




Article

Incidence and Severity of End-Splitting in Plantation-Grown *Eucalyptus pellita* F. Muell. in North Borneo

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Abstract: *Eucalyptus pellita* F. Muell. is currently the predominant tree species deployed for tree plantation establishment in some parts of Borneo, particularly Sabah state, Malaysia. Its low disease susceptibility, good growth and form, and desirable wood properties make *E. pellita* particularly suitable for plantation development in the wet tropical regions of south-east Asia. In spite the many positive traits, practical field observations indicate that the species is susceptible to end-splitting. There is some anecdotal evidence to suggest a genetic relationship with the incidence of end-split, although these observations were not statistically tested. This study evaluates the occurrence of end-splitting in five-year old plantation *E. pellita* in Sabah as affected by family and growth attributes. An existing progeny tree breeding trial, involving seeds that originated from Papua New Guinea, China, Vietnam, Australia, Sabah, and Sarawak with 106 families, was used to carry out the split assessment. Logs from the second thinning were cut into 2.2-m-long sections. The end splits were measured three days later; the incidence and severity of splitting were assessed at both the large and small ends of each log by using a designated split scoring system. The study shows that 99% of all log cross sections (per cut surface) experienced signs of splitting, with an average of 2.7 splits per cut surface. Overall, 54% of all splits were classed as ‘Three-Quarter Radial Splits’ while the occurrence of internal splits was negligible. Split severity showed a heritable and significant difference ($h^2 = 0.24$ at $p \leq 0.05$) among the family levels. Splitting was also significantly related to growth factors such as tree height and diameter at breast height (DBH). The findings suggest that end-splitting is caused by family–environment interactions. This offers the opportunity to improve the wood resource of *E. pellita* via breeding strategies.



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1. Introduction

Eucalyptus pellita F. Muell., also known as red mahogany, occurs naturally in the tropical regions of north-eastern Queensland, Australia, and the island of New Guinea [1]. It can reach heights of up to 40 m and about 1 m diameter at breast height with a usually straight stem form. It grows in gentle to moderate sloping terrain mixed with other eucalypt species in tall open forests and at the fringes of tropical rainforests. It prefers sand to loam soil types with good drainage at altitudes from sea level to 800 m above sea level with moderate to high rainfall of 900 to 4000 mm annually. It is one of the few *Eucalyptus* species that is adapted to the wet tropical climate and thus less susceptible to fungal leaf

pathogens [2]. This adaptation, together with other positive traits, makes it suitable for plantation establishment in wet tropical regions outside of its natural range.

The recent devastation caused by *Ceratocystis* vascular wilt disease [3,4] has resulted in almost all *Acacia mangium* Willd. plantations in the Malaysian state of Sabah being replaced by *E. pellita*. Since 2012, large-scale *E. pellita* plantations and tree breeding orchards have been established in Sabah and Sarawak states in the north of the island of Borneo [5]. Up until 2020, Sabah had planted about 36,200 ha (source: company data) with *Eucalyptus*, with the main species being *E. pellita*, along with *E. grandis* W. Hill., *E. urophylla* S.T. Blake., and eucalypt hybrids. A study by Japarudin et al. [6] showed that *Eucalyptus pellita* had highly productive growth in Sabah (Mean annual increment (MAI) $27.6 \text{ m}^3 \text{ ha}^{-1} \text{ year}^{-1}$) compared to other potential species in a taxa trial. A study revealed that among the three species, namely, *E. grandis*, *E. urophylla*, and *E. pellita*, *E. pellita* has superior characteristics in both the growth rate and wood properties [7]. Hii et al. [8] and Japarudin et al. [9] studied the properties of *E. pellita* from Sarawak and Sabah and found that it possesses good properties for solid wood and veneer, