005*BH RBD)	0.422	1.068	**101.07**(1)

Table 2c.4. Generalised linear models for predicting whole-tree Klason lignin (KL) from breast-height properties. Models show predictor variables, regression equations, coefficient of determination (R^2), root mean squared error (RMSE), and Akaike Information Criterion (AIC) values. Lower AIC values indicate better model fit. WH: whole-tree; BH: breast-height.

For kraft pulp yield prediction, the best single-predictor model using Resi basic density alone explained 14.4% of variation. However, incorporating additional predictors (DBH, cell wall thickness, and microfibril angle) substantially improved model performance, explaining 42.2% of variation with reduced RMSE (1.1%) and AIC (101.07). This indicates that anatomical traits provide valuable additional information for predicting kraft pulp yield beyond density measurements alone. Overall, these models demonstrate that simple field-based measurements can effectively estimate laboratory-derived chemical properties, providing an efficient approach for rapid wood quality assessment in plantation forestry.

Key Findings

Whole-tree mapping feasibility: Akima's interpolation method effectively maps whole-tree wood properties in *E. pellita* and its hybrids using only three sampling heights (bottom, middle, top), with prediction accuracy comparable to approaches using more sampling points.

Radial and longitudinal patterns: Radial wood property patterns are generally similar across genotypes, with air-dry density, cell wall thickness, and fibre coarseness increasing from pith to bark, whilst microfibril angle decreases. Upper stem exhibits greater variability than lower stem.

Breast-height predictability: Breast-height pith-to-bark measurements reliably predict whole-tree averages (R^2 = 0.67–0.88), supporting the use of breast-height sampling for non-destructive wood quality assessment in standing trees.

Trait interrelationships: Strong correlations among wood properties reflect shared developmental controls, with density measures positively correlated, and microfibril angle negatively correlated with mechanical properties and kraft pulp yield.

Predictive model performance: Multiple-trait models incorporating Resi basic density, DBH, cell wall thickness, and microfibril angle effectively predict chemical properties (Klason lignin and kraft pulp yield), explaining 40–45% of variation with practical feasibility for plantation management.

Recommendations for Plantation Management and Processing

Wood quality assessment: Breast-height sampling using non-destructive tools (Resi for density, SilviScan for anatomical properties, NIRS for chemical composition) provides sufficient accuracy for predicting whole-tree wood properties and can support rapid quality assessment in standing trees.

Processing optimisation: Understanding within-tree variation in wood properties enables processors to optimise log allocation and processing strategies based on stem position and radial location, potentially improving recovery and product quality.

Breeding strategies: The demonstrated ability to predict whole-tree properties from breast-height measurements supports the integration of wood quality assessment into breeding programs, enabling more efficient selection of superior genotypes for specific end-use applications.

2d. Identifying candidate genes controlling growth and wood quality traits of *Eucalyptus pellita*

Improving wood quality requires understanding the genetic basis of wood traits—that is, which genes control the development of desirable wood properties. Traditional breeding approaches rely on selecting trees with superior phenotypes (observable characteristics), but this is slow and labour-intensive. Modern genomic approaches using DNA markers can accelerate breeding by identifying genetic variants associated with desirable traits, enabling marker-assisted selection of superior genotypes before they reach maturity. However, for *E. pellita*, the genetic control of complex wood quality traits remains largely unknown. Previous studies have identified genes associated with growth traits, but comprehensive investigation of genes controlling anatomical, physical, mechanical, and chemical wood properties is lacking. Additionally, understanding which genes influence multiple traits simultaneously (pleiotropy) can explain why growth and wood quality traits are often correlated, and can inform breeding strategies to balance these objectives. This section uses association analysis to identify candidate genes significantly associated with growth and wood quality traits in a large population of *E. pellita* trees. By determining which genes control wood properties and understanding their biological functions, we can identify opportunities for genetic improvement using marker assisted selection, and potentially support future genetic engineering approaches to enhance wood quality in this commercially important species.

Objectives

To identify candidate genes associated with growth and wood quality traits in *E. pellita* through genetic association studies (GAS) using single nucleotide polymorphisms (SNPs), and to understand the biological functions and pathways underlying wood formation and trait variation.

Methods and Results

Study population and phenotypic data

A total of 1,502 *E. pellita* trees from two plantation trial sites on Melville Island were assessed for growth traits (diameter at breast height, height, volume) and wood quality traits (anatomical, physical, mechanical, and chemical properties). Wood quality traits were measured using non-destructive testing methods including SilviScan (for anatomical properties such as cell wall thickness, fibre diameter, microfibril angle, and air-dry density), near-infrared spectroscopy (NIRS, for chemical properties including kraft pulp yield, lignin, and cellulose content), and IML-Resistograph (Resi, for wood density and mechanical properties including modulus of elasticity and acoustic wave velocity). A total of 5,328 SNP markers were used for genetic association analysis.

Genome-wide association analysis identified 348 significant SNPs

Association analysis using the FarmCPU (Fixed and Random Model Circulating Probability Unification) model identified 348 SNPs significantly associated with growth and wood quality traits at a stringent Bonferroni threshold ($\alpha = 0.05$, $p < 9.38 \times 10^{-6}$) (Fig. 2d.1). These SNPs were distributed across four growth traits (121 SNPs) and twelve wood quality traits (227 SNPs), explaining between 0.13% and 2.43% of phenotypic variance. Growth-related traits (diameter, height, volume) showed the highest number of significant associations (121 SNPs), explaining 1.78–2.43% of phenotypic variance. Wood density traits (measured by Resi and SilviScan) had 137 significant SNPs explaining 1.77–2.19% of variance. Mechanical properties (modulus of elasticity and acoustic wave velocity) were associated with 72 SNPs explaining 1.47–2.07% of variance. Anatomical traits (microfibril angle and fibre coarseness) had 16 SNPs explaining 0.13–1.92% of variance. Chemical traits (Klason lignin) showed only 2 significant SNPs explaining 2.11% of variance. Notably, kraft pulp yield, extractives content, total lignin, cell wall thickness, and fibre diameter showed no significant associations under the stringent Bonferroni threshold, suggesting these traits may require larger sample sizes or different analytical approaches for detection.

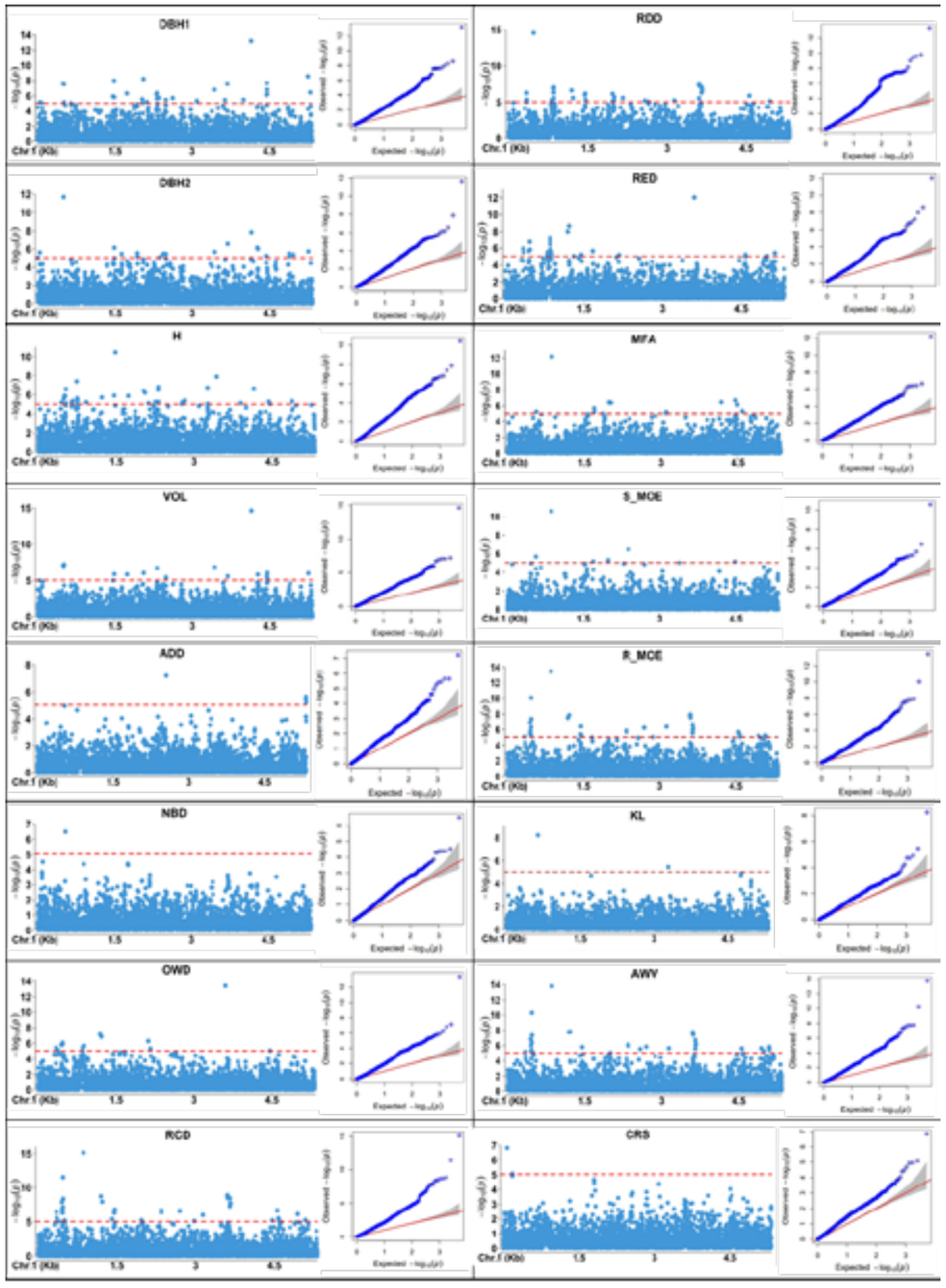


Figure 2d.1. Manhattan plots and quantile-quantile (QQ) plots from genome-wide association analysis. Manhattan plots show the distribution of SNP associations across the genome for selected traits, with the dashed red line indicating the significance threshold (Bonferroni-corrected $p < 9.38 \times 10^{-6}$) with dots above being considered significant. QQ plots compare observed versus expected p-value distributions, with the solid red line representing the expected null distribution. The QQ plots demonstrate good agreement between observed and expected distributions, indicating appropriate model calibration. DBH1: diameter at breast height at 9 years, DBH2: diameter at breast height at 10 years, H: tree height at 9 years, VOL: tree volume at 9 years, MFA: microfibril angle, ADD: air-dry density, NBD: NIRS-derived basic density, OWD: outer wood basic density, RCD: Resi core basic density, RDD: Resi disk basic density, RED: Resi entry basic density, CRS: fibre coarseness, KL: Klason lignin, R_MOE and S_MOE: modulus of elasticity/wood stiffness derived from Resi and SilviScan, respectively.

Annotation identified 112 candidate genes

All 348 significant SNPs were annotated by aligning marker positions with the *Eucalyptus grandis* reference genome, resulting in identification of 112 candidate genes. The SNPs were distributed across different genomic regions: 60% in intron variants (non-coding regions), 10% in intergenic regions, 9% missense variants, 8% synonymous variants, 5% in 5′ untranslated regions (5′ UTR), 3% in 3′ untranslated regions (3′ UTR), 2% intragenic, 2% splice region, and 1% stop gained variants. The predominance of non-coding variants suggests that regulatory rather than structural changes may be driving phenotypic variation in wood traits.

Comparison of significant genes across traits revealed substantial overlap, with 98 genes identified in total (Fig. 2d.2). Several genes were associated with multiple traits, indicating pleiotropic effects. For example, Eucgr. F00593 (gibberellin-regulated family protein, GASA11) was significantly associated with five traits (acoustic wave velocity, growth traits, wood density, microfibril angle, and modulus of elasticity). Other genes showed associations with specific trait combinations: twelve genes were shared between wood density and both modulus of elasticity and acoustic wave velocity, whilst three additional genes were shared among these three traits and microfibril angle. Forty genes were associated with growth-related traits, with some overlapping with wood quality traits. These overlapping associations suggest coordinated genetic control of growth and wood properties.

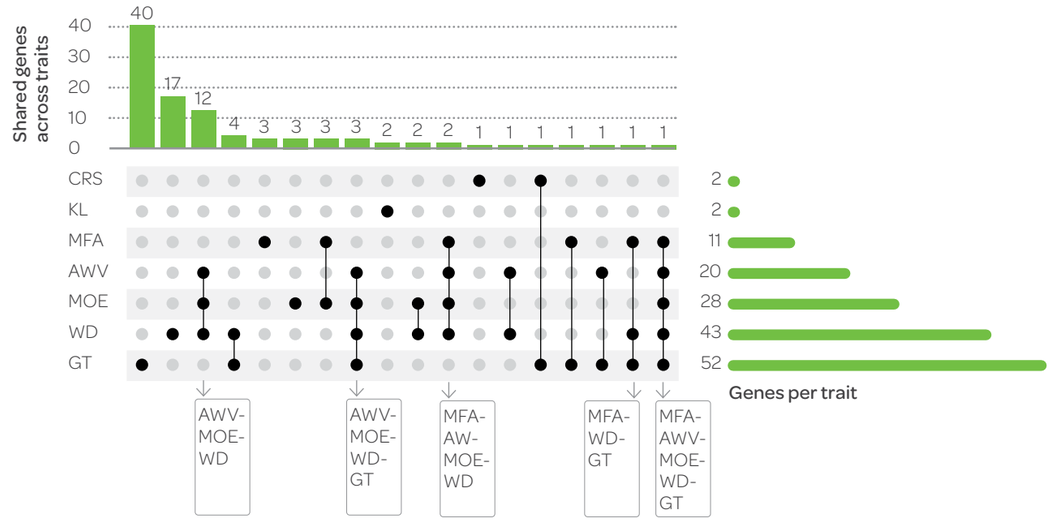


Figure 2d.2. Diagram showing overlap of genes associated with different wood traits. Connected dots indicate overlapping trait categories that share common genes, whilst single dots represent genes associated with a single trait. WD: wood density (RCD, RED, OWD, RDD, ADD, NBD); GT: growth traits (DBH, height, volume); MOE: modulus of elasticity; AWV: acoustic wave velocity; CRS: fibre coarseness; MFA: microfibril angle; KL: Klason lignin. The diagram demonstrates substantial pleiotropy, with many genes influencing multiple traits simultaneously.

Gene ontology enrichment revealed biological pathways

Gene ontology (GO) enrichment analysis identified 31 significantly enriched biological process terms, 19 molecular function terms, and 8 cellular component terms (Fig. 2d.3). The most frequently represented GO terms were protein binding, metabolic process, GTP binding, multicellular organism development, and catalytic activity. Genes associated with growth traits and fibre coarseness showed similar representation in metabolic process and catalytic activity GO terms. Genes linked to Klason lignin were predominantly involved in multicellular organism development, whilst microfibril angle-related genes were annotated in transmembrane and monoatomic cation transport. Genes associated with multiple traits (wood density, modulus of elasticity, and acoustic wave velocity) showed strong representation in nucleotide binding and metal ion binding GO terms.

Gene ontology biological process



GO:0034755 iron ion transmembrane transport
GO:0007018 microtubule-based movement
GO:0007017 microtubule-based process
GO:0043413 macrotubule glycosylation
GO:0030036 actin cytoskeleton organisation
GO:0009100 glycoprotein metabolic process
GO:0034220 monoatomic ion transmembrane transport
GO:0098662 inorganic cation transmembrane transport
GO:0000045 autophagosome assembly
GO:0006812 monoatomic cation transport
GO:0006811 monoatomic ion transport
GO:0006486 protein glycosylation
GO:0097435 supramolecular fibre organisation
GO:0009101 glycoprotein biosynthetic process
GO:0098655 monoatomic cation transmembrane transport
GO:0042168 heme metabolic process
GO:0098660 inorganic ion transmembrane transport
GO:0016236 macroautophagy
GO:0006826 iron ion transport
GO:G000041 transition metal ion transport
GO:0007015 actin-filament organisation
GO:0030029 actin-filament-based process
GO:007008S glycosylation
GO:0055085 transmembrane transport
GO:0006779 porphyrin-containing compound biosynthetic
GO:0046148 pigment biosynthetic process
GO:0030042 actin filament depolymerisation

Gene ontology molecular function



GO:0005381 iron ion transporter activity
GO:0008324 monoatomic cation transmembrane transport
GO:0008378 gatactosyltransferase activity
GO:0015631 tubulin binding
GO:0046915 transition metal ion transmembrane transporter
GO:0015075 monoatomic ion transmembrane transporter
GO:0008092 cytoskeletal protein binding
GO:0003777 microtubule motor activity
GO:0008017 microtubule binding
GO:0003774 cytoskeletal motor activity
GO:0022857 transmembrane transporter activity
GO:0005215 transporter activity

Gene ontology cellular component



GO:0005856 cytoskeleton
GO:0015630 microtubule cytoskeleton
GO:0030137 COP I-coated vesicle
GO:0005871 kinesin complex
GO:0015629 actin cytoskeleton
GO:0030663 COPI-coated vesicle membrane

Figure 2d.3. Frequency of significantly enriched genes according to gene ontology (GO) term classification. Bars show the number of genes (indicated inside bars) associated with each GO term, colour coded by GO category. Enrichment was determined using Fisher's exact test ($p < 0.05$).

Hierarchical analysis of enriched GO terms revealed three major functional clusters (Fig. 2d.4). The biological process hierarchy showed specialisation from general cellular and localisation processes to metal and iron ion transport, with the final node strongly overrepresented in iron ion transmembrane transport pathways (FDR = 0.0002). The molecular function hierarchy identified three main clusters: ion transport and metal-cation binding, catalytic enzymes, and cytoskeletal protein binding. Pathways that emerged included ion transporters (ion and metal cations), polysaccharide biosynthesis, and cytoskeletal interactions involving tubulin and microtubule protein binding. Cellular component analysis showed genes with highest enrichment in cytoskeleton (FDR = 0.001) and microtubule cytoskeleton (FDR = 0.02).

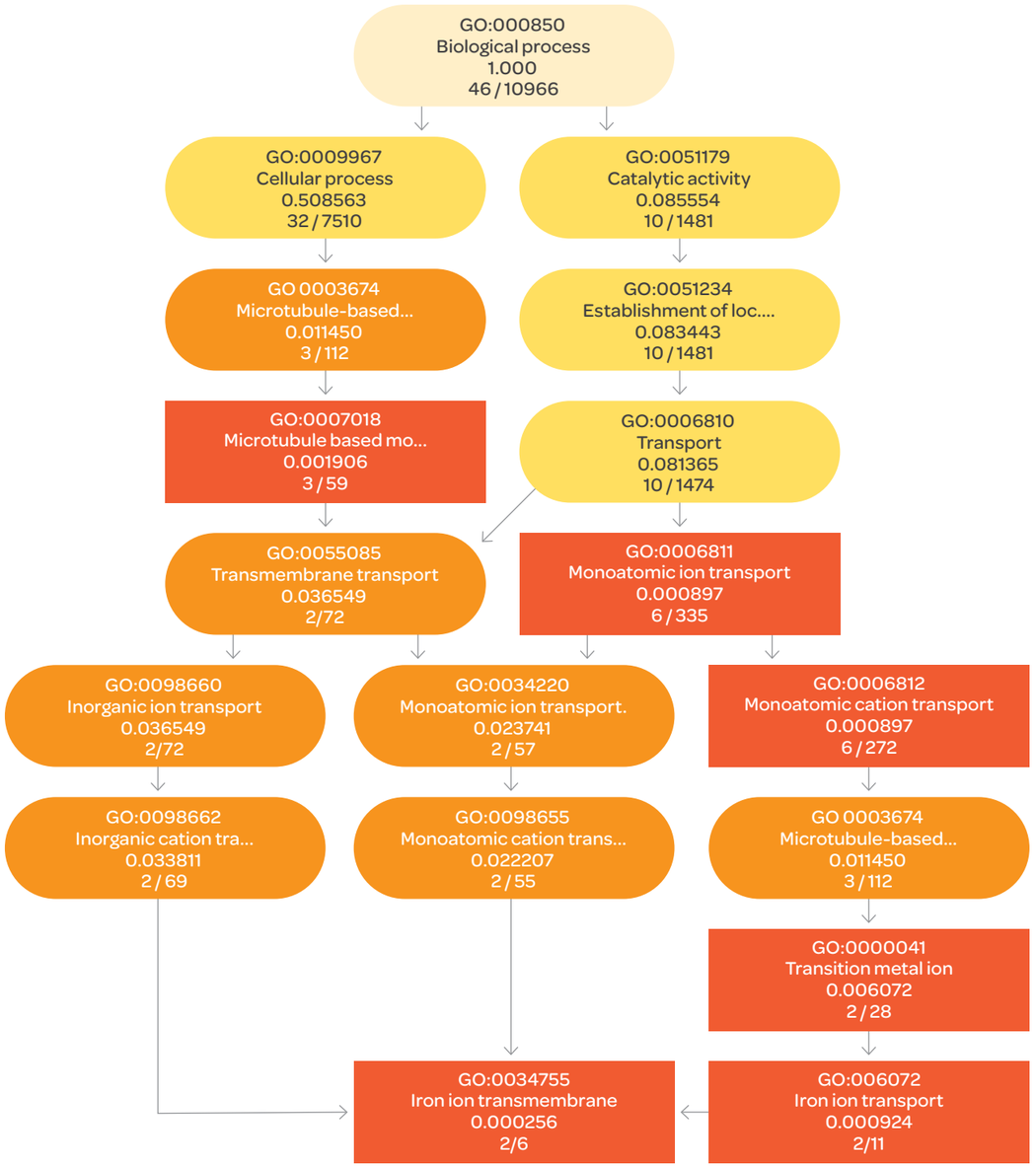


Figure 2d.4. Hierarchical structure of significantly enriched gene ontology biological process terms (FDR < 0.01). Rectangles indicate GO terms, with colour representing relative significance (dark red = most significant; bright yellow = least significant). Each node shows the GO identifier, GO name, FDR-adjusted p-value (Benjamini-Hochberg correction), and the number of significant genes annotated to that term.

Gene co-expression network analysis identified hub genes

Gene co-expression network analysis using normalised expression data from different plant tissues (xylem, tension wood xylem, leaves, roots, flowers) identified hub genes, resulting in 50 genes with strong network connectivity (Fig. 2d.5). Gene families with highest intermodular connectivity included GASA11 (gibberellin-regulated family protein), MRH1, DUF547, IRX14-L (irregular xylem 14-like), NAT9, CH, Eucgr.E03247, DUF707, FL2 (forked-like 2), and HGPT1. GASA11 showed the highest degree of connectivity, linked to 22 genes including the other nine top gene families. IRX14-L, associated with wood density, modulus of elasticity, and acoustic wave velocity, was predominantly linked to growth trait-related genes but also connected to wood density, modulus of elasticity, and acoustic wave velocity trait-related genes including CH, PATL3, and GA2, as well as microfibril angle-related genes such as Eucgr.E03247 and GASA11.

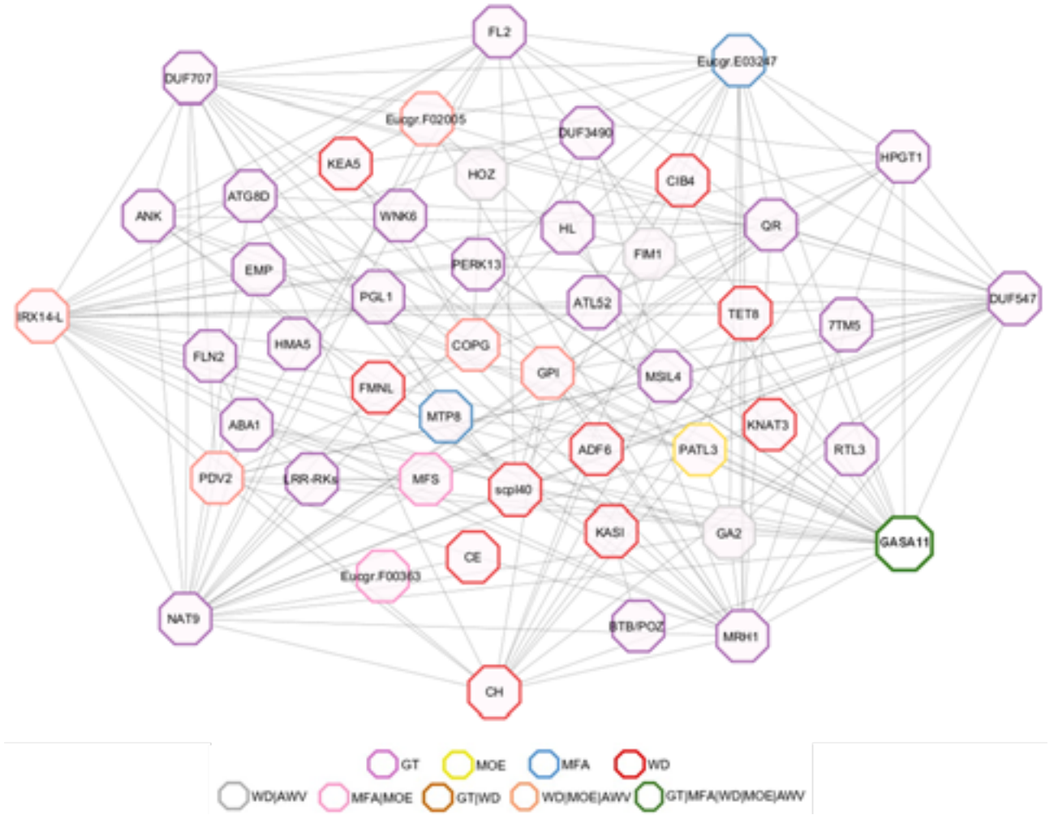


Figure 2d.5. Gene co-expression network of highly connected hub genes significantly associated with wood traits. Coloured octagon nodes represent genes associated with different wood trait categories: GT (growth traits), MOE (modulus of elasticity), MFA (microfibril angle), WD (wood density), AWV (acoustic wave velocity), and combinations thereof. Grey edges depict co-expression relationships between genes.

Key Findings

Significant SNP-trait associations: Association analysis identified 348 SNPs significantly associated with growth and wood quality traits, with growth traits showing the highest number of associations and chemical traits showing the fewest.

Candidate genes identified: The 348 SNPs were annotated into 112 candidate genes, with 60% located in non-coding regions (introns), suggesting regulatory rather than structural variation drives phenotypic differences.

Pleiotropic effects: Multiple genes were associated with more than one trait, indicating shared genetic control of growth and wood properties. GASA11 (gibberellin-regulated family protein) was associated with five traits, suggesting coordinated regulation of multiple wood quality characteristics.

Biological pathways: Gene ontology enrichment revealed genes involved in secondary cell wall biosynthesis, cytoskeletal development, metal ion transport (particularly iron), and hormone signalling pathways.

Gene co-expression networks: Hub genes with highest connectivity include GASA11, IRX14-L, FL2, and other genes involved in cell wall biosynthesis and hormone signalling, indicating coordinated regulation of wood formation processes.

Implications for Tree Improvement

Understanding trait correlations: The pleiotropic effects of genes controlling multiple traits explain the observed correlations among growth and wood properties. Understanding these genetic correlations can inform breeding strategies to balance growth with wood quality objectives.

Functional genomics: The identified candidate genes involved in secondary cell wall biosynthesis, cytoskeletal development, and hormone signalling provide targets for functional genomics studies to confirm their roles in wood formation and potentially enable genetic engineering approaches to improve wood quality.

Breeding strategy optimisation: The identification of genes with stable associations across multiple traits suggests that selection for these genes could simultaneously improve multiple wood quality characteristics, increasing breeding efficiency.

2e. Genotype x Environment interaction of *E. pellita* populations on Tiwi

Productivity of a tree plantation is dependent on-site conditions such as the environment and soil. Trees grown in favourable environments can produce large amounts of biomass in a relatively short time, maintaining their yield capacity over many years. However productivity can vary greatly from site to site, illustrating the importance of understanding the genetic characteristics of the planting material, and its interaction and response to site characteristics that can affect growth.

Genotype by environment (GxE) interaction in a population arise when genetic entities differ in their response to an array of environmental conditions. The patterns of response across environments involve both or either changes in the ranking of the genotypes and/or alterations in the scale. In forestry, GxE can led to unpredictability of some genotypes' performance across different environments, reducing heritability and overall genetic gains. When it occurs, GxE complicates the design of breeding programs but it also provides an opportunity for matching the most appropriate planting stocks to targeted deployment conditions to optimise forest health, growth and wood quality in intensively managed. Therefore, characterising and understanding GxE interactions of *E. pellita* on Tiwi, may lead to higher productivity when these optimal populations for suitable environments are identified.

Objectives

We looked at the growth traits and wood properties of 10 subpopulations of *E. pellita* at two locations to (i) determine whether GxE interactions exists between the subpopulations and sites assessed for the traits measured (growth and wood properties), and for traits that show significant GxE interactions (ii) evaluate the stability and adaptability of the tested subpopulations.

Due to the significant age difference between the 5 sites studied so far, investigations into GxE interactions for the traits measured was conducted as two separate assessments; Firstly, GxE interactions were investigated at KI64 and YP28 as these stands were established in the same year (2012), and the ten subpopulations are represented at both sites. Different soil types were reported at these two sites (Table 1). The second assessment was performed at Y48, A3b and I18, where two subpopulations were represented at these three sites (P6 and P9), and the sites differed by reported soil type, and A3b had a higher annual rainfall compared to I18 and Y48 (Table 1).

GxE interactions at KI64 and Y48

Initial visual assessment of trees at KI64 and Y28 suggested that the trees at Y28 appeared to be smaller and have less dense canopies than those at K64. The stand floor at Y28 also had substantial grass growth, whereas KI 64 had none (Fig 2e.1). Both sites were reported to have the same annual rainfall (1200-1400 mm per annum), however YP28 appeared to be the dryer site.



Figure 2e.1. Yapilika 28 (left) and Kilu Impini 64 (right).

As reported in Section 2a (Growth traits and wood properties of the 10 subpopulations at KI64 and Y28), significant differences in all but three measured traits (KPY, total lignin and density measured by Resi) exist between KI64 and Y28, indicating that site has a significant influence on the growth and wood properties of the trees grown on these two sites (Table 2e.1). And significant differences were also detected between the ten subpopulations for all the traits measured, suggesting that the tree's genotype also contributed to its performance with regard to the measured traits. The genotypes contributed to most of the variability seen in all the traits (as determined by sum of squares) except for Bark thickness, where site was determined to have the main effect.

Two-way ANOVA results (Table 2e.1) show that the interaction between site and subpopulations to be statistically significant for height, as well as for the wood properties measured by NIRS including, Basic Density, Klason Lignin, Extractives and Total lignin. These findings suggest that for these five traits, differential response of the genotypes across the two site exists, therefore indicating that GxE interactions are significant for these five traits at KI64 and Y28.

Table 2e.1. Two-way ANOVA table of main effects for 10 subpopulations of *E. pellita* across 2 sites, KI64 and Y48.

Source of variation	df	Sum of squares	Mean squares	F-value	p-level (>F)
Height					
Genotypes	9	1937.2	215.24	14.223	<0.001
Environments	1	1628.1	2628.08	173.658	<0.001
Interactions (GxE)	9	304.8	33.87	2.2379	0.018 (<0.05)
Residuals	1373	20778.5	15.13		
NIRS Cellulose					
Genotypes	9	377.9	41.986	11.7457	<0.001
Environments	1	137.2	137.241	38.394	<0.001
Interactions (GxE)	9	16.5	1.828	0.512	0.867
Residuals	1373	4907.9	3.575		
NIRS Basic Density					
Genotypes	9	130570	14508	15.428	<0.001
Environments	1	56893	56893	60.504	<0.001
Interactions (GxE)	9	18829	2092	2.225	0.018 (<0.05)
Residuals	1373	1291077	940		
NIRS KYP					
Genotypes	9	1085.0	120.554	14.263	<0.001
Environments	1	30.2	30.201	3.573	0.059
Interactions (GxE)	9	108.8	12.093	1.431	0.170
Residuals	1373	11604.7	8.452		
NIRS Klason Lignin					
Genotypes	9	135.3	15.029	5.408	<0.001
Environments	1	62.5	62.545	22.506	<0.001
Interactions (GxE)	9	49.1	5.455	1.963	0.040 (<0.05)
Residuals	1373	3815.6	2.779		
NIRS Extractives					
Genotypes	9	148.9	16.541	6.8407	<0.001
Environments	1	14.5	14.489	5.9920	0.015 (<0.05)
Interactions (GxE)	9	52.1	5.792	2.3953	0.011 (<0.05)
Residuals	1373	3320.0	2.418		
NIRS Total Lignin					
Genotypes	9	43.53	4.837	2.485	0.008 (<0.01)
Environments	1	0.12	0.121	0.062	0.803
Interactions (GxE)	9	38.16	4.240	2.178	0.021 (<0.05)
Residuals	1373	2672.31	1.946		

Source of variation	df	Sum of squares	Mean squares	F-value	p-level (>F)
Resi DBHOB					
Genotypes	9	1797.3	199.7	11.027	<0.001
Environments	1	1311.3	1311.34	72.408	<0.001
Interactions (GxE)	9	131.0	14.55	0.804	0.613
Residuals	1373	24865.7	18.11		
Resi Bark Thickness					
Genotypes	9	300	33.336	4.868	<0.001
Environments	1	128.9	128.926	18.826	<0.001
Interactions (GxE)	9	53.9	5.984	0.874	0.548
Residuals	1373	9402.8	6.848		
Resi Core Density					
Genotypes	9	358896	39877	20.375	<0.001
Environments	1	2426	2426	1.240	0.266
Interactions (GxE)	9	148879	1653	0.845	0.575
Residuals	1373	2687142	1957		
Resi DBHUB					
Genotypes	9	1589.5	176.61	11.547	<0.001
Environments	1	1264.0	1263.99	82.639	<0.001
Interactions (GxE)	9	109.8	12.20	0.798	0.618
Residuals	1373	21000.6	15.30		
Resi PrAWV					
Genotypes	9	14.204	1.578	17.676	<0.001
Environments	1	0.023	0.023	0.260	0.610
Interactions (GxE)	9	0.770	0.086	0.958	0.474
Residuals	1373	122.592	0.089		
Resi Pr MOE					
Genotypes	9	3451.4	383.49	18.608	<0.001
Environments	1	11.1	11.12	0.5395	0.463
Interactions (GxE)	9	140.9	15.66	0.760	0.654
Residuals	1373	28296.3	20.61		

AMMI analysis: Biplots of genotype-environment interactions

The Additive Main Effects and Multiplicative Interaction (AMMI) model is a quick and relevant tool to judge environmental behaviour and genotypic stability. It is a biplot based graphical unique linear-bilinear model, that combines both ANOVA for the genotype and environmental main effects and the PCA with multiplicative indices (Gauch 1989). The AMMI analysis provides a meaningful graphical representation or biplot to summarise information on the main effects and the first principal component scores of the interactions (IPCA1) of both genotype and environments, simultaneously, from which direct interpretation of the relationship between specific environments and between particular genotypes.

In an AMMI biplot, genotypes that are distributed near the origin have minimal interactions with the environment. And a genotype showing this low interaction with environment is considered to be stable over a range of environments. However, genotypes that are further away from the origin are more sensitive to interactions with the environment.

In our study, GxE interaction for height at KI64 and Y28 was significant. The AMMI biplot for height (Fig. 2e.2) also shows that subpopulation P9 has the highest mean height out of all ten subpopulations, whereas P10 has the lowest.

The AMMI biplot of Ht shows that P6 and P9 do not deviate far from the origin and are therefore considered to be stable genotypes for both sites KI64 and Y28, that these two subpopulations exhibited the same characteristics regardless of the environment. Whereas P10 deviated the furthest from the origin and is deemed the most unstable genotype. Subpopulations P8 and P3 have a positive associating with KI64, indicating that this site would be more favourable for these two genotypes with regard to height, whereas P2 would perform better on a site similar to Y28. The markers for P4 and P7 are positioned very close to each other suggesting these two genotypes present similar interaction patterns, and they are very different to P1 and P5.

A summary of the key findings from the AMMI biplots for the highest value for each trait is presented below in Table 2e.2.

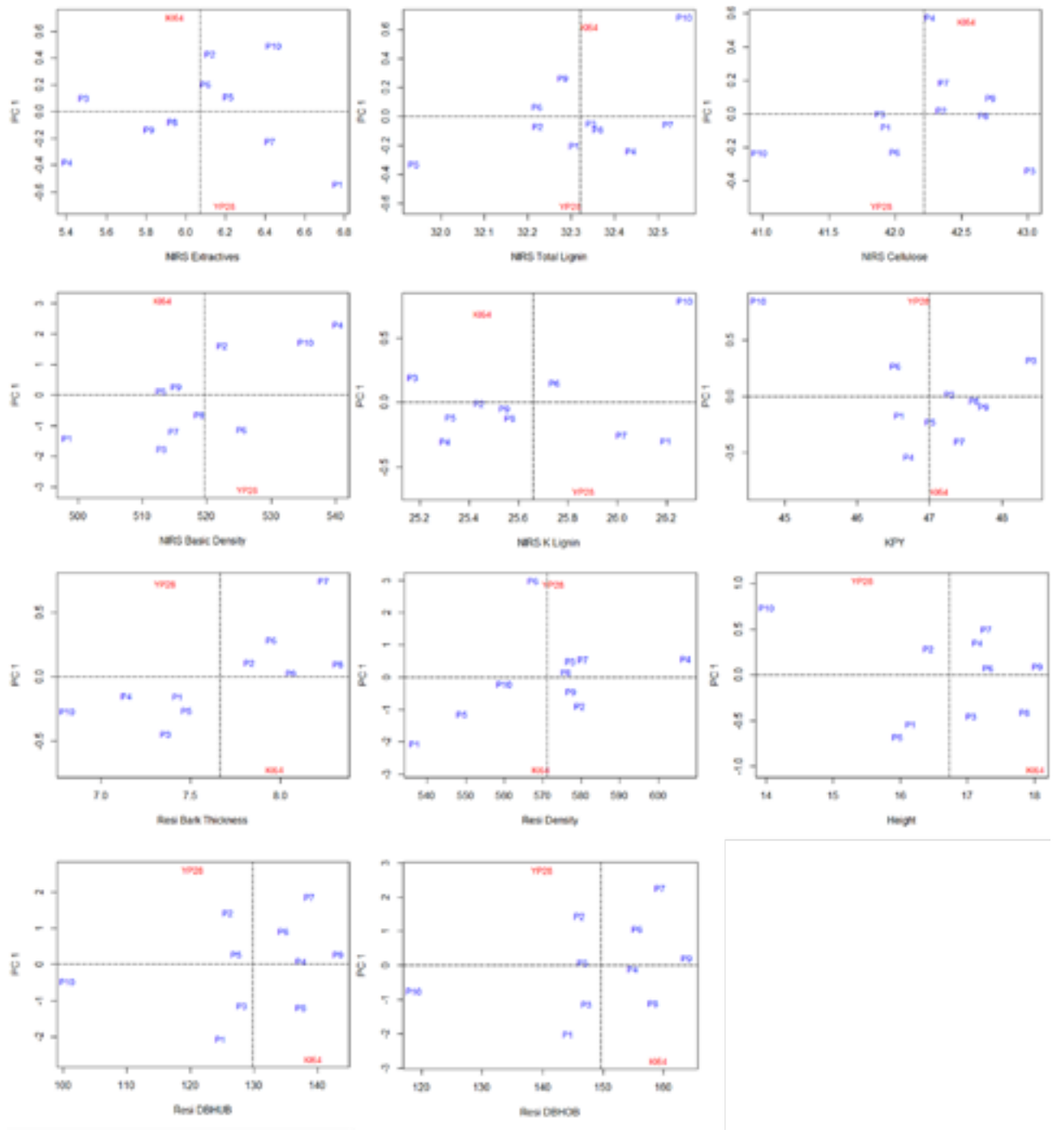


Figure 2e.2. AMMI Biplot for the primary component of interaction (PC1) and average growth and wood properties listed. Vertical line is the general grand mean for that trait. Displacement along the abscissa (x-axis) reflected differences in main effects (trait), whereas displacement along the ordinate (y-axis) exhibited differences in interaction effects.

Table 2e.2. Summary of key findings from AMMI analysis, showing best subpopulations for KI64 and Y28, for traits with the highest mean values.

Trait	Sub pop. with highest mean value	Sub pop. with lowest mean value	Stable sub pop.	Unstable Sub pop.	Best for KI64	Best for Y28
NIRs Basic Density	P4	P1	P5, P9	P4	P4	P6
NIRs KYP	P3	P10	P2, P8, P9	P10	P7	P3
NIRS Total Lignin	P10	P5	P3, P2, P6	P10	P9	P4
NIRs Klason Lignin	P10	P3	P2, P9	P10	P10, P6	P7
NIRs Extractives	P1	P4	P8	P1	P2, P10	P1, P7
NIRs Cellulose	P3	P10	P5, P2, P8	P4	P9	P3
DBHOB	P9	P10	P5, P4	P7	P8	P7
DBHUB	P9	P10	P5, P4	P7	P8	P7
Resi Density	P4	P1	P8, P10	P6	P2	P4
Bark Thickness	P8	P10	P9	P7	P5	P7
Height	P9	P10	P6, P9	P10	P8	P7

Summary/Key findings

The subpopulation/genotypes of the trees grown at KI64 and Y28 was determined to be responsible to most of the variability seen in all measured traits (expect bark thickness), therefore selecting the right genotype for future plantings is important to minimise variability in trait response. Significant differences were observed between sites for the traits measured, also illustrating the importance of selecting optimal sites for maximum tree performance.

Significant GxE interactions were identified for the following traits at KI64 and Y28; Height, NIRS Basic Density, Total Lignin, Klason lignin and Extractives. Therefore, for any future deployment of these subpopulations for these specific traits, consideration should be given for selecting the most favourable genotype specific to site, or utilising genotypes that were identified to be stable across KI64 and Y28.

The AMMI statistical model was used to diagnose the G × E interaction pattern of growth and wood properties of *E. pellita* subpopulations on Tiwi, and provided meaningful graphical displays of performance which allows growers to see the relationship between sites and genotypes. Depending on the trait of interest, subpopulations were identified that were either stable or unstable across the two sites assess, and the most favourable subpopulations were identified for each trait specific to site.

Limitations

A major limitation in the GxE assessment is that only two environments/sites were assessed. Testing these ten subpopulations across more diverse sites and environments would provide valuable information on the stability and/or adaptability of the tested genotypes.

Also, more detailed environmental and soil information about each of the sites needs to be obtained in order to develop a better understanding of the factors that contribute to the seen variation in traits between the sites as well as any significant GxE interactions that may exist. Currently we only have very general details of the soil type and annual rainfall from TCP maps, however detailed information on soil nutrient composition, ground water availability and accurate rainfall and temperature data specific to each site, will provide valuable information on what specific environmental factors are involved in any detected GxE interactions for the traits of interest. These then can be applied to other sites on Tiwi with similar environmental and climatic characteristics.

Recommendations

Based on the traits of interest, findings from the AMMI analysis can be utilised to select genotypes that are not sensitive to environmental changes or selecting genotypes specific to environments, in order to maximise expected gains resulting in higher stand productivity.

Establish research trials across various sites on Tiwi Islands to validate the performance of identified best seedlings in the nursery stage for species – site interaction & adaptability

GxE interactions at Y48, A3b and I18

Visual assessment of sites Y48, A3b and I18 showed that trees at Y48 were taller and straighter, and at A3b, trees appeared to be denser and lusher. Whereas I18 was very dry, with smaller trees and high tree mortality (Fig. 2e.3).



Figure 2e.3. Yapilika 48 (left), Andranangoo 3b (middle) and Imalu 18 (right).

Significant differences were observed between these three sites for height, density (NIRs and Resi) and wood properties including KPY, total lignin and cellulose content (Table 2e.3), indicating that the site these trees are grown at has a significant impact on these measured traits.

Trees at I18 were significantly smaller, less dense (Resi) than those at A3b and Y48, as well as having lower cellulose content, KPY, and higher density (NIRs).

In this GxE assessment, the environment/site was identified to be the main contributor to the variation seen in all measure traits at A3b, I18 and Y48, and not the two genotypes. Whereas genotype was determined to have the main effect at KI64 and Y28, where more genotypes were tested.

Significant differences were detected between the two subpopulations (P6 and P9) for only cellulose, KPY and density measured by NIRs. No significant genotype x environment interactions were identified at these three sites for the two subpopulations grown there.

Table 2e.3. Two-way ANOVA table of 2 genotypes across 3 sites, A3b, I18 Y48.

Source of variation	df	Sum of squares	Mean squares	F-value	p-level (>F)
Height					
Genotypes	1	1.9	1.94	0.073	0.788
Environments	2	1080.8	540.42	20.262	<0.001
Interactions (GxE)	2	49.5	24.73	0.927	0.398
Residuals	180	4801	26.67		
NIRS Cellulose					
Genotypes	1	11.18	11.175	4.588	0.034(<0.05)
Environments	2	64.36	32.178	13.211	<0.001
Interactions (GxE)	2	4.76	2.381	0.978	0.378
Residuals	180	438.43	2.436		
NIRS Basic Density					
Genotypes	1	6400	6400.3	10.033	0.002(<0.05)
Environments	2	12963	6481.3	10.160	<0.001
Interactions (GxE)	2	2082	1041.0	1.632	0.199
Residuals	180	114827			
NIRS KYP					
Genotypes	1	51.18	51.176	9.414	0.003(<0.05)
Environments	2	158.64	79.322	14.591	<0.001
Interactions (GxE)	2	5.98	2.991	0.550	0.578
Residuals	180	978.56	5.436		
NIRS Klason Lignin					
Genotypes	1	0.02	0.022	0.008	0.930
Environments	2	6.17	3.084	1.075	0.344
Interactions (GxE)	2	0.33	0.165	0.057	0.944
Residuals	180	516.47	2.869		
NIRS Extractives					
Genotypes	1	0.644	0.644	0.401	0.527
Environments	2	6.575	3.288	2.048	0.132
Interactions (GxE)	2	0.210	0.105	0.065	0.937
Residuals	180	288.928	1.605		
NIRS Total Lignin					
Genotypes	1	0.045	0.045	0.026	0.872
Environments	2	12.059	6.029	3.515	0.032(<0.05)
Interactions (GxE)	2	0.017	0.009	0.005	0.995
Residuals	180	308.686	1.715		

Source of variation	df	Sum of squares	Mean squares	F-value	p-level (>F)
Resi DBHOB					
Genotypes	1	1605	1605.4	0.429	0.513
Environments	2	10723	5361.6	1.434	0.241
Interactions (GxE)	2	3016	1507.9	0.403	0.669
Residuals	180	673248	3740.3		
Resi Bark Thickness					
Genotypes	1	11.42	11.417	1.435	0.233
Environments	2	16.88	8.439	1.061	0.348
Interactions (GxE)	2	7.07	3.536	0.444	0.6419
Residuals	180	1432.39	7.958		
Resi Core Density					
Genotypes	1	8817	8817	3.277	0.072
Environments	2	53892	26945.9	10.015	<0.001
Interactions (GxE)	2	1456	728.0	0.271	0.763
Residuals	180	484314	2690.6		
Resi DBHUB					
Genotypes	1	1242	1242	0.385	0.536
Environments	2	11006	5502.8	1.706	0.185
Interactions (GxE)	2	2320	1210.1	0.375	0.688
Residuals	180	580677	3226.0		
Resi PrAWV					
Genotypes	1	0.446	0.446	3.991	0.042(<0.05)
Environments	2	2.416	1.208	10.820	<0.001
Interactions (GxE)	2	0.095	0.048	0.426	0.654
Residuals	180	20.096	0.112		
Resi Pr MOE					
Genotypes	1	105.6	105.56	3.147	0.078
Environments	2	744.8	372.38	11.103	<0.001
Interactions (GxE)	2	9.6	4.80	0.143	0.867
Residuals	180	6037.2	33.54		

Findings

No significant GxE interactions were detected between subpopulations P6 and P9 at site A3b, Y48 and I18. However, the site at which these trees are grown at has a significant impact on growth traits such as height, and wood properties including density, KPY, total lignin and cellulose content. Trees at I18 underperformed for many traits, compared with trees at A3b and Y48.

Therefore, for future plantings of trees from subpopulations P6 and P9, site will have a significant influence of the tree's performance and sites similar to A3b and Y48 would be recommended.

3. Wood Products and Processing

This work program aimed to understand the genetic and phenotypic relationship between growth traits and wood property traits of *E. pellita* and hybrids grown on the Tiwi Islands in northern Australia. Wood properties were assessed and characterised across genotypes. Shrinkage was measured at different moisture levels in the tangential and radial directions, while mechanical properties were tested at different longitudinal (bottom, middle, top) and radial (inner, outer) positions. Wood recovery and resource quality were assessed through sawing and veneer peeling trials. As part of this program, options were developed for wood processing methods and product development.

To achieve these objectives, 10-year-old plantation trees were sampled from two sites: Kilu Impini 64, a high-productivity site, and Yapilika 28, a moderate-productivity site. A combination of physical and mechanical property testing, log conversion trials, and genetic association analysis was conducted. The study included *E. pellita* trees and hybrids from first- generation (F1) and backcrosses (BC) involving one parent species. Properties assessed included physical properties (density and shrinkage) and mechanical properties (modulus of elasticity (MOE), modulus of rupture (MOR), and compressive strength (CS), with mechanical properties measured radially and longitudinally. Phenotypic correlations were explored between wood properties, growth traits, and chemical and pulping properties. Genetic analysis was performed to identify single nucleotide polymorphism (SNP) markers linked to key wood traits. Sawing and veneer trials were conducted to evaluate recovery rates and defect patterns. LVL panels were fabricated using hybrid veneers and tested for strength, stiffness, and bond quality.

3.1 Methods

For this research program, trees with small-end diameters of ≥15 cm were purposively selected from each genotype group. From the full population of 1,500 trees, six individuals per genetic group, based on species classification from the initial hybrid identification analysis using LEA (Section 1a), were randomly chosen within three wood density classes ranging from low (≤550 kg/m³), medium (550 kg/m³ to 620 kg/m³) and high (≥620 kg/m³). This selection was independently carried out at both plantation sites to ensure balanced representation across density classes. Trees with defects such as multiple stems, termite damage, or decay were excluded, resulting in a final sample of 58 trees. These trees were felled at 10 years of age. In addition, four mother trees (approx. 30-year-old *E. pellita* trees) were selected and included in the present testing program. Assessing the properties of these "older" trees provided an indication of what the current plantation-grown *E. pellita* trials could be if left to grow to older age and has given an idea of how the properties of short-rotation *E. pellita* could be improved to have properties similar to older trees through breeding. Table 3.1 provides a summary of the selected trees by genotype group and plantation site.

Table 3.1: Selected trees from Kilu impini 64 and Yapilika 28 plantation sites according to genotype group for solid wood properties testing and processing trials.

Genotype	KILU IMPINI 64		YAPILIKA 28	
	Mechanical properties/ sawing trials	Peeling trials	Mechanical properties/ sawing trials	Peeling trials
E. pellita x *E. brassiana (BC)*	5	1	5	1
E. pellita x *E. brassiana (F1)*	5	1	5	-
E. pellita x *E. urophylla (BC)*	5	1	5	1
E. pellita x *E. urophylla (F1)*	5	1	5	-
E. pellita	5	1	5	1
Total	25	5	25	3
Total number of trees	58			
Mother trees	4			

Note: F1 is the first-generation tree and BC is the back cross (i.e., first-generation crossed with one of the parents which is *E. pellita*). Trees in the *E. pellita* x *E. brassiana* (F1) and *E. pellita* x *E. urophylla* (F1) genotype groups did not meet the selection criteria for peeling trials.

Trees for the determination of wood properties were selected according to standard practice for sampling forest trees for the determination of clear wood properties. Random sampling and cruciform sampling (secondary method) were used due to the small diameter of the plantation trees. Selection of the number of trees, number of billets, and collection of materials to be tested was carried out according to the steps outlined in ASTM D5536-17. Figure 3.1 shows the method of cutting up the billets.

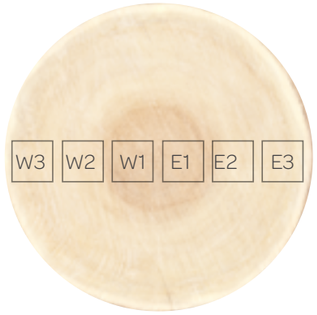
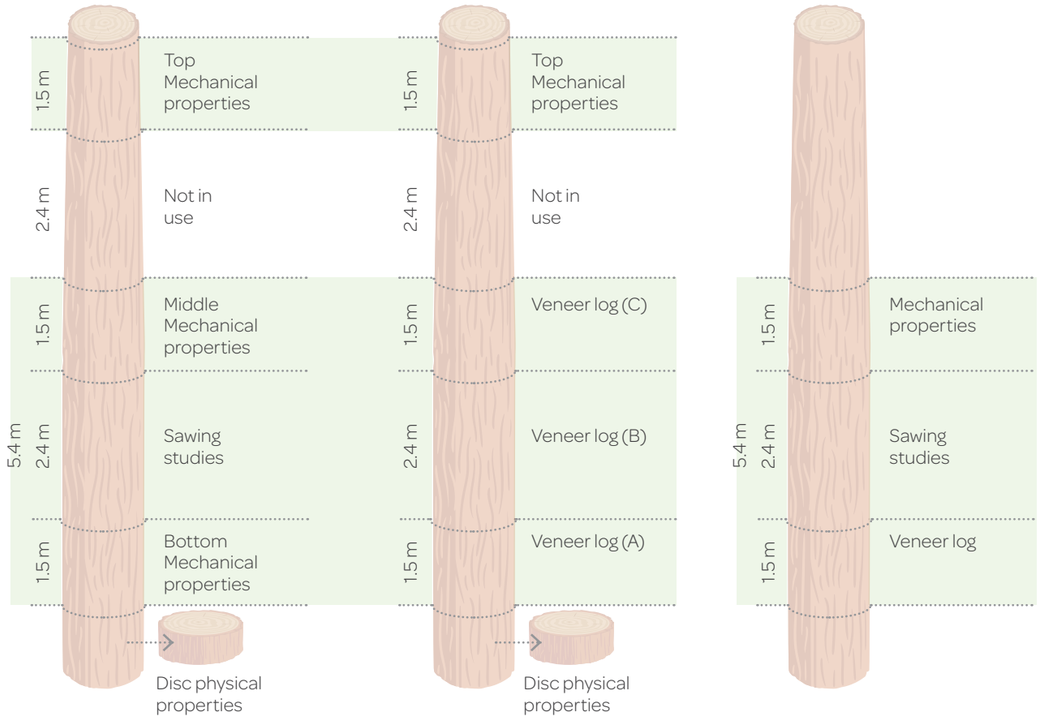


Figure 3.1: Method of cutting up the bolt and marking the sticks along the East (E) to West (W) axis (adapted from ASTM, 2017).

Tree samples were collected and prepared according to the plantation sites, genotype groups, and mature trees. Figure 3.2 illustrates the sampling and log breakdown procedures used for trial trees from different genotype groups at the Yapilika 28 and Kilu Impini 64 plantation sites, as well as mature *E. pellita* trees from the Bremer site. Each tree was sectioned to enable targeted assessment of physical, mechanical, and processing properties. For five trees per genotype group, a 50 mm-thick disc was collected at the base of the stem for physical property analysis. Following this, a 1.5 m billet was cut from the bottom portion, a 2.4 m segment was allocated for sawing studies, and another 1.5 m billet was taken to represent the middle position. After skipping a 2.5 m section to avoid overlapping zones, a final 1.5 m billet was taken from the upper stem to represent the top position. These billets were used to assess mechanical properties at different stem heights. In addition, one tree per genotype group was selected for peeling trials. From each of these, three 1.5 m veneer billets were collected from the bottom, middle, and top stem positions, along with a basal disc for physical property testing.

Four mature *E. pellita* trees (approximately 30 years old) from the Bremer site were also included as reference material. Given the limited number of mature trees, sample use was maximised. From each, a 5.4 m stem section was processed: the bottom 1.5 m was used for veneer peeling, the central 2.4 m for sawing studies, and the upper 1.5 m for mechanical testing, corresponding to the middle stem position of the younger trees. This sampling allowed for comparisons across genetic background, site productivity, and tree age. It provided valuable insights into how these factors influence wood properties and suitability for various end-use applications.



5 trees from each genotype group
Mechanical properties and sawing trials

1 tree from each genotype group
Peeling trials

Mother tree
Mechanical properties, sawing, and peeling trials

Figure 3.2: Collection of discs and billets from genotype trees and mother trees for physical properties (disc), mechanical properties, sawing, and peeling trials.

3.1.1 Tree Harvesting

Tree harvesting was carried out using chainsaws. The selected trees were felled and extracted to the roadside (Figure 3.3). Before debarking, discs were collected from the bottom. To preserve the moisture content, these discs were wrapped and stored in an insulated cooler for onward transportation. Debarking was performed at the roadside using two methods, manual debarking and mechanical debarking with a harvester head. Following debarking, the logs were crosscut into billets. The ends of each billet were sealed with end sealers and fitted with nail plates to minimise rapid moisture loss and reduce the risk of end splitting. The harvested logs were divided into lengths of 1.5 m and 5.4 m to facilitate transportation.



Figure 3.3: Tree harvesting activities, including identification and marking of selected trees (A); felling with a chainsaw (B and C); extraction of logs to the roadside (D); collection and storage of discs (E); manual debarking (F); debarking with a harvester head (G); identification of debarked logs (H); application of seal and nail plates (I); and loading for transportation (J).

3.1.2 Sawmilling

Back sawing, also referred to as flat sawing, where the growth rings intersect the surface of the board at an angle generally less than 45° has been favoured for its high recovery rate and efficiency, yielding wider boards and arched grain patterns that are highly valued for their decorative appeal. After deposition of harvested logs at the sawmill, the logs were placed at the log yard under a water sprinkler system to release internal stresses and to minimise the rate of surface drying in preparation for milling. The logs were placed under the water sprinkling system for 8 weeks before the commencement of the milling operation. Sawmilling was performed using a portable sawmill (LUCAS mill, Model 6-18) (Figure 3.4). Logs were crosscut into smaller billet sizes. Billets were backsawn to an initial board thickness of 35 mm to allow for shrinkage and machining during drying and dressing processes. This approach ensured sufficient material for producing final board thicknesses suitable for mechanical testing and product evaluation.



Figure 3.4: Sawmilling operations showing cross-cut billets (A), under a water sprinkling system (B), portable LUCAS mill (C), back-sawing (D), and stacked sawn boards (E).

3.1.3 Drying

After sawing operations, the sawn boards were moved to an air-drying shed. They were air-dried following the recommended drying schedules for Australian hardwood species. After reaching the appropriate intermediate moisture content, the boards were kiln-dried using an industrial kiln drier to a final target moisture content, 12%. After kiln drying, the boards were rip-sawn and dressed prior to subsequent quality assessment (Figure 3.5). This process ensured compliance with standards required for mechanical testing and engineered wood product fabrication.



Figure 3.5: Drying and processing of sawn boards: air-drying under an air-drying shed (A); kiln drying (B); and boards after rip-sawing and dressing (C).

3.1.4 Determination of Dimensional Stability of *E. pellita* and Hybrids

Dimensional stability refers to a wood's ability to maintain its original dimensions when exposed to changes in moisture content. It is a critical property for sawn timber and EWPs, as wood tends to shrink or swell with fluctuations in environmental humidity. From the discs collected during harvesting, tangential and radial samples were extracted and subjected to a series of conditioning steps, including moisture adjustment, reconditioning, and oven-drying (Figure 3.6). Samples were measured in the green state, then conditioned to 17%, 12%, and 5% moisture content (MC) under controlled temperature and relative humidity conditions. At each stage, samples were allowed to reach equilibrium moisture content (EMC) before weight and dimensions were recorded. A reconditioning step was included at 12% MC using an autoclave to relieve drying stresses. Shrinkage was measured at each MC stage (17%, 12% before and after reconditioning, and 5%), and unit shrinkage was calculated in both tangential and radial directions. In addition, green density, oven dry density, and basic density were determined.



Figure 3.6: Determination of dimensional stability: unwrapping of round wood discs (A and B); collection of tangential and radial samples (C); conditioning in the conditioning room (D) and conditioning chamber (E); reconditioning using an autoclave (F); reconditioned test samples (G); followed by final conditioning and oven drying (H).

3.1.5 Determination of Strength Properties of *E. pellita* and Hybrids

In this study, sample collection for mechanical testing was adapted from the standard clear wood sampling procedures as stated in ASTM D-5536 (Figure 3.7). After kiln drying the sawn boards, samples for bending and compressive strength testing were prepared and conditioned in the conditioning room. Sapwood proportion for each sample was determined using iodine and potassium iodide solution in a 2:1 ratio. The solution was applied to the cross-sectional surface of each sample to measure the sapwood area was then measured (Figure 3.8). The samples were subsequently conditioned to 12% moisture content. Mechanical testing was performed using a universal testing machine (UTM) equipped with appropriate load cells and fixtures. For bending tests, boards were placed on supports and loaded at mid-span using a three-point bending setup to determine MOE and MOR (Figure 3.9). For compression tests, small clear specimens were loaded axially until failure to determine compressive strength parallel to the grain (Figure 3.10).

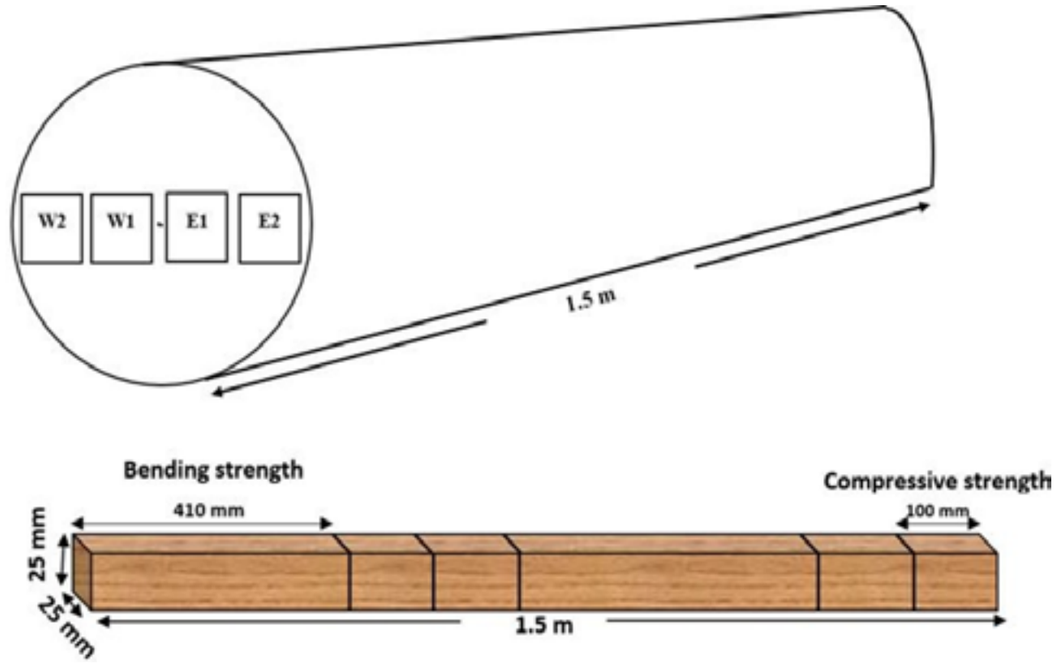


Figure 3.7: Schematic diagram showing test sample collection.

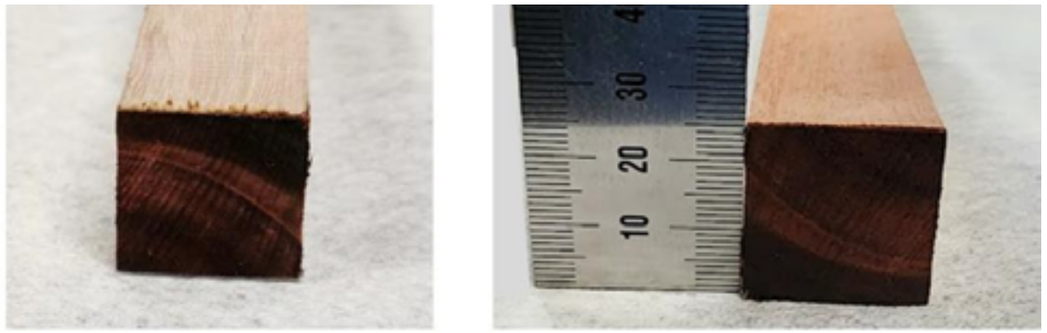


Figure 3.8: Determination of sapwood proportion on test samples

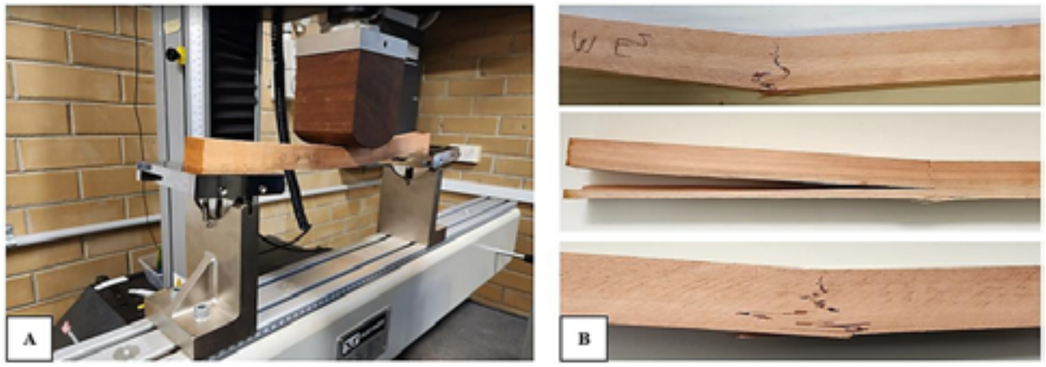


Figure 3.9: 3-point bending test (A) and tension surface failure in bending test (B).

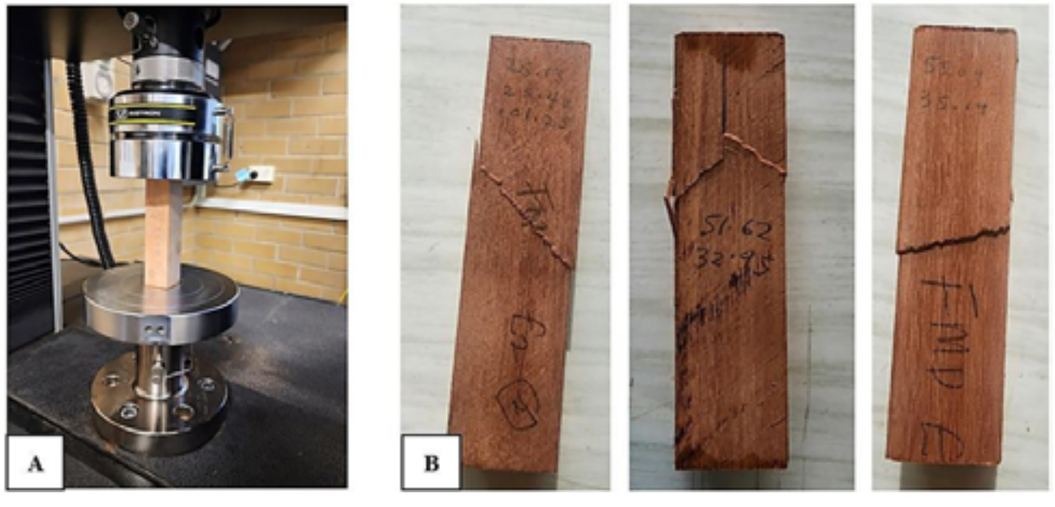


Figure 3.10: Compression test parallel to grain (A) and failures in compression test (B).

3.1.6 Log Traits Determination

Log traits were measured on logs selected for sawing and rotary peeling trials to assess their influence on wood recovery and product quality. The traits evaluated included heartwood and sapwood proportion, knot diameter and frequency, taper, sweep, and end splits. Measurements were taken using a measuring rule, tape, and calliper. Heartwood and sapwood areas were assessed from log cross-sections, while knots were evaluated based on their size and frequency along the log surface. Taper was calculated from diameter measurements at both ends of the log, and sweep was measured as the maximum deviation from a straight axis. End splits were recorded by measuring the length and depth of cracks at the log ends (Figure 3.11). Understanding the variability in these traits helps guide more informed log selection. This improves sawing and peeling recovery. It also contributes to the production of higher-grade structural and veneer products.



Figure 3.11: Log traits including heart to sap wood proportion (A), end splits (B), taper (C), knot diameter (D), and sweep (E).

3.1.7 Recovery and Quality Assessment of Veneer

Veneers were produced from *E. pellita* and its hybrids using the rotary peeling method with a spindle lathe. Green measurements were recorded immediately after peeling (Figure 3.12). The veneers were then conditioned and dried. After drying, the rotary-peeled veneers were visually inspected and graded into quality classes based on surface appearance and the presence of defects. This grading process distinguished veneers suitable for high-grade structural applications from those intended for non-structural or core layers. After grading, veneer samples (500 mm x 500 mm) were collected for LVL fabrication and oven dried at 40 °C to a moisture content of 8 - 12%.



Figure 3.12: Peeling operations which involved rounding of veneer logs (A); steaming (B); peeling (C); clipped veneer (D); measurement of green veneer (E); and veneer ribbon (F).

3.1.8 Manufacture of Laminated Veneer Lumber

5-ply LVL panels were fabricated from rotary-peeled veneers of *E. pellita* and its hybrids. Veneers were graded, dried, glued, assembled, and pressed according to standard LVL production procedures (Figure 3.13). The resulting LVL samples were then prepared for mechanical property testing and bond quality evaluation.

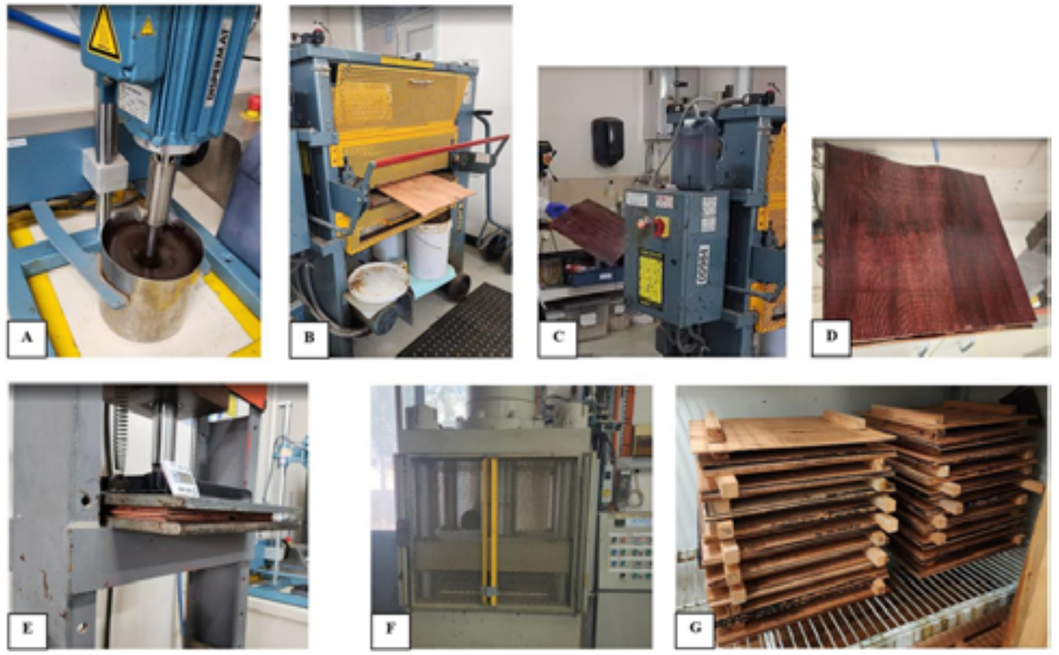


Figure 3.13: Laminated veneer lumber fabrication process showing preparation of adhesive (A); adhesive application via roller coating on both surfaces (B and C); adhesive-coated veneer (D); cold pressing (E); hot pressing (F); and conditioning (G).

Mechanical testing of LVL samples was conducted following AS/NZS 4357. Test specimens were conditioned to 12% moisture content (MC) before testing. A three-point bending test was used to determine the moduli of elasticity and rupture (Figure 3.14). Bond quality was assessed following AS/NZS 2098. Samples were conditioned before testing. The bond quality evaluation involved steaming and the chisel test. (Figure 3.15).



Figure 3.14: Laminated veneer lumber sample for three-point bending test (A) and testing setup (B).



Figure 3.15: Bond quality test samples (A); steaming process (B); chisel test (C); and veneer sheets showing bond line failure (D).

3.1.9 Sawn Timber Recovery and Visual Grading

Sawn timber recovery was assessed to evaluate the efficiency of converting logs into usable boards and to determine the quality of the resulting sawn products. Logs were sawn using conventional back-sawing or through-sawing methods, depending on log characteristics and dimensions, with the aim to maximise recovery and produce boards suitable for structural and appearance-grade applications. After sawing, the sawn recovery rate was calculated by comparing the volume of usable boards to the original log volume. Board volumes were determined based on their measured dimensions (thickness, width, and length). Recovery rates were analysed to understand how log traits such as diameter, straightness, taper, and defects influenced sawn yield. Subsequently, visual assessment of sawn board characteristics was conducted. Boards were assigned structural grades, including Structural Grade No. 1, No. 2, No. 3, No. 4, and appearance grades based on specific visual criteria. The grading criteria included the size, length, and frequency of defects such as knots, borer holes, termite galleries, slope of grain, heartwood presence, heart shakes, gum veins, ring shakes, bow, and twist, among others. After grading, variations in structurally graded lumber were evaluated to identify patterns related to the initial log properties. This analysis aimed to provide insights into key factors affecting product quality, allowing for better resource allocation and targeted plantation management practices to enhance both yield and timber quality.

3.2 Results and Discussion

3.2.1 SNP-Based Genetic Analysis of Dimensional Stability and Wood Density in *Eucalyptus pellita* and Hybrids

The study revealed variation in shrinkage and density among *Eucalyptus pellita* and its hybrids, influenced by both genetic background and site conditions. As expected, tangential shrinkage exceeded radial shrinkage across all taxa, reflecting wood's well-known anisotropic behaviour (Table 3.1). For instance, *E. pellita* × *E. urophylla* (F1) recorded the lowest unit shrinkage at Kilu Impini 64 (0.16% tangential, 0.08% radial), while *E. pellita* × *E. brassiana* (F1) showed the highest values in the tangential direction (0.21%). These findings suggested that *E. urophylla* hybrids have the potential to offer superior dimensional stability. Reconditioning consistently reduced shrinkage across hybrids, indicating its effectiveness in relieving internal stresses and enhancing the dimensional stability of the wood, thereby improving overall product quality. While density values varied among genotypes (e.g., 587–781 kg/m^3 oven-dry at Kilu Impini 64), differences within each site were often not statistically significant, possibly due to uniform site conditions (Table 3.2). Across all hybrids and sites, green, oven-dry, and basic densities ranged from 1,041 to 1,156 kg/m^3, 582 to 781 kg/m^3, and 526 to 643 kg/m^3, respectively, with hybrids involving *E. brassiana* consistently exhibiting the higher values, pointing to a favourable genetic effect for wood strength.

Shrinkage was negatively correlated with tree height and diameter, indicating that faster growth may reduce dimensional stability (Figure 3.16). Meanwhile, higher wood density was positively correlated with shrinkage, highlighting the challenge of simultaneously maximising both strength and stability. Chemical traits such as lignin content and extractive content also showed negative correlations with shrinkage in the radial direction, implying that wood composition contributes to dimensional behaviour.

From the genetic analysis, moderate diversity was observed across the population, with individual heterozygosity values ranging from 0.30 to 0.35. Only one SNP (SNP2554) surpassed the significance threshold ($-\log_{10}(p) > 5$) for tangential shrinkage at 12% moisture content after reconditioning. However, several others, including SNP4963 and SNP2981, showed consistent associations with shrinkage and density traits across different conditions (Tables 3.3-3.4). These markers represent promising candidates for future validation and potential use in marker-assisted selection.

These findings emphasised the complexity of managing trade-offs between rapid growth and wood stability. For breeding programs, the findings emphasised the importance of considering both site conditions and genotype interactions when targeting optimised, stable, and industrially valuable wood products. This is supported by the lack of significant differences in shrinkage among hybrids at Kilu Impini 64, in contrast to the significant variation observed at Yapilika 28, highlighting the strong influence of site-specific environmental factors on trait expression.

Table 3.1: Means, LSD, and p-values for shrinkage values among the hybrids at Kilu Impini 64 (KI64) and Yapilika 28 (YP28) plantation sites.

Plantation sites/Hybrids	Green to 17% (%)		Green to 12% BR (%)		Green to 12% AR (%)		Green to 5% (%)		Unit shrinkage (%)	
	T	R	T	R	T	R	T	R	T	R
KI64										
E. pellita	2.31 [a]	1.20 [a]	4.00 [a]	2.16 [a]	3.00 [a]	1.45 [a]	6.14 [a]	4.67 [a]	0.20 [a]	0.18 [a]
E. pellita x *E. brassiana* (BC)	3.86 [a]	1.60 [a]	5.27 [a]	2.71 [a]	4.34 [a]	2.34 [a]	6.67 [a]	4.58 [a]	0.19 [a]	0.15 [a]
E. pellita x *E. brassiana* (F1)	4.09 [a]	1.75 [a]	5.70 [a]	3.30 [a]	4.26 [a]	2.60 [a]	7.49 [a]	4.79 [a]	0.21 [a]	0.13 [a]
E. pellita x *E. urophylla* (BC)	2.33 [a]	1.49 [a]	3.95 [a]	2.95 [a]	2.96 [a]	2.02 [a]	5.76 [a]	4.09 [a]	0.19 [a]	0.13 [a]
E. pellita x *E. urophylla* (F1)	3.48 [a]	1.42 [a]	5.05 [a]	2.36 [a]	4.05 [a]	1.99 [a]	6.65 [a]	3.27 [a]	0.16 [a]	0.08 [a]
LSD (p=0.05)	2.14	0.85	2.18	1.45	2.08	1.40	1.69	2.22	0.07	0.10
LSD (p=0.05) - Tukey	3.15	1.22	3.16	2.08	3.06	2.01	2.42	3.18	0.10	0.14
p-value	0.15	0.62	0.23	0.41	0.27	0.41	0.20	0.60	0.68	0.24
YP28										
E. pellita	2.01 [a]	1.42 [a]	3.54 [a]	2.56 [a]	2.86 [a]	2.13 [a]	6.04 [a]	4.69 [a]	0.21 [a]	0.15 [a]
E. pellita x *E. brassiana* (BC)	3.29 [a]	1.36 [a]	4.88 [a]	2.51 [a]	3.11 [a]	1.87 [a]	6.93 [a]	3.54 [a]	0.22 [a]	0.11 [a]
E. pellita x *E. brassiana* (F1)	6.83 [b]	3.01 [b]	8.06 [b]	4.21 [a]	7.09 [b]	3.84 [a]	8.70 [b]	4.56 [a]	0.11 [b]	0.09 [a]
E. pellita x *E. urophylla* (BC)	2.30 [a]	1.29 [a]	3.92 [a]	2.68 [a]	2.99 [a]	2.28 [a]	6.28 [a]	4.59 [a]	0.22 [a]	0.16 [a]
E. pellita x *E. urophylla* (F1)	3.63 [a]	1.57 [a]	4.88 [a]	2.44 [a]	3.94 [a]	2.14 [a]	6.47 [a]	4.85 [a]	0.16 [a]	0.18 [a]
LSD (p=0.05)	2.00	0.94	1.93	1.44	1.72	1.46	1.63	2.65	0.05	0.15
LSD (p=0.05) - Tukey	2.88	1.35	2.78	2.08	2.49	2.11	2.35	3.84	0.07	0.22
p-value	0.00	0.00	0.00	0.01	0.00	0.00	0.02	0.55	0.00	0.45

* F1, first generation; BC, back cross; B.R., Before reconditioning; A.R., After reconditioning; T, Tangential; R, Radial. Level of significance (p<0.05), Confidence level used = 0.95, hybrids that are not significantly different from each other have the same letter while hybrids that are significantly different from each other have different letters (based on the Tukey LSD)

Table 3.2: Means, LSD, and p-values for density values among the hybrids at Kilu Impini 64 (KI64) and Yapilika 28 (YP28) plantation sites.

Plantation sites/Hybrids	Green density (kg/m³)		Oven dry density (kg/m³)		Basic density (kg/m³)	
	T	R	T	R	T	R
KI64						
E. pellita	1,085 [a]	1,044 [a]	701 [a]	589 [a]	593 [a]	531 [a]
E. pellita x *E. brassiana* (BC)	1,156 [a]	1,085 [a]	766 [a]	647 [a]	643 [a]	573 [a]
E. pellita x *E. brassiana* (F1)	1,136 [a]	1,090 [a]	781 [a]	626 [a]	627 [a]	553 [a]
E. pellita x *E. urophylla* (BC)	1,087 [a]	1,058 [a]	695 [a]	587 [a]	588 [a]	534 [a]
E. pellita x *E. urophylla* (F1)	1,093 [a]	1,069 [a]	693 [a]	605 [a]	571 [a]	545 [a]
LSD (p=0.05)	93.64	58.12	129.40	110.15	102.65	93.85
LSD (p=0.05) - Tukey	134.15	83.30	184.90	160.85	146.75	136.75
p-value	0.23	0.35	0.360.60		0.41	0.81
YP28						
E. pellita	1,103 [a]	1,041 [a]	682 [a]	582 [a]	579 [a]	526 [a]
E. pellita x *E. brassiana* (BC)	1,155 [a]	1,114 [a]	765 [a]	673 [a]	638 [a]	599 [a]
E. pellita x *E. brassiana* (F1)	1,108 [a]	1,065 [a]	742 [a]	631 [a]	596 [a]	551 [a]
E. pellita x *E. urophylla* (BC)	1,120 [a]	1,056 [a]	750 [a]	619 [a]	620 [a]	551 [a]
E. pellita x *E. urophylla* (F1)	1,117 [a]	1,104 [a]	716 [a]	663 [a]	606 [a]	591 [a]
LSD (p=0.05)	93.50	111.21	131.62	135.95	102.75	111.85
LSD (p=0.05) - Tukey	135.40	160.55	189.90	196.10	148.05	181.30
p-value	0.50	0.21	0.37	0.22	0.52	0.24

* F1, first generation; BC, back cross; B.R., Before reconditioning; A.R., After reconditioning; T, Tangential; R, Radial. Level of significance (p<0.05), Confidence level used = 0.95, hybrids that are not significantly different from each other have the same letter while hybrids that are significantly different from each other have different letters (based on the Tukey LSD).

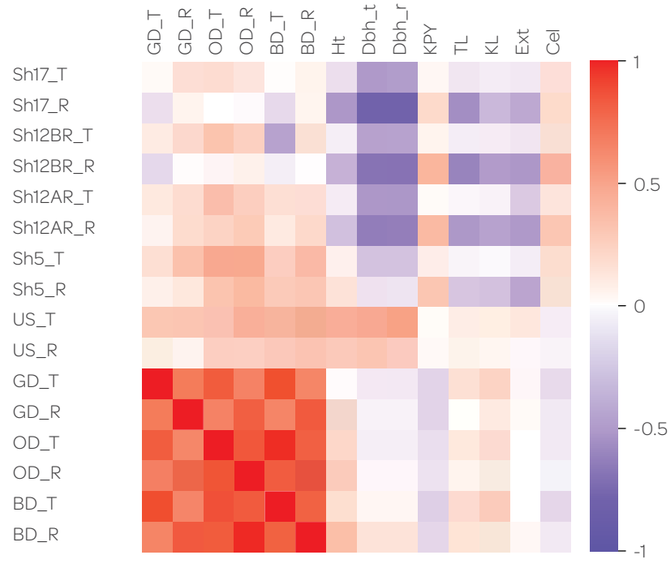


Figure 3.16: Correlation matrix for combined plantation sites between shrinkage properties, density, growth traits, and chemical components.

Table 3.3: Identified Single Nucleotide Polymorphisms (SNPs) associated with shrinkage property traits at the Tangential (T) and Radial (R) directions.

Molecular markers	Traits	Alleles	Chr	Pos	p-value	MAF	Allelic effect
SNP2554	Green to 12% AR (T)	T/C	1	2554	0.000**	0.167	-2.303
	Green to 17% (T)	T/A	1	4963	0.000**	0.118	1.996
SNP4963	Green to 12% BR (T)	T/A	1	4963	0.000**	0.118	1.888
	Unit shrinkage (T)	T/A	1	4963	0.000**	0.118	-0.080
	Green to 17% (T)	G/A	1	4976	0.000**	0.118	1.996
SNP4976	Green to 12% BR (T)	G/A	1	4976	0.000**	0.118	1.888
	Unit shrinkage (T)	G/A	1	4976	0.000**	0.118	-0.080
	Green to 17% (T)	A/C	1	4979	0.000**	0.118	-1.996
SNP4979	Green to 12% BR (T)	A/C	1	4979	0.000**	0.118	-1.888
	Unit shrinkage (T)	A/C	1	4979	0.000**	0.118	0.080
SNP1641	Green to 12% BR (R)	C/G	1	1641	0.002*	0.153	0.998
	Green to 12% AR (R)	C/G	1	1641	0.001**	0.153	1.010
SNP2256	Green to 12% BR (R)	G/A	1	2256	0.002*	0.122	0.922
	Green to 12% AR (R)	G/A	1	2256	0.000**	0.122	1.065
SNP117	Green to 5% (R)	G/A	1	117	0.001**	0.490	0.950
	Unit shrinkage (R)	G/A	1	117	0.000**	0.490	0.052

**p < 0.001, *p < 0.01, Chr: chromosomes; Pos: single nucleotide polymorphisms (SNPs) position in the population structure; MAF: minor allele frequency; BR (Before reconditioning); AR (After reconditioning).

Table 3.4: Identified Single Nucleotide Polymorphisms (SNPs) associated with density property traits at the Tangential (T) and Radial (R) directions.

Molecular markers	Traits	Alleles	Chr	Pos	p-value	MAF	Allelic effect
SNP2981	Green density (T)	G/T	1	2981	0.000**	0.098	69.245
	Oven dry density (T)	G/T	1	2981	0.002*	0.098	78.225
	Basic density (T)	G/T	1	2981	0.001**	0.098	70.362
SNP3459	Oven dry density (T)	G/A	1	3459	0.002*	0.333	-46.823
	Basic density (T)	G/A	1	3459	0.001**	0.333	-39.114
SNP4216	Oven dry density (T)	A/T	1	4216	0.002*	0.363	42.607
	Basic density (T)	G/A	1	3459	0.001**	0.333	-39.114
SNP2507	Oven dry density (R)	T/C	1	2507	0.001**	0.194	-62.993
	Basic density (R)	T/C	1	2507	0.000*	0.194	-56.888
SNP2508	Oven dry density (R)	T/C	1	2508	0.001**	0.194	-62.993
	Basic density (R)	T/C	1	2508	0.000**	0.194	-56.888
SNP2509	Oven dry density (R)	T/C	1	2509	0.001**	0.194	-62.993
	Basic density (R)	T/C	1	2509	0.000**	0.194	-56.888

**p < 0.001, *p < 0.01, Chr: chromosomes; Pos: single nucleotide polymorphisms (SNPs) position in the population structure; MAF: minor allele frequency; BR (Before reconditioning); AR (After reconditioning).

3.2.2 Effect of Genotype on Selected Properties of Young Plantation-Grown *Eucalyptus pellita* and its hybrids for Structural Applications

The results from this section highlight the structural potential of young *E. pellita* hybrids grown in tropical plantations. Mechanical properties varied across hybrid types, sites, and positions within the stem, reflecting the combined effects of genetics and growing environment. At Kilu Impini 64, MOE ranged from 10,670 to 16,580 MPa, MOR from 103 to 135 MPa, and CS from 49 to 70 MPa. At Yapilika 28, MOE ranged from 10,499 to 17,674 MPa, MOR from 68 to 147 MPa, and CS from 47 to 69 MPa (Tables 3.5 and 3.6). Among the hybrid groups, those involving *E. brassiana*, particularly the backcross, consistently demonstrated the highest stiffness, strength, and compressive performance. Variation within the stem was another important factor influencing mechanical performance. Wood from the outer and middle zones had higher values than the core wood. These patterns are relevant to processing and grading decisions, where log position can affect structural classification and end-product value. The mechanical properties observed in these hybrids are comparable to those reported for *E. pellita* grown in other tropical environments, as well as for other commercially used hardwood species. This positioned the hybrids as viable candidates for expanding structural timber supply from fast-grown plantation sources.

While older trees naturally exhibited higher mechanical values, predictions based on regression models showed that some 10-year-old hybrids could match or even exceed the performance of 30-year-old *E. pellita* by rotation age (Figure 3.2). The mean values for hybrid clones met the Australian structural standards for stiffness (MOE), bending strength (MOR), and compression strength (CS), with stress grades ranging from F14–F17 (MOE), F34 (MOR), and F27–F34 (CS) based on AS 1720.1. This indicated early suitability for solid wood products and highlighted the potential to improve economic returns by reducing rotation age in plantation forestry.

Strong correlations between density and mechanical traits further confirmed the central role of density as a predictor of wood performance. This supports the use of density as a practical selection trait for both industrial grading and genetic improvement. Moderate positive relationships were also observed between mechanical properties and tree growth traits such as height and diameter, indicating that some fast-growing trees can still produce structurally sound wood. Chemical and anatomical traits also influenced performance. Higher lignin content was associated with improved strength, while higher microfibril angle had a negative effect. These relationships offer additional selection opportunities, particularly for improving mechanical stability without compromising growth.

Genetic analysis identified three SNPs that exceeded the significance threshold for mechanical traits, particularly in outer wood, while several others showed strong and consistent associations across traits. These findings provided evidence of underlying genetic control over wood stiffness, strength, and compressive performance. The presence of both trait-specific and multi-trait associations suggested that multiple genomic regions influence mechanical behaviour in *E. pellita* hybrids. For breeders, these markers offered practical targets for developing genomic tools aimed at enhancing wood quality. Their integration into marker-assisted selection strategies could enhance the precision and efficiency of breeding programs targeting structurally reliable timber from fast-grown plantation resources.

The results demonstrate that *E. pellita* hybrids, particularly those involving *E. brassiana*, have promising potential as plantation-grown structural material. The findings support early harvesting strategies and help identify hybrid types most likely to meet structural standards. For breeders, the results underscore the importance of selecting for density, growth, and specific genetic markers to enhance structural performance while balancing productivity with wood quality.

Table 3.5: Mean table for MOE and MOR in Kilu Impini 64 and Yapilika 28.

	MOE (MPa)						MOR (MPa)					
	Top		Middle		Bottom		Top		Middle		Bottom	
	Outer	Inner	Outer	Inner	Outer	Inner	Outer	Inner	Outer	Inner	Outer	Inner
Kilu Impini 64												
E. pellita	15,670 [a]	13,767 [a]	16,115 [a]	14,212 [a]	14,238 [a]	12,336 [a]	131 [a]	114 [a]	134 [a]	117 [a]	124 [a]	108 [a]
E. pellita x *E. brassiana* (BC)	16,136 [a]	14,233 [a]	16,580 [a]	14,678 [a]	14,704 [a]	12,802 [a]	135 [a]	118 [a]	138 [a]	121 [a]	128 [a]	112 [a]
E. pellita x *E. brassiana* (F1)	15,708 [a]	13,805 [a]	16,152 [a]	14,250 [a]	14,276 [a]	12,374 [a]	131 [a]	115 [a]	135 [a]	118 [a]	125 [a]	108 [a]
E. pellita x *E. urophylla* (BC)	15,604 [a]	13,701 [a]	16,049 [a]	14,146 [a]	14,172 [a]	12,270 [a]	130 [a]	114 [a]	133 [a]	117 [a]	124 [a]	107 [a]
E. pellita x *E. urophylla* (F1)	14,004 [a]	12,101 [a]	14,449 [a]	12,546 [a]	12,572 [a]	10,670 [a]	126 [a]	110 [a]	130 [a]	113 [a]	120 [a]	103 [a]
LSD (Tukey)	2,957.00						26.20					
p-value (Hybrid)	0.27						0.91					
p-value (Long_Pos)	0.00 (Top = a, Middle = ab, Bottom b)						0.00 (Top = ab, Middle = b, Bottom = a)					
p-value (Rad_Pos)	0.00 (Inner = a, Outer = b)						0.00 (Inner = a, Outer = b)					
Yapilika 28												
E. pellita	16,013 [ab]	13,638 [ab]	16,307 [ab]	13,932 [ab]	15,222 [ab]	12,848 [ab]	129 [ab]	105 [ab]	138 [ab]	115 [ab]	135 [ab]	111 [ab]
E. pellita x *E. brassiana* (BC)	17,380 [a]	15,005 [a]	17,674 [a]	15,299 [a]	16,589 [a]	14,214 [a]	137 [a]	114 [a]	147 [a]	123 [a]	143 [a]	119 [a]
E. pellita x *E. brassiana* (F1)	14,208 [ab]	11,833 [ab]	14,502 [ab]	12,128 [ab]	13,417 [ab]	11,043 [ab]	92 [b]	68 [b]	102 [b]	78 [b]	98 [b]	74 [b]
E. pellita x *E. urophylla* (BC)	16,432 [a]	14,057 [a]	16,726 [a]	14,351 [a]	15,641 [a]	13,266 [a]	129 [a]	106 [a]	139 [a]	115 [a]	135 [a]	112 [a]
E. pellita x *E. urophylla* (F1)	13,664 [b]	11,290 [b]	13,959 [b]	11,584 [b]	12,874 [b]	10,499 [b]	110 [ab]	86 [ab]	119 [ab]	96 [ab]	116 [ab]	92 [ab]

* F1: first-generation hybrid; BC: backcross hybrid. Significance at $p < 0.05$, 95% confidence. Means with the same letter within each factor are not significantly different (Tukey-adjusted, Mixed Linear Model). Different letters indicate significant differences. The same LSD value applies across all hybrid comparisons within each longitudinal and radial position for each trait.

Table 3.6: Mean table for compressive strength in Kilu Impini 64 and Yapilika 28

	Top		Middle		Bottom	
Kilu Impini 64	Outer	Inner	Outer	Inner	Outer	Inner
E. pellita	64 [a]	56 [a]	66 [a]	58 [a]	60 [a]	52 [a]
E. pellita x *E. brassiana* (BC)	68 [a]	60 [a]	70 [a]	62 [a]	64 [a]	56 [a]
E. pellita x *E. brassiana* (F1)	62 [a]	53 [a]	63 [a]	55 [a]	58 [a]	50 [a]
E. pellita x *E. urophylla* (BC)	61 [a]	52 [a]	62 [a]	54 [a]	57 [a]	49 [a]
E. pellita x *E. urophylla* (F1)	62 [a]	54 [a]	64 [a]	56 [a]	58 [a]	50 [a]
LSD (Tukey)	10.85					
p-value (Hybrid)	0.29					
p-value (Long_Pos)	0.00 (Top = b, Middle = ab, Bottom = a)					
p-value (Rad_Pos)	0.00 (Inner = a, Outer = b)					
Yapilika 28						
E. pellita	63 [a]	54 [a]	65 [a]	55 [a]	60 [a]	51 [a]
E. pellita x *E. brassiana* (BC)	68 [a]	58 [a]	69 [a]	60 [a]	64 [a]	55 [a]
E. pellita x *E. brassiana* (F1)	62 [a]	53 [a]	63 [a]	54 [a]	59 [a]	50 [a]
E. pellita x *E. urophylla* (BC)	62 [a]	53 [a]	64 [a]	54 [a]	59 [a]	50 [a]
E. pellita x *E. urophylla* (F1)	60 [a]	51 [a]	61 [a]	52 [a]	57 [a]	47 [a]
LSD	10.78					
p-value (Hybrid)	0.23					
p-value (Long_Pos)	0.00 (Top = b, Middle = ab, Bottom = a)					
p-value (Rad_Pos)	0.00 (Inner = a, Outer = b)					

* F1: first-generation hybrid; BC: backcross hybrid. Significance at $p < 0.05$, 95% confidence. Means with the same letter within each factor (hybrid, longitudinal position, radial position) are not significantly different (Tukey-adjusted, Mixed Linear Model). Different letters indicate significant differences. The same LSD value applies across all hybrid comparisons within each longitudinal and radial position.

3.2.3 Examining Hybrid Effects on Peeling and Sawing Recovery, Wood Quality of *Eucalyptus pellita*, and Strength Properties of Engineered Wood Product

This section demonstrates how log form, processing recovery, and wood product quality are shaped by both hybrid genetics and plantation site conditions. More consistent stem form was observed at the high-productivity site, Kilu Impini 64, with minimal differences among hybrids. In contrast, hybrids grown at the moderate-productivity site, Yapilika 28, exhibited greater variation in log traits, including diameters, volume, and knot characteristics (Tables 3.7 and 3.8). These findings indicated that high-productivity sites not only minimised the expression of genetic differences but also promoted improved stem form and log quality across hybrids. In contrast, moderate-productivity sites tend to magnify variation in form-related traits. This underscored the importance of matching hybrid selection to site productivity to achieve consistent wood quality and optimise processing performance in plantation forestry.

Product recovery outcomes varied by site and hybrid. Sawn board recovery and grading were generally higher across most hybrids in the high-productivity environment, while the moderately productive environment yielded lower-grade material (Table 3.9). Veneer recovery followed a similar trend, with net recovery reaching up to 70% in the high-productivity environment. In contrast, recovery was lower in the moderate-productivity environment, where a higher incidence of defects limited performance (Table 3.10). The mature *E. pellita* produced the highest-quality sawn and veneer products, indicating how current plantation material might perform if allowed to mature.

Correlations between log traits and recoveries revealed important relationships. Traits such as log volume, large end and small end diameters, and DBH were positively associated with sawn and veneer recovery. Conversely, traits linked to form irregularity, such as taper and end-splitting, had strong negative effects on veneer yield. Knot size showed weaker but negative correlations with recovery. These highlighted the need to manage log form through both hybrid selection and silvicultural practices, to maximise resource efficiency and product value.

The performance of hybrid veneers in LVL also confirmed their structural suitability. Despite variation in density ($p < 0.001$), stiffness and bending strength remained consistent across combinations (Table 3.11), and bonding quality was high. This confirmed that hybrid cores can be structurally integrated with mature *E. pellita* face veneers without compromising performance. Such flexibility enhanced the industrial utility of hybrids, especially when mature resource supply is limited.

Genetic analysis identified SNPs associated with key log traits affecting processing, including end split, heartwood proportion, and knot diameter (Table 3.12). These markers offer practical targets for improving log form and reducing defect risk through selection. Their incorporation into breeding programs could accelerate the development of hybrids with improved processing recovery and product quality.

These findings support the broader utilisation of *E. pellita* hybrids, highlighting their suitability for a range of solid and engineered wood applications, including structural timber, veneers, and laminated products. Aligning hybrid selection with site productivity is essential to optimise stem form and recovery outcomes, ensuring more consistent log quality. Hybrids showed the capacity to meet structural standards and minimise downgrade losses, enhancing their value for processing. The identification of key phenotypic traits and associated genetic markers also provided a foundation for breeding programs focused on improving log quality, recovery efficiency, and overall product performance.

Table 3.7: Mean variation among sawn log traits: volume, large-end diameter (LED), small-end diameter (SED), large-end heartwood diameter (LEHD), small-end heartwood diameter (SEHD), and heartwood proportion (HP).

Hybrid/Plantation site	No of logs	Volume (m³)	LED (mm)	SED (mm)	LEHD (mm)	SEHD (mm)	HP (%)
Kilu Impini 64 (Site A)							
E. pellita	5	0.05 [a]	178.4 [a]	162.7 [a]	147.6 [a]	129.9 [a]	66.1 [a]
		(0.01)	(17.1)	(18.5)	(15.8)	(16.8)	(3.8)
E. pellita x *E. brassiana* (F1)	5	0.03 [a]	139.7 [a]	124.9 [a]	118.2 [a]	102.2 [a]	65.7 [a]
		(0.03)	(50.9)	(48.02)	(56.9)	(52.2)	(15.2)
E. pellita x *E. brassiana* (BC)	5	0.05 [a]	177.6 [a]	161.5 [a]	149.9 [a]	129.3 [a]	68.0 [a]
		(0.01)	(14.3)	(19.8)	(18.9)	(18.9)	(10.7)
E. pellita x *E. urophylla* (F1)	5	0.05 [a]	176.6 [a]	147.1 [a]	131.3 [a]	115.1 [a]	60.4 [a]
		(0.02)	(37.4)	(10.8)	(6.7)	(6.6)	(14.1)
E. pellita x *E. urophylla* (BC)	5	0.05 [a]	174.0 [a]	157.8 [a]	147.7 [a]	129.5 [a]	70.5 [a]
		(0.01)	(22.7)	(23.4)	(16.6)	(18.0)	(8.8)
Yapilika 28 (Site B)							
E. pellita	5	0.04 [a]	163.3 [ab]	148.7 [a]	140.6 [a]	126.5 [a]	73.9 [a]
		(0.02)	(26.5)	(31.8)	(25.2)	(28.6)	(13.8)
E. pellita x *E. brassiana* (F1)	5	0.02 [b]	94.73 [c]	85.7 [b]	81.8 [c]	71.2 [c]	72.1 [a]
		(0.01)	(16.7)	(12.7)	(19.5)	(15.7)	(16.4)
E. pellita x *E. brassiana* (BC)	5	0.05 [a]	177.3 [a]	150.1 [a]	152.3 [a]	123.7 [a]	71.2 [a]
		(0.01)	(10.2)	(17.4)	(9.1)	(14.3)	(5.2)
E. pellita x *E. urophylla* (F1)	5	0.03 [ab]	126.3 [bc]	113.2 [ab]	98.2 [bc]	82.6 [bc]	60.7 [ab]
		(0.01)	(21.4)	(21.1)	(22.7)	(19.6)	(7.6)
E. pellita x *E. urophylla* (BC)	5	0.05 [a]	169.2 [a]	152.5 [a]	130.8 [ab]	119.6 [ab]	56.2 [b]
		(0.01)	(21.9)	(17.2)	(23.6)	(16.3)	(6.0)

Standard deviation in parentheses. Different letters indicate significant differences between means ($p < 0.05$).

Table 3.8: 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 (Site A)						
E. pellita	4.2 [a]	55.1 [a]	3.9 [a]	0.004 [a]	0.94 [a]	0.0 [a]
	(3.5)	(19.7)	(5.6)	(0.001)	(0.04)	(0.0)
E. pellita x E. brassiana (F1)	3.6 [a]	40.1 [a]	13.1 [a]	0.003 [a]	0.97 [a]	5.0 [a]
	(2.9)	(25.2)	(10.0)	(0.001)	(0.02)	(11.2)
E. pellita x E. brassiana (BC)	4.8 [a]	45.7 [a]	17.6 [a]	0.004 [a]	0.98 [a]	0.0 [a]
	(3.0)	(13.2)	(12.3)	(0.002)	(0.02)	(0.0)
E. pellita x E. urophylla (F1)	6.0 [a]	42.4 [a]	2.2 [b]	0.007 [a]	0.94 [a]	3.8 [a]
	(3.2)	(3.9)	(5.0)	(0.002)	(0.03)	(8.5)
E. pellita x E. urophylla (BC)	6.2 [a]	38.8 [a]	6.7 [a]	0.004 [a]	0.94 [a]	0.0 [a]
	(5.6)	(23.6)	(6.2)	(0.002)	(0.03)	(0.0)
Yapilika 28 (Site B)						
E. pellita	6.8 [a]	49.4 [a]	33.6 [a]	0.003 [a]	0.92 [a]	0.0 [a]
	(5.2)	(8.8)	(38.8)	(0.002)	(0.81)	(0.0)
E. pellita x E. brassiana (F1)	5.0 [a]	11.6 [b]	9.3 [a]	0.002 [a]	0.95 [a]	0.0 [a]
	(8.7)	(20.1)	(8.5)	(0.001)	(0.05)	(0.0)
E. pellita x E. brassiana (BC)	7.2 [a]	24.9 [ab]	12.6 [a]	0.006 [a]	0.95 [a]	14.0 [a]
	(8.9)	(23.5)	(9.5)	(0.004)	(0.02)	(26.1)
E. pellita x E. urophylla (F1)	4.6 [a]	32.4 [ab]	8.4 [a]	0.003 [a]	0.96 [a]	0.0 [a]
	(4.7)	(18.5)	(12.4)	(0.001)	(0.02)	(0.0)
E. pellita x E. urophylla (BC)	7.2 [a]	55.8 [a]	6.2 [a]	0.004 [a]	0.94 [a]	0.0 [a]
	(3.1)	(8.6)	(9.3)	(0.002)	(0.04)	(0.0)

Standard deviation in parentheses. Different letters indicate significant differences between means ($p < 0.05$).

Table 3.9: 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.

		SR	SGR	DDR	G1	G2	G3	G4
Kilu Impini 64 (Site A)								
E. pellita	199	45.1	36.0	19.7	23.5	20.9	10.7	45.0
E. pellita x *E. brassiana* (F1)	156	49.2	37.4	20.8	10.0	29.9	11.2	48.9
E. pellita x *E. brassiana* (BC)	192	42.5	21.4	11.8	10.4	29.9	15.7	44.1
E. pellita x *E. urophylla* (F1)	186	40.1	25.8	14.3	0.0	33.1	29.4	37.5
E. pellita x *E. urophylla* (BC)	197	45.2	29.5	16.1	21.4	30.0	37.0	11.7
Yapilika 28 (Site B)								
E. pellita	195	43.2	27.8	15.7	15.0	0.0	0.0	85.0
E. pellita x *E. brassiana* (F1)	114	0.0	0.0	0.0	0.0	0.0	0.0	0.0
E. pellita x *E. brassiana* (BC)	187	48.4	22.8	13.7	0.0	10.9	21.0	68.1
E. pellita x *E. urophylla* (F1)	154	50.8	27.1	15.0	0.0	0.0	0.0	100.0
E. pellita x *E. urophylla* (BC)	191	44.7	24.6	14.5	19.7	8.1	8.1	64.1
Bremer								
Mature *E. pellita*	362	40.0	35.6	21.1	58.8	6.0	9.9	25.3

Table 3.10: Green (GR), dry (DR), net (NR) recoveries and veneer grades from *E. pellita* and hybrids.

Hybrid	Site	Dbh	Veneer recovery (%)			Veneer grade proportion (%)					
			GR	DR	NR	A	S	B	C	D	Rejects
E. pellita	Kilu Impini 64	20	76.0	65.3	55.5	0.0	0.0	0.0	0.0	46.6	53.4
E. pellita x *E. urophylla* (F1)	Kilu Impini 64	19	80.1	74.7	63.5	0.0	0.0	0.0	0.0	100	0.0
E. pellita x *E. urophylla* (BC)	Kilu Impini 64	20	82.2	78.3	66.6	0.0	0.0	0.0	0.0	73.4	26.6
E. pellita x *E. brassiana* (BC)	Kilu Impini 64	19	83.6	83.1	70.7	0.0	0.0	0.0	0.0	77.5	22.5
E. pellita x *E. urophylla* (BC)	Yapilika	18	53.5	43.5	37.0	0.0	0.0	0.0	0.0	0.0	100.0
Mature *E. pellita* tree	Bremer	36	79.3	64.4	54.8	67.1	18.2	0.0	8.9	0.0	5.8

Table 3.11: 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/m³)	MOE (MPa)	MOR (MPa)
Layup 1	703 (31.77) ^{d}	14,376 (403.53) ^{a}	122 (8.43) ^{a}
Layup 2	788 (2.90) ^{abc}	15,793 (2408.78) ^{a}	124 (22.87) ^{a}
Layup 3	791 (18.45) ^{ab}	18,802 (2345.72) ^{a}	139 (8.83) ^{a}
Layup 4	815 (14.44) ^{a}	14,931 (5179.14) ^{a}	123 (33.68) ^{a}
Layup 5	774 (33.23) ^{abc}	16,271 (2538.10) ^{a}	132 (12.48) ^{a}
Layup 6	732 (50.34) ^{cd}	15,403 (4374.10) ^{a}	127 (23.85) ^{a}
Layup 7	736 (24.69) ^{bcd}	14,534 (654.99) ^{a}	127 (5.62) ^{a}
Layup 8	756 (13.59) ^{abcd}	16,619 (1060.52) ^{a}	138 (11.80) ^{a}
p-value	0.000***	0.271	0.711
F value	5.573	1.334	0.65

Standard deviation in parentheses. Different letters indicate significant differences between means ($p < 0.05$).

Table 3.12: Identified SNPs associated with log traits (end split (ES), heartwood proportion (HP), knot diameter, large-end diameter (LED), and small-end diameter (SED)).

SNP	Traits	Alleles	Chr	Pos	P-value	MAF	Allelic effect
SNP1358	ES	A/G	1	1358	0.000**	0.045	50.867
SNP66		T/A	1	66	0.000**	0.091	22.785
SNP4964		A/T	1	4964	0.001*	0.076	-34.726
SNP2187	HP	T/A	1	2187	0.000**	0.283	-10.549
SNP3547		G/A	1	3547	0.000**	0.321	8.591
SNP3544		C/T	1	3544	0.001*	0.123	-8.574
SNP3201	Knot diameter	T/C	1	3201	0.000**	0.228	-8.863
SNP991		A/G	1	991	0.000**	0.370	-5.069
SNP4093		T/C	1	4093	0.000**	0.402	5.410
SNP13	LED	T/A	1	13	0.000**	0.236	-30.320
SNP14		T/C	1	14	0.000**	0.236	-30.320
SNP4505		G/A	1	4505	0.000**	0.113	39.617
SNP3055	SED	C/T	1	3055	0.000**	0.151	-38.175
SNP672		T/G	1	672	0.000**	0.179	-27.566
SNP13		T/A	1	13	0.001*	0.236	-26.356

**p < 0.001, *p < 0.01, Chr: chromosomes; Pos: SNP position in the population structure; MAF: minor allele frequency

3.3 Implications and Limitations

3.3.1 Physical Properties as Early Indicators of Wood Quality

The evaluation of physical properties revealed significant variation in density and shrinkage among *E. pellita* and its hybrids, highlighting genetic and environmental influences on basic wood quality. Higher basic density was generally associated with improved structural performance, and strong correlations with kraft pulp yield and lignin content indicated the relevance of this trait for both structural and pulp applications. Genotypes involving *E. urophylla* showed favourable shrinkage characteristics and lower unit shrinkage values, which are important indicators of dimensional stability and product reliability during drying and service life. These findings supported the use of density and shrinkage as effective early selection criteria in breeding programs. Selecting genotypes with higher density and lower shrinkage could improve processing efficiency and product quality, thereby enhancing the commercial competitiveness of plantation-grown timber.

A key limitation in this component of the study was the restricted sampling of shrinkage discs to the bottom of the tree. This prevented the assessment of longitudinal variation in shrinkage, which could have provided a more complete understanding of dimensional stability along the stem.

3.3.2 Mechanical Strength and Structural Suitability of Plantation Timber

Mechanical testing provided key insights into the structural potential of *E. pellita* and its hybrids. MOE, MOR, and CS varied significantly by genotype, stem position, and plantation site, highlighting the influence of both genetic and environmental factors. Hybrids involving *E. brassiana* consistently outperformed others, with many samples exceeding the AS 1720.1:2010 F-grade thresholds. These results confirmed that selected hybrids are suitable for structural timber applications, including engineered products such as LVL. The observed correlations between unit shrinkage and mechanical traits highlighted a relationship between physical and structural properties. While not predictive, these associations suggested that traits such as density and shrinkage could offer useful insights during early-stage selection in breeding programs. Their relatively straightforward measurement made them practical reference points for identifying genotypes with potential for superior mechanical performance. Knowledge of genotype-specific strength performance supported targeted log allocation, processing optimisation, and improved product yield. High-performing hybrids could be directed to structural applications, while others may be better suited for pulp or non- structural use. The findings also underscore the need to align genotype deployment with site conditions to maximise performance. Overall, the study provided a compelling foundation for integrating structural traits into breeding, plantation management, and processing strategies.

There was a challenge with obtaining consistent sampling across the top, middle, and bottom sections of the stem. In plantation-grown trees, the upper logs had smaller diameters and greater taper, which limited their suitability for standard test specimens. Due to these constraints, mechanical testing was carried out using small, clear specimens prepared according to the secondary method outlined in ASTM D143-21. While this approach enabled comparative assessments across genotypes and sites, it may not fully represent the behaviour of full-size members under structural loading. Additionally, comparisons with mature *E. pellita* were limited to specimens taken from the middle stem and sourced from a different site (Bremer). This restricted the ability to comprehensively assess age-related variation and its interaction with stem position.

3.3.3 Processing Efficiency and Product Recovery from Plantation Logs

This study on sawing and product recovery demonstrated that genetic variation and plantation site conditions significantly influenced processing outcomes in plantation-grown *E. pellita* and its hybrids. Notable differences were observed in sawn board recovery, veneer yield, and LVL fabrication. Logs from the high-productivity site, Kilu Impini 64, consistently outperformed those from the moderate-productivity site, Yapilika 28. This was largely due to their larger size, straighter form, and lower incidence of defects. Key log traits such as diameter, taper, and knot severity were strongly linked to recovery rates, reinforcing their importance in both breeding objectives and operational decision-making. The performance of certain hybrids as core material in LVL production, with acceptable bonding quality, highlighted their potential for use in engineered product applications. These findings offered practical guidance for mill operations, suggesting that targeted log grading and allocation based on genotype and site could enhance processing efficiency and product value. They also supported the inclusion of log quality traits in early selection criteria to improve processing efficiency and reduce waste across plantation forestry value chains.

A key challenge in this study was the limited sampling for veneer recovery. Although the aim was to peel 1.8 m logs from three stem positions per tree, only a single bottom log was processed. This limitation was due to capacity constraints of the peeling line. As a result, variation in veneer yield and quality along the stem could not be assessed. For LVL, only bending properties (MOE and MOR) were assessed. Key structural traits, such as shear and compressive strength, were not evaluated, which limits the ability to fully determine product suitability for applications such as beams, load-bearing walls, and columns in structural and engineered wood systems. Future work should include these tests, along with long-term performance evaluations (e.g., durability, creep, and weathering), to support structural applications of plantation-grown hybrids. Another challenge encountered was in the sawing trials. Only one 2.4 m log at a fixed height was collected per tree, restricting the assessment of full-stem recovery and excluding some hybrids.

3.3.4 Genomic Insights and Deployment Strategies

This study provided novel evidence supporting the integration of genomic tools and phenotypic performance data to enhance wood quality improvement and deployment strategies in tropical plantation forestry. The identification of SNPs associated with key wood and log traits (density, shrinkage, mechanical strength, and log form) provided valuable genetic insight. These findings demonstrated the potential for applying marker-assisted selection (MAS) in *E. pellita* and its hybrids. Although only a small number of SNPs surpassed the significance threshold, several showed consistent associations across all traits, suggesting potential biological relevance that needs further validation. The capacity to link genotypic variation with traits of commercial importance opened a path toward more targeted and data-driven breeding programs that can accelerate genetic gain, reduce breeding cycle times, and optimise resource use. In addition to the molecular findings, the study highlighted the value of aligning genotype performance with plantation site conditions and intended product outcomes. Genotypes with superior structural and processing characteristics could be strategically deployed on high- productivity sites (such as Kilu Impini 64) to maximise log quality, recovery rates, and product value. Conversely, moderate-productivity sites (Yapilika 28) may require tailored silvicultural strategies to support consistent growth and stem form. These results provided practical guidance for breeders, forest managers, and industry stakeholders. They supported efforts to improve wood quality, reduce processing inefficiencies, and increase the market competitiveness of plantation-grown hardwoods. The combined use of phenotypic and genotypic information advanced the principles of precision forestry. It also supported the long- term goal of developing resilient, high-yield plantation systems that are both economically and environmentally sustainable.

The genetic analysis was limited by a relatively small sample size ($n \approx 60$), which reduced statistical power and increased the likelihood of false negatives. The SNP panel (~5,500 markers) may not have captured the full extent of genomic variation. In addition, the limited genome annotation constrained the biological interpretation of associated markers. Future studies should increase the number of sampled individuals and apply higher-density genotyping or whole-genome sequencing to improve resolution. Integrating functional genomic tools such as transcriptomics would also help validate candidate genes and clarify their roles in trait expression. Unbalanced genotype representation, particularly among the first-generation (F1) hybrids, across the two sites limited the ability to make comprehensive comparisons between hybrid groups. A more balanced experimental design, with replicated genotype blocks across sites, would support more precise conclusions on deployment strategies. Including economic and environmental factors, such as cost–benefit analysis and carbon assessment, would add practical value to these findings. This would support more informed decision-making in sustainable plantation management.

3.3.5 Translating Research into Practice

The findings of this study provided a promising foundation for practical application across the forestry value chain. By integrating wood quality data, including density, shrinkage, and mechanical strength, with processing outcomes such as sawn and veneer recovery and LVL performance, the study provides a holistic understanding of the utilisation potential of *E. pellita* hybrids in plantation forestry. When combined with molecular insights from SNP associations, these results offered actionable evidence for improving both genetic selection and resource utilisation in plantation-grown Eucalyptus. For breeders, traits such as density, shrinkage, and log form could serve as reliable indicators of processing performance and product suitability. The identification of promising hybrids supported the development of structurally capable, fast-growing genotypes. The observed site effects highlighted the importance of matching genotype to site conditions to maximise log quality, minimise defects, and improve recovery efficiency. Processors and product developers could also benefit from this integrated approach.

Knowledge of genotype-specific performance in sawing, veneer peeling, and LVL manufacturing enabled better log segregation and allocation, ultimately improving product yield and value. More broadly, this study contributed to advancing sustainable tropical hardwood plantation forestry by supporting the targeted use of improved hybrids. This approach helped reduce pressure on native forests and expanded the role of plantation resources in high-value, structural applications.

3.3.6 Recommendation for Future Research

This study has advanced understanding of the integrated relationships among wood quality, processing recovery, and genetic associations in *Eucalyptus pellita* and its hybrids, providing a valuable foundation for applied breeding and resource optimisation. While the findings offer important insights, several factors highlight opportunities for further research. Limited sample sizes, unbalanced genotype representation across plantation sites, and small log diameters, particularly at the upper stem, restricted inclusion in certain processing stages. These factors reduced the statistical power of the genetic analyses and constrained the extent to which the findings could be applied more widely. Future research should aim to address these gaps by expanding sampling across a wider range of genotypes and sites. A larger and more balanced dataset would improve the reliability of trait comparisons and strengthen the detection of SNP– trait associations. It is also essential to validate the significant SNPs identified in this study using independent, genetically diverse populations. This will help confirm their value for use in marker-assisted selection. Including more plantation sites with contrasting silvicultural histories, such as variations in pruning, spacing, and thinning, would offer insights into how genotype-by-environment interactions affect wood development and defect formation. Further work is recommended to investigate the production and mechanical testing of engineered wood products, such as LVL and glulam, across diverse hybrids, sites, and processing conditions to assess their structural performance and commercial potential. These tests should use logs with commercial dimensions to better reflect industry applications. It is recommended to expand the production and testing of LVL and glulam using commercially sized logs. Additional tests should cover shear strength and durability. Weathering under different climates will help assess long-term performance and structural suitability. Recovery performance and mechanical properties should be linked to cost–benefit and sustainability analyses. This will help breeders and forest managers evaluate the long-term value of different hybrids. This integrated approach would support the strategic deployment of superior genotypes across plantation landscapes, optimising both productivity and end-use performance. This study provided the foundational evidence needed for such integration, offering novel insights into how wood quality, processing recovery, and genetic variation interact to inform breeding, product development, and resource optimisation in *E. pellita* and its hybrids.

3.4 Key findings

Significant variation in shrinkage and density of *E. pellita* and its hybrids was observed, driven by both genetic background and site conditions. The impact of site was evident, as differences between the high-productivity and moderate-productivity sites influenced wood formation, contributing to the observed variation in shrinkage and density across genotypes. *E. pellita* × *E. urophylla* (F1) exhibited the most stable shrinkage behaviour among all genotype groups. Reconditioning reduced shrinkage, indicating improved dimensional stability. Basic density ranged from 527 to 651 kg/m^3, with *E. pellita* × *E. brassiana* (BC) recording the highest values. Shrinkage traits were positively correlated with density and negatively correlated with growth traits, lignin content, and extractives. As expected, tangential shrinkage was consistently higher than radial shrinkage, reflecting wood anisotropy.

Mechanical properties varied across sites, genotypes, and wood positions. At high-productivity site, hybrid differences were not statistically significant. However, radial and longitudinal variations were observed. Outer and middle wood showed higher MOE, MOR, and CS values. In contrast, hybrid effects were evident at moderate-productivity site, with hybrids involving *E. brassiana* consistently showed superior mechanical performance. Several groups, at just 10 years, met Australian standards for stiffness, strength, and compression, highlighting their potential for early harvesting. Mechanical properties were influenced by both genetic background and log position, with outer stem zones yielding stiffer, stronger wood. These results reinforced the value of selecting specific hybrids and applying targeted processing strategies to produce high-performance timber at a young rotation age. Strong correlations between density, growth traits (height and diameter at breast height), and mechanical performance, together with key SNPs associated with these traits, highlighted opportunities for targeted genetic improvement in Eucalyptus breeding programs.

Processing trials revealed strong genotype and site effects on log quality, recovery, and defect patterns. At the high-productivity site, *E. pellita* × *E. brassiana* (F1) showed the highest sawn recovery, while limited log size at moderate-productivity site restricted processing. Veneer recovery was highest for *E. pellita* × *E. brassiana* (BC), and mature *E. pellita* yielded the highest veneer grade. Recovery was positively associated with log size and negatively with defect traits such as end split and taper. LVL combining hybrid core veneers with mature *E. pellita* faces demonstrated high bond quality and mechanical performance, reinforcing their potential for structural applications. Genome-wide association analyses identified SNPs linked to shrinkage, density, mechanical properties, and log traits, highlighting opportunities for marker-assisted improvement of processing and product outcomes.

These findings demonstrated the strong potential of *Eucalyptus pellita* and its hybrids for structural applications and value-added wood products. By integrating phenotypic assessment with molecular marker analysis, this study established a foundation for targeted breeding to improve dimensional stability, mechanical strength, and processing efficiency. The results also underscored the importance of genotype-by-environment interactions, showing how site productivity and log traits influenced wood quality and recovery outcomes. To optimise plantation performance, the deployment of superior hybrids should consider both genetic potential and site-specific factors. Future research should aim to validate SNP–trait associations in diverse populations and evaluate engineered wood products under commercial processing conditions, supporting broader adoption of improved genotypes across tropical hardwood plantation systems.

4. Breeding and Deployment

4a. Genomic Selection

Forest tree breeding, together with forest management, aims at providing genetically superior material for various traits and management of forest trees based on the application of genetics, reproductive biology and economic principles, and has become an integral part of forestry operations today. Any tree breeding program aims to deliver genetically superior trees in an economically sustainable manner, by maximising genetic gain per unit time at a lower cost. The application of latest molecular tools and genomic technologies recently has helped in the enhancement of physical and chemical wood traits and increment in forest productivity thereby becoming an important significant strategy to continue the sustainability and development of the wood-based industries Integration of genomic technology with quantitative genetics of complex traits is rapidly becoming the approach of choice for exploring fundamental genetic questions with practical implications for tree breeding applications. Genomic Selection (GS) offers promising strategy towards increasing genetic gains per year by accelerating the tree breeding cycle. GS is a prospective approach to create new marker-based prediction models to devise innovative tree breeding programs for evaluation of genetic merit by using molecular marker. GS offers modern approach to improve genetic advantage of complex traits by reducing cost and unit time in tree breeding. GS enables the selection of complex quantitative traits using data from a sizeable number of genome-wide markers.

Objectives

Genomic selection (GS) helps to speed up genetic progress by improving the selection accuracy and reducing the generation interval. Can GS in an unstructured population accurately measure the genetic parameter estimates using markers? Also, compare the GS models performance used in the study and find the top performing models for Tiwi dataset used in the study.

Machine learning approaches are increasingly being used in GS investigations because they are simple to apply, need no assumptions about the traits and can effectively capture complicated non-linear correlations while also improving prediction accuracy. Is machine learning better than previous GS approaches for predicting breeding values?

Methods and Results

Genomic selection models – Building Genomic relationship Matrix, developing GBLUP model – estimation of genetic parameters and genomic estimated breeding values (GEBV), Identification of top-ranking trees in the research trials

Genomic selection models – Development of GS models – GBLUP, rrBLUP, Bayes A, Bayes B, Bayes C, Bayesian Lasso, Bayesian Ridge Regression – Comparison of prediction ability among the models using various R programming packages.

Genomic selection models – Development of machine learning models – Random Forest, Bayesian recurrent neural network, Support vector machine – Prediction ability comparison & machine learning models performs for Tiwi dataset.

A GBLUP model was constructed using the phenotypic and genotype data, using a genomic relationship matrix (GRM) to calculate the breeding values for the Tiwi dataset. Using genomic estimated breeding values, we have selected the trees that score highest in the research trials based on trait weightage recommendation from Midway: 60% volume, 30% density and 10% KPY.

The top 100 trees were distributed across seven subpopulations, with over half (58%) of trees belonging to subpopulation P8 and P9, with the majority of these trees located at KI64.

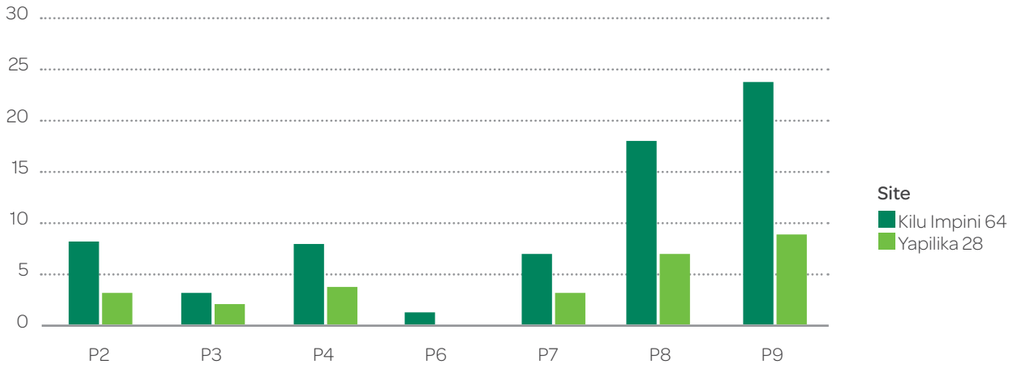


Figure 4a.1. Populations to which the Top 100 ranked trees for Volume, Density and KPY, weighted 60%, 30%, 10% respectively, based on estimated breeding values from GBLUP analysis.

Prediction ability of different GS models using genotyped trees in two research trials

We compared the prediction abilities of seven different GS models – GBLUP, rrBLUP, Bayes A, Bayes B, Bayes C, Bayesian Lasso, Bayesian Ridge Regression for all the six traits using all the 1425 genotyped trees from two research trials. Predictive abilities were estimated by correlating breeding values/genetic values from cross-validation with the adjusted phenotypes. Fractional cross-validation method was used for testing predictive abilities of the GS models. For each trait, various cross-validation tests for the GS models were done by varying the size of the training and test/validation population size such as Frac 0.5,0.6,0.7,0.8 and 0.9. Cross-validation using various training and test population size helped to analyse & compare the results of the effect of training population size in determining the prediction ability of the GS models for various traits.

For growth traits, cross-validation results from Frac 0.8 & Frac 0.9 (Table 4a.2) are similar for all the GS models and are better compared to results from Frac 0.5,0.6 and 0.7 for Height. However, we have BL model from Frac 0.7 performing slightly better than all other models across the cross-validation tests. Cross-validation results for Diameter for Frac 0.9 were better than other Frac sizes (Table 4a.2). GBLUP model prediction ability result of 0.34 in Frac 0.9 was slightly better compared to other GS models. GS models rrBLUP, Bayes A, BL and BRR with a prediction ability of 0.34 (Table 3a.2) for Frac 0.9 cross- validation performed better than other GS models for volume trait.

Cross- validation results for Density were almost similar for Frac 0.7, 0.8 and 0.9. GS models with highest prediction ability of 0.45 was observed for Density compared to all the other traits across the various cross-validation results (Table 4a.2). However, there was a substantial decrease in prediction ability for KPY and Cellulose. Cross-validation results showed KPY had the lowest prediction ability compared to all the other traits (Table 4a.2). KPY prediction ability results for all the Frac methods were almost similar and were ranging from 0.19 to 0.21 for the different GS models (Table 4a.2). Cellulose cross – validation results were slightly better than KPY (Table 4a.2). GS models rrBLUP and BRR with prediction ability result of 0.25 for Frac 0.9 cross-validation were better than the other models. Overall, analysing the cross -validation results for all the traits using different GS models, it is observed that prediction ability for Frac 0.9 cross – validation method is better than all the other Frac methods for the Tiwi dataset.

Table 4a.2. Prediction ability of different GS models using genotyped trees in two research trials.

Cross-Validation	Traits	GS Models						
		GBLUP	rrBLUP	Bayes A	Bayes B	Bayes C	BL	BRR
FRAC 0.5	Height	0.23	0.26	0.26	0.24	0.25	0.27	0.26
	Diameter	0.25	0.28	0.27	0.26	0.27	0.27	0.27
	Volume	0.28	0.3	0.3	0.28	0.29	0.3	0.3
	Density	0.41	0.41	0.41	0.4	0.4	0.42	0.41
	KPY	0.19	0.21	0.2	0.18	0.2	0.21	0.2
	Cellulose	0.19	0.22	0.21	0.19	0.21	0.22	0.21
FRAC 0.6	Height	0.25	0.26	0.26	0.25	0.25	0.26	0.26
	Diameter	0.26	0.3	0.3	0.28	0.29	0.3	0.3
	Volume	0.28	0.31	0.31	0.29	0.3	0.31	0.3
	Density	0.41	0.42	0.42	0.41	0.41	0.42	0.42
	KPY	0.22	0.21	0.2	0.19	0.2	0.22	0.2
	Cellulose	0.21	0.23	0.22	0.2	0.21	0.23	0.22
FRAC 0.7	Height	0.26	0.27	0.27	0.26	0.27	0.29	0.27
	Diameter	0.27	0.3	0.29	0.28	0.28	0.3	0.29
	Volume	0.3	0.32	0.32	0.3	0.31	0.32	0.32
	Density	0.44	0.44	0.44	0.43	0.43	0.45	0.44
	KPY	0.21	0.22	0.21	0.2	0.21	0.22	0.21
	Cellulose	0.21	0.23	0.22	0.2	0.21	0.22	0.22
FRAC 0.8	Height	0.26	0.28	0.28	0.27	0.28	0.28	0.28
	Diameter	0.29	0.3	0.3	0.29	0.3	0.31	0.3
	Volume	0.31	0.32	0.32	0.31	0.31	0.32	0.32
	Density	0.42	0.45	0.45	0.43	0.44	0.45	0.45
	KPY	0.21	0.21	0.21	0.19	0.2	0.21	0.21
	Cellulose	0.21	0.24	0.23	0.21	0.22	0.24	0.23
FRAC 0.9	Height	0.27	0.28	0.28	0.26	0.27	0.28	0.28
	Diameter	0.34	0.33	0.33	0.31	0.32	0.33	0.33
	Volume	0.32	0.34	0.34	0.32	0.33	0.34	0.34
	Density	0.44	0.45	0.45	0.44	0.44	0.45	0.45
	KPY	0.22	0.23	0.22	0.2	0.22	0.23	0.23
	Cellulose	0.23	0.25	0.24	0.22	0.24	0.24	0.25

Machine Learning vs GBLUP Model

Machine learning models like Random Forests & SVM are transforming tree breeding by enabling accurate and efficient prediction of genetic merit of individuals. These powerful tools hold immense promise for accelerating tree breeding cycles, improving resource allocation, and ultimately, developing superior tree varieties for a more sustainable future. We constructed Machine learning GS models & compared its performance with GBLUP Model. From the figure below (Fig 4a.2.), we can see that the prediction ability of Random Forest GS model is better than SVM & GBLUP model. However for wood quality parameters the prediction ability of random forest model is similar to GBLUP model.

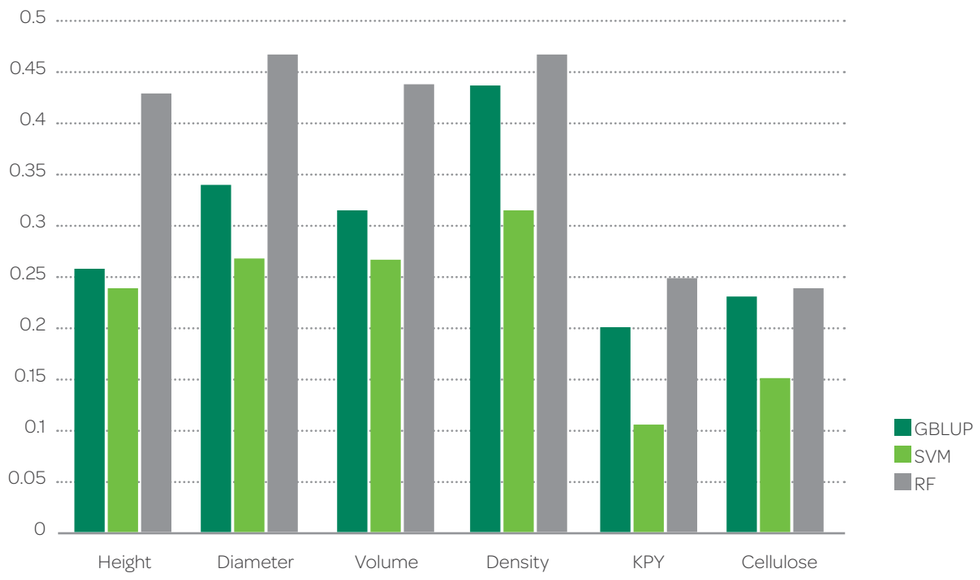


Figure 4a.2. Machine Learning vs GBLUP Model.

Key findings/Recommendations

- Top ranked trees were identified.
- Prediction ability for Frac 0.9 cross validation method is better than all the other Frac methods for the Tiwi dataset
- The prediction ability of Random Forest GS model is better than SVM & GBLUP model. However for wood quality parameters the prediction ability of random forest model is almost similar to GBLUP model.
- Seed or cuttings from the highest-ranked trees may be gathered and cultivated for subsequent planting cycles, or the top-ranked trees can be transformed into seed orchards to ensure their propagation for future generations.
- Majority of top 100 ranked trees were identified to be pure *E. pellita* and belong to subpop P8 and P9.

4b. Pollen dispersal/Seed orchard design

Open pollinated seed orchards are relatively simple to establish and cost effective, and the use of open-pollinated seeds from large scale seed orchards is a common strategy for the development and development of genetically improved eucalypts (Gonzaga et al., 2016 for *Eucalyptus globulus*). However, there are two factors that can negatively impact seed genetic quality from such open pollination systems; (i) the rate of self-pollination (selfing), which is known to cause diminished growth, survival and developmental abnormalities in the resulting progeny (Pulpin et al., 2019); and (ii) the degree of contamination from unimproved pollen outside the orchard is another factor that can influence the genetic quality of seed.

Therefore, it is important to understand patterns of pollen movement within and throughout a planted eucalypt forest stand, as it not only provides insight into population genetics, evolutionary biology and patterns of gene movement by pollen dispersal of the tree species, but it also has practical significance in forestry.

Pollen dispersal data are essential for determining the ideal distance to which seed orchards should be established away from commercial stands, germplasm banks or unimproved forests, so as to avoid undesired pollen contamination and its resulting negative impact on the genetic quality of the seed crop. Pollen dispersal influences seed orchard performance metrics such as seed set, pollen distance, effective pollen number and indirectly, the inheritance of genetic diversity across generations. Furthermore, quantifying the distance of pollen flow from a trial site/seed orchard, may provide guidelines to contain or minimise gene flow from eucalypt stands into native forests.

Objectives

A systematic assessment of pollen dispersal within KI64 was carried out to:

- Determine the pollen dispersal pattern of *E. pellita* within the site;
- Identify the rate of pollination success over increasing distances between the mother tree and pollen donors
- Determine the prevalence of selfing and pollen contamination from outside sources

Pollen flow in the KI64 population of *E. pellita* was estimated using the same molecular markers previously described and paternity analysis. SNP genotyping was used to identify pollen donors to progeny from one mother tree (K-R3T9-25). Of the 186 progeny analysed, 136 (73.1%) were assigned to pollen parents within the research trial site at 95% confidence, and another 13 seedlings (7%) were assigned to pollen parents with 80% confidence. Identified pollen donors were located between 5 – 180 m from the mother tree at the trial site, with an average pollination distance of 49.3 meters. Over half of the progeny (54.4%) were from pollen donors located within 20 m from the mother tree, and 87.3% were located within 80 m of the tree, suggesting that the majority of the pollination of the mother tree was outcrossed, by nearest neighbours (Fig, 4b.1). Nearly 20% of the progeny that could not be assigned pollen parents within the population with confidence (<80%) may have resulted from foreign pollen immigration from outside the trial site. No evidence of selfing was detected in the tested progeny.

In total, 60 pollen donors were identified, representing 60 full-sib families, with 31 families comprising of more than one offspring. Four full-sib family groups accounted for 26.9% of all the assigned offspring (Fig 4b.2).

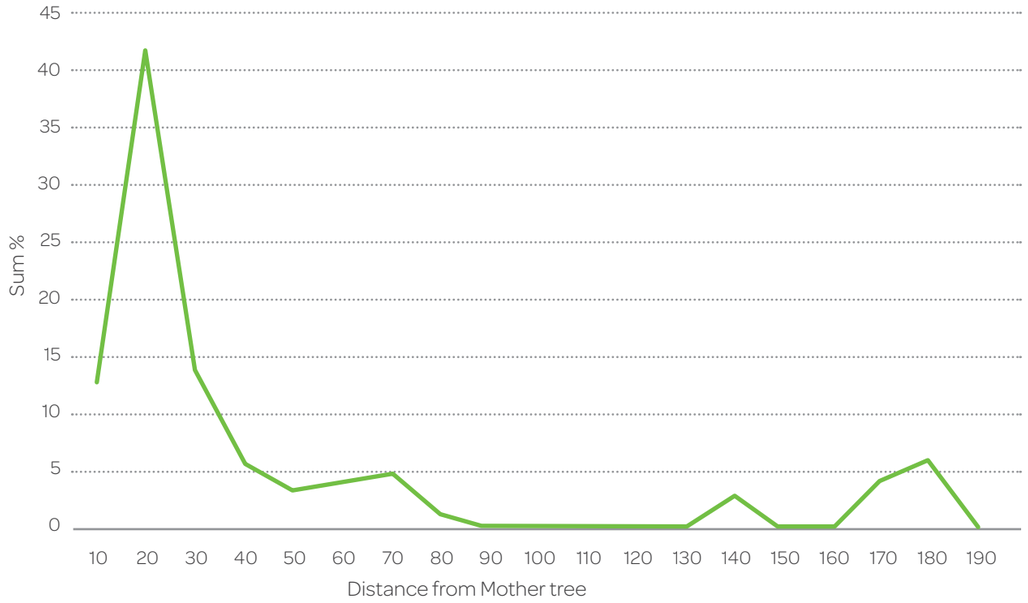


Figure 4b.1. The distance of effective pollen distribution in KI64. Progeny assigned to pollen parents within the trial site were divided into classes based on the distance between the pollen parent and the mother tree. The number of progeny in each class is represented as a percentage of the total number of seedlings analysed from assigned within the trial site.

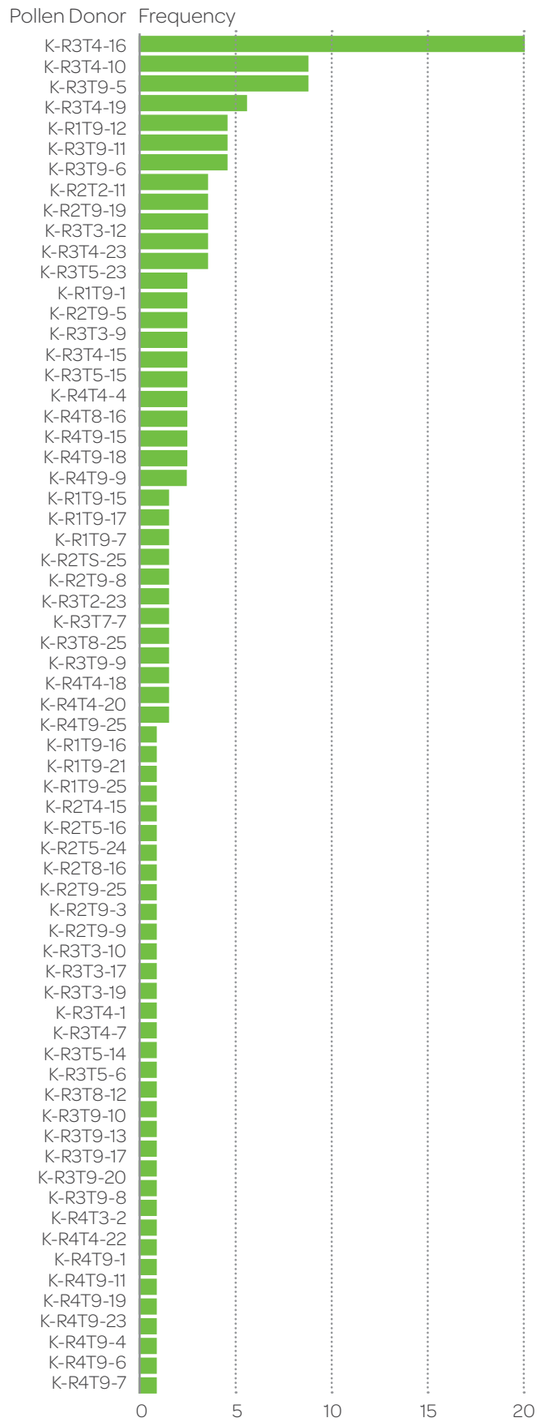


Figure 4b.2. Identified pollen donors and family distribution.

Weather conditions were not considered to play a major role in the dispersal of pollen at KI64, as no correlation was identified between the direction from which the majority of pollen originated and wind direction and speed during time of flowering. Many Eucalypt species are predominantly pollinated by insects, and it has been previously reported that the main pollination mechanism for *E. pellita* in Yogyakarta, Indonesia, was through flower visitors from the order *Hymenoptera: Apidae, Vespidae* and *Formicidae,* with the bee of *Apidae* being the most effective pollinator (Ratnaningrun et al., 2001).

These pollen flow parameters provide useful information about the dynamics of pollen movement within a *E. pellita* population and may be used in the design of seed orchards for *E. pellita* breeding programs, as well as in risk assessment of gene flow from plantations to adjacent areas of native forest in Tiwi.

Recommendations

With designing an open pollination seed orchard of *E. pellita* on Tiwi for seed production for second rotation deployment, the following recommendation should be considered:

- Utilising the top ranked trees identified from genomic selection as parents.
- The majority of pollen at KI64 was determined to be dispersed locally (54% at 20m; 87% at 80m) therefore keep selected trees for crossing within 20-80 m of each other.
- Ensure trees selected for crossing flower simultaneously, as this is likely to increase the likelihood of outcross mating and pollen dispersal. Further investigation looking at flower synchrony of existing populations of *E. pellita* on Tiwi is required and an important factor when considering selecting populations for future orchards for seed production. Seed production trees should be monitored carefully to record the flowering window of each tree, and seed from trees that flower without unrelated synchronously flowering individuals can be removed or overlooked at harvest. Flowering can be artificially stimulated by application of hormones such as paclobutrazol once the trees are fully established, however its use on *E. pellita* will require further investigation.
- Pollen contamination from sources outside KI64 was estimated to be approximately 19%. This illustrates the potential risk of unimproved pollen from outside the site/orchard negatively impacting the genetic quality of seed produced in an OP orchard. Open pollination orchards will also contain a large source of foreign pollen that may impact adjacent native forests through pollen dispersal and hybridisation. Implementation of risk management strategies would greatly reduce the likelihood of foreign pollen moving in and out of an open pollination orchard. Such strategies include the use of buffer zones and guard rows of non-compatible trees to catch the majority of dispersed pollen.
- As *E. pellita* has been reported to be primarily pollinated by insects/bees, they play a vital role in the wide dispersal of pollen. The use of honey bee hives inside a eucalypt seed orchard can increase pollen transfer, outcrossing rates and viable seed production. With that, it is also important to provide suitable habitat for pollinators to improve their abundance. The planting of unrelated heavy-flowering species near the *E. pellita* orchard, that do not overlap with the flowering period of *E. pellita* could assist in maintaining bee populations.

4c. Deployment Strategies (clonal/seed)

Seed production and clonal propagation

Seed production is a critical step in realising genetic gains from tree improvement programs as well as providing a reliable source of seedlings for deployment into next rotation plantations. A simple and cost-effective means to obtain seeds for second rotation plantings of *E. pellita* on Tiwi is to utilise the existing *E. pellita* sites at KI64 and Y28 can be utilised as seed production areas. These trial sites can be thinned to only include the top ranked trees as determined by genomic selection analysis, and remove underperforming trees, so that they cannot pass on their genes to the next generation.

A clonal seed orchard utilising cuttings from the top ranked trees can be established to increase seed production and direct deployment into plantation estates. Cloning can be achieved by grafting, rooted cuttings and tissue culture propagation. The advantage in using clonal seed orchards is the greater genetic gain due to more intensive selected orchard trees, and faster flowering due to the physiological mature nature of the scion. However clonal seed orchards can incur higher establishment costs and poorer genetic diversity.

Optimisation of clonal propagation methods for *E. pellita* using coppice shoots, cuttings and/or tissue culture protocols will be required in order to support clonal deployment of seedlings. However, these cloned seedlings from top ranked trees can also be used to establish an open pollinated seed orchard for seed production.

Open pollinated (OP) seed orchards are also relatively simple to establish and cost effective, and their use for large scale seed orchards is a common strategy for the development and deployment of genetically improved eucalypts. Outcrossing with elite but unrelated individuals in open pollinated seed orchards is encouraged a high degree of genetic diversity within the orchard. Reducing the number of relationships within the orchard is essential to avoid inbreeding depression. Increasing the range of represented provenances/populations contributes another level of genetic diversity to produced seed, ensuring the resultant stands have a wider range of genes that may be important for overcoming unforeseen biological and climatic challenges in the decades to come. A Genomic Relationship Matrix (GRM) was created for the trees assessed in this project, which can be utilised to select elite but unrelated individuals for the establishment of any OP seed orchards.

Coppice for clonal propagation or stand re-establishment

Coppicing is a sustainable forestry technique that involves cutting back trees to ground level, leading to a strong vegetative response and regeneration of new shoots from the stump. Utilising coppice for clonal propagation can be an efficient and sustainable way to produce large numbers of genetically identical plants, for deployment as well as for the establishment of a seed orchard. Like several other Eucalyptus species, *E. pellita* has an ability to resprout from the cut stump via dormant epicormic buds under the live bark, and this has been demonstrated in trees harvested at KI64 and Y28 (Fig 4c.1). Significant regrowth seven months post harvesting was seen on all inspected stumps, providing a reliable source for clonal propagation and maintaining the existing germplasm on Tiwi.

Following any harvesting of top-ranking trees, and coppiced shoots have grown and matured, healthy and vigorous shoots can be selected for clonal propagation, for creating new plants. Another possible means of producing coppice without harvesting the whole tree may be through a 'scarring' technique, whereby an incision is made into the stem of a standing tree to induce coppicing from that point. This method will require significant development and optimisation for it to be successfully applied to *E. pellita* trees in Tiwi.



Figure 4c.1. Coppice regrowth seven months post tree harvest at KI64 and Y28.

A harvested *E. pellita* stand can also be regenerated through coppice. Reports have been made from a *E. pellita* site in South Sumatra, where at the end of rotation (6 years after establishment) a coppice stand had substantially higher productivity compared to a replanted seedling stand (Hardiyanto et al., 2022). The coppice stand also had higher biomass production but slightly lower wood density than the seedling stand. Coppice reduction to one stem at 2 months after tree felling produced the stand with slightly greater diameter than that at 4 months after tree felling, but had approximately the same volume. Therefore, if the existing *E. pellita* plantations on Tiwi were to be harvest, these sites could possibly be re-established through coppice regrowth, which would also maintain the existing germplasm on the islands.

Summary of project's key findings and recommendations

1. Characterisation of standing trees by genotype

- The hybrid analysis of trees at KI64 and Y28 revealed that the documented provenance details based on seedlot information and hybrid identities was unreliable. LEA genetic structure analysis assigned the individual trees from 10 seedlots at KI64 and Y28 to clusters, confirming the identity of each tree as either pure *E. pellita*, *E. pellita* x E. urophylla hybrid or *E. pellita* x E. brassiana hybrids.
- Further in-depth genomic structure analysis of *E. pellita* and hybrid trees assessed at KI64, Y28, A3b, I18 and Y48 identified ten subpopulations for which subsequent phenotypic and genetic analyses was conducted.
- It is important that the existing population be as genetically diverse as possible to sustain multiple generations of selection and improvement without exhausting useful genetic variance. Genetic diversity within the population of trees assessed at KI64 and Y28 was determined to be moderate, indicating that there is a reasonable degree of genetic variation among individual trees within the Tiwi *E. pellita* population, ensuring its adaptive potential to environmental changes. No significant differences were detected between observed and expected heterozygosity in all subpopulations, therefore a seed orchard consisting of these trees can be expected to maintain its genetic structure in the next generation, through open pollination and thereby support genetic resource conservation. Utilisation of GRM for any potential OP seed orchards and breeding program can help guide selection of elite but unrelated trees to maintain genetic diversity.

2. Characterisation of standing trees by phenotype

- Significant differences in wood properties exist between sites and genotypes, with trees at red sandy soil sites showing faster growth and higher pulp yield, whilst sandstone soil sites produce denser, stiffer wood. Recommend selecting site-specific genotypes and considering soil type when establishing plantations to optimise wood quality for target end-uses.
- Faster growth correlates with lower kraft pulp yield but higher mechanical properties and lignin content. Recommend balancing rotation length based on intended product—shorter rotations (5–7 years) for pulpwood, longer rotations (>7 years) for solid wood applications requiring mature wood.
- Pure *E. pellita* excels in growth traits; *E. pellita* × E. brassiana (backcross) demonstrates superior density and mechanical properties. Recommend deploying genotypes strategically based on site conditions and specific product objectives.
- Xylem maturation occurs at approximately 6–7 years in large trees based on microfibril angle stabilisation, with smaller trees maturing slower. Recommend establishing minimum harvest rotation thresholds based on growth class to ensure adequate mature wood proportion in harvested logs.
- At high-productivity sites, growth class significantly affects wood properties; at low-productivity sites, properties are more uniform. Recommend competitive thinning at productive sites to reduce wood property variability and promote more uniform wood quality.
- Wood density exhibits greater seasonal variability during juvenile compared to mature phase. Recommend monitoring wood density during early growth as an indicator of environmental stress responses and water availability impacts.
- Breast-height measurements reliably predict whole-tree wood properties. Recommend using breast-height sampling with non-destructive tools for rapid, cost-effective population-level wood quality assessment in standing trees.
- Strong positive correlations exist between density measures and cell wall thickness; negative correlations between microfibril angle and mechanical properties. Recommend developing multiple-trait selection strategies in breeding programs to simultaneously improve correlated traits.
- Significant genotype × environment interactions exist for height, basic density, total lignin, klason lignin, and extractives at different sites. Recommend developing site-specific deployment strategies and validating genotype performance across diverse environments before large-scale deployment.

- The AMMI statistical model was used to diagnose the G × E interaction pattern of growth and wood properties of *E. pellita* subpopulations on Tiwi. Based on the traits of interest, findings from the AMMI analysis can be utilised to select genotypes that are not sensitive to environmental changes or selecting genotypes specific to different environments, in order to maximise expected gains resulting in higher stand productivity.
- A major limitation in the GxE assessment is that only two environments/sites were assessed, therefore testing these ten subpopulations across more diverse sites and environments would provide valuable information on the stability and/or adaptability of the tested genotypes.
- SilviScan, NIRS, and Resi provide reliable, rapid assessment of wood properties without tree damage, enabling assessment of large populations. Recommend integrating non-destructive testing into routine plantation monitoring and breeding programs for efficient resource characterisation.
- Trade-offs between growth and wood properties vary by trait and genotype, requiring multi-objective breeding strategies. Recommend developing breeding objectives that balance productivity with wood quality, considering market demands and end-use applications for *E. pellita* plantations.

3. Wood Products and Processing

- *Eucalyptus pellita* hybrids demonstrated strong potential as plantation grown structural timber resources. Hybrids involving E. brassiana consistently showed superior stiffness, strength and compressive performance, meeting Australian structural grading requirements and supporting their use in both solid wood and engineered wood products.
- Wood quality was influenced by both genetics and site productivity. High productivity sites produced trees with better stem form, higher processing recovery and more consistent wood properties, highlighting the importance of matching hybrid deployment to site conditions.
- E. urophylla hybrids exhibited favourable dimensional stability with lower shrinkage values, while E. brassiana hybrids generally produced higher wood density and mechanical performance. These complementary traits provide valuable opportunities for targeted breeding and product development.
- Processing trials confirmed the suitability of selected hybrids for sawn timber, veneer and laminated veneer lumber (LVL) manufacture. Veneer recoveries exceeded 70% in some cases, and LVL products achieved satisfactory strength, stiffness and bond quality, demonstrating commercial potential for value added processing.
- Several genetic markers (SNPs) associated with wood density, shrinkage, mechanical properties and log quality traits were identified. These markers provide a foundation for marker assisted selection to accelerate breeding programs and improve wood quality, processing recovery and product performance.
- Future breeding, plantation management and deployment strategies should integrate both phenotypic and genomic information. Priority should be given to selecting hybrids with favourable density, dimensional stability, mechanical properties and log form, while aligning genotype choice with site productivity to maximise value recovery, resource efficiency and long term plantation profitability.

4. Breeding and Deployment

- Utilising genomic selection models to calculate the estimated breeding values for the Tiwi *E. pellita* resource, the top 100 ranked trees were identified based on trait weightage recommendation from Midway: 60% volume, 30% density and 10% KPY (Table 4a.1).
- These top ranked trees can be utilised for seed production, clonal propagation and establishment of an open pollinated seed orchard, to support deployment of *E. pellita* seedlings to plantation estate.
- Utilise the available genetic information and molecular marker data to implement an optimised tree breeding and mating design to achieve long-term and sustainable genetic gain. Genomic mating will help to develop superior trees by selecting the best parental genotypes for breeding.
- Pollen dispersal was investigated at KI64 and the majority of pollen was determined to be dispersed locally (54% at 20m; 87% at 80m). Therefore in an open pollinated seed orchard, keep selected trees for crossing within 20-80 m of each other.
- Self-pollination was not detected, however pollen contamination from sources outside KI64 was estimated to be approximately 19%. This illustrates the potential risk of unimproved pollen from outside the site/orchard negatively impacting the genetic quality of seed produced in an OP orchard. Implementation of risk management strategies will be required to reduce the likelihood of foreign pollen moving in and out of an open pollination orchard.
- Further investigation into flowering synchronicity is required as timing of flowering can impact seed production and the likelihood of outcross mating and pollen dispersal.

Program 3 – Increasing First Nations participation in northern Australia's forestry sector

Submission to the ForestWorks Scoping Study for the Department of Agriculture, Fisheries and Forestry (DAFF), Forestry Workforce Training Program

A submission was coordinated by Alicia Boyle at Charles Darwin University and prepared by the members of the Forestry Industry Association Northern Territory, Tiwi Plantation Corporation (TPC), Gumatj Corporation, Charles Darwin University, the Northern Territory Government's Department of Industry, Tourism and Trade, and Midway Limited to DAFFs $10 million Forestry Workforce Training Program. This Program aims to support the delivery of skills and training to meet the requirements of Australia's forest and wood products sectors.

Alicia used the knowledge gained by preparing the Tiwi Islands Forestry Workforce Profile and her work alongside the TPC to contribute to multiple online workshops and interviews with ForestWorks. She recognised the importance and need for a coordinated, collaborative First Nations voice to the national Scoping Study. Over four months authors and designers prepared the submission that identified a locally developed, collaborative pathway to increased and sustainable employment. ForestWorks provided their final report to the Australian Government in November 2023, setting out 19 recommendations for piloting action and implementation of the Program. All of the recommendations included in the 'Increasing First Nations Participation in Northern Australia's Forestry Sector' submission were adopted in the final report to DAFF.

Implications of the work for Tiwi forestry

Tiwi aspire to own and manage forestry operations on their land, which creates jobs, business opportunities and economic self-determination. To achieve this objective, training and development opportunities must be structured to create the capabilities to work effectively in complex commercial operations, while also maximising opportunities for employment and career progression from entry level jobs through to executive management and business governance.

Three key platforms were identified in the submission and ultimately supported for delivery and funding ($780,000) as part of the Forestry Workforce Program. These platforms are:

- Coordination of training and development for the Northern Australian Forestry Industry
- Building awareness through engagement
- Appropriate training and development initiatives for First Nations people in the Northern Australian forestry industry

For Tiwi forestry this means an opportunity to benefit from:

- An identified position working across Tiwi governance structures, forestry managers, employment service providers, Registered Training Organisations (RTOs), Group Training Organisations (GTOs) and schools that can assist to better understand the workforce needs of industry, and coordinate efforts to increase the awareness of employment opportunities in Tiwi forestry, assist in the identification of potential employees and support the development and delivery of appropriate education and training of all Tiwi forestry employees
- Tiwi mentors, employed to raise awareness of the benefits of forestry in their communities (and schools), to mentor new Tiwi forestry employees, to assist with the delivery of forestry training, and to support all Tiwi forestry workers to flourish in the intercultural workplace
- The identification and development of local workplace trainers (and assessors)
- The development of a tiered yet comprehensive training framework that includes locally contextualised subject matter and culturally appropriate materials
- Contributing to and learning from a national forestry workforce development program

Skill development and workforce exposure performance dashboard figures to May 2026 include:

- 55 Tiwi plantation employment placements since June 2025
- $600,00 salary and $60,000 super paid to Tiwi workers as of January 2026
- 21 Enrolments and 18 Completions in the Tiwi Ready Pre-Employment 5-day program, including Workforce Credentials, Financial Literacy, Tiwi Health, and Tiwi Tech – Digital literacy
- 16 Enrolments and 7 Completions, with 2 more Completions by June 2026 in Certificate II in Forest Operations
- 6 Senior First Aid Completions
- 7 Forklift licence Completions
- 25 Deadly Thinking – Mental Health First Aid Completions
- 8 Bushfire/Wildfire training Completions
- 25 Talking About Suicide Completions
- 16 Alcohol and Drugs in the Workplace Completions

Codesigning the future in the intercultural workspace of the Tiwi Islands forestry industry

PhD Candidate, Alicia Boyle, Charles Darwin University

Alicia Boyle is undertaking a PhD project, part-time based Charles Darwin University in Darwin. The study will take advantage and build on the existing relationships Alicia has developed over the past four years whilst working on the Cooperative Research Centre for Developing Northern Australia (CRCNA) project 'Maximising Northern Tropical Forestry – Linking Communities and Cutting-Edge Technology'. Her project aims to better understand and potentially redesign the intercultural workspace in Tiwi forestry to make it a place where Tiwi people not only want to work but also flourish, and that meets the commercial goals set by the Tiwi Plantations Corporation and its forestry management partners.

The Tiwi want the forestry industry to play an integral role in their future economic independence and skills-building strategy. The 30,000-ha plantation site is on Tiwi land and is Tiwi-owned, governed by the Tiwi Plantation Corporation (TPC), and managed by the TPC-appointed company, Midway. Whilst the majority of the first rotation of *Acacia Mangium* has been chipped and exported, a second rotation of *Eucalyptus pellita* is underway. Despite the plantation's existence for over 20 years, there has been no consistent progress toward high levels of Tiwi employment. The purpose of the research is to explain and address this ongoing employment challenge by examining past and future undertakings surrounding the plantation workspace from an intercultural perspective.

Rather than approaching this challenge solely as a workforce participation issue, the study conceptualises Tiwi forestry as an intercultural workspace, a space where Tiwi governance systems, cultural responsibilities, organisational practices, and broader economic structures intersect. The project asks not only how more Tiwi people can participate in forestry, but more fundamentally:

What does a good job in Tiwi forestry look like from a Tiwi perspective?

To explore this question, the study adopts an integrated theoretical framework combining Amartya Sen's Capability Approach and Pierre Bourdieu's Theory of Practice, underpinned by Indigenous Standpoint Theory. Sen's framework provides a way of understanding whether forestry expands people's opportunities and freedoms to live lives they value. Bourdieu contributes an understanding of how power, recognition, and different forms of capital shape participation and opportunity within organisational and intercultural settings. Indigenous Standpoint Theory ensures that Tiwi knowledge, values, and collective priorities remain central to how these experiences are interpreted and understood.

Methodologically, the project uses Participatory Narrative Inquiry (PNI) to collect stories from current and former Tiwi forestry workers, Tiwi Plantations Corporation Directors, and others connected to forestry over time. Narrative approaches enable participants to share experiences in ways that foreground relationships, meaning, and lived experience rather than relying on externally defined categories. Stories will explore experiences of work, leadership, learning, culture, governance, recognition, and future aspirations.

The project also incorporates collaborative sense-making processes, allowing participants to collectively reflect on emerging themes and consider future opportunities for Tiwi forestry. Rather than seeking to fit Tiwi experiences within existing workplace models, the project aims to understand how forestry can better align with Tiwi priorities and support both individual and collective wellbeing.

Potential outcomes of the research include:

- A stronger understanding of what meaningful and valued work in Tiwi forestry looks like from a Tiwi perspective
- Greater understanding of the relationship between employment, culture, governance, and collective futures
- Practical insights to support future workforce development and planning
- Improved pathways for Tiwi participation and leadership in forestry
- Contributions to broader discussions concerning Indigenous economic participation and intercultural workplaces globally

Tiwi Forestry Workforce Plan 2026–2030 and Tiwi Forestry Seasonal Calendar

Alongside the PhD research, collaborative work undertaken with Tiwi Plantations Corporation, Midway, Tiwi Islands Training and Employment Board and partner organisations resulted in the development of the Tiwi Forestry Workforce Plan 2026–2030 and the accompanying Tiwi Forestry Seasonal Calendar. These resources have now been published and distributed across the Tiwi Islands and to schools on both the Tiwi Islands and in Darwin to support awareness of forestry career pathways, seasonal work patterns, and future education and training opportunities.

The Tiwi Forestry Workforce Plan 2026–2030 and the supporting Tiwi Forestry Seasonal Calendar are available online

Report: Boyle, A. and P. Tremblay (2022) Tiwi Islands workforce profile

- Overall WAP participation over the last 2 decades appears to have decreased, in part related to COVID and changes associated with CDP – in ways similar to other remote NT regions
- Dominating industries of employment also comparable to other remote regions (without mining) usually dominated by public administration, education and other services (although these are somewhat declining) and with health being less significant than elsewhere due to the proximity of Darwin's hospitals. Data exploring jobs filled and unfilled in Wurrumiyanga, Milikapiti and Pirlangimpi replicate the same patterns and inter-connected employment offerings.
- The Agriculture, forestry and fishing sector employs relatively small numbers of locals (although some Tiwi locals residing in Darwin and FIFOs are less documented).
- Forestry employment over the various phases of the plantation has been fragmented, given the changing approaches reflecting different ownership priorities, commercial strategies, infrastructure developments (Port Melville in particular) and management emphasis. Data pertaining to the first rotation was not sufficiently detailed and dependable to support an historical analysis, but provides some clues as to the activities which provide greatest employment opportunities for locals around the plantation cycle and related port activities.
- Second rotation employment needs, investments and monitoring will need to be properly documented and systematic if locals are to benefit from plantation work opportunities.

Report: P. Tremblay (2024) Tiwi Plantation micro-business opportunities

An exploration of business or commercial opportunities related (but notionally external) to the Tiwi Islands plantation made use of multiple information sources and incorporated an extensive literature review of international sources considering forestry, plantations in particular, First Nations remote regions, Indigenous small business entrepreneurship, and challenges or barriers to Aboriginal business participation in remote regions. It overviewed Tiwi-related documents and interviews, stakeholders' perspectives, and stated Tiwi aspirations related to employment, business control and current or realistic access to skills and capabilities in the short-run (as opposed to potential larger-scale investments in the competences and business know-how that could be imported or developed in the long-term). The report identifies a set of "micro" business opportunities that feature the following attributes:

- They arise because of the presence of the plantation (its continued existence) and the activities it generates locally (in Tiwi), but they are not completely dependent on the latter and could potentially supersede and extend their business scope while continuing to employ Tiwi locals. The ability of a small local business to satisfy the needs of the plantation at competitive conditions (if they offer essential goods or services) and secure lasting contracts without imposing a burden on the latter is a complex issue;
- They fit the long-term commercial vision of the Tiwi leadership to create jobs and business activities that don't simply reflect the provision of traditional welfare or support services (education, health, safety, basic amenities, other government services, etc.) and could contribute towards building business skills (the first report appendix overviews those aspirations as stated over many decades), decreasing reliance on external transfers and fickle government pledges and assistance (and instead "build a Tiwi private economy");
- They would be of limited scale and not excessively demanding in terms of business skill requirements, as well as technological capabilities (or could be realistically and locally connected with the acquisition and upkeep of required vocational skills and relevant technological inputs to ensure their competitive advantage);
- It would be feasible for individuals (or small groups) to navigate the local politics associated with the provision of any set of goods or services without competing with established corporations, and to obtain the required legal and regulatory permissions needed to operate in selected locations.
- There would be sufficient readiness to operate relatively quickly without excessive dependency on either government or the plantation direct financial or technical support (although this varies across the types of opportunities listed below).

The report ultimately highlights some business opportunities and domains which differ with respect to their likelihood of success, their timeframes, the potential balance between advantages, risks and disadvantages, and their potential to extend beyond the plantation activities themselves. Those examined include:

- Nursery businesses
- Childcare services
- Transport-related services (including infrastructure maintenance)
- Vehicle maintenance, workshop services and trades
- Environmental, biosecurity and waste management services connected with the plantation
- Timber milling and processing
- Outsourcing plantation basic services (hospitality services and workplace trainers and assessors)

The report includes a discussion of the some cross-cutting and interdependent issues linked with competition (with other business organisations), independence from the plantation (and the latter's need to not in turn see its operations undermined by being locked-in agreements with non-competitive local suppliers), the reliability of training providers and the nature of the employment market in Tiwi.

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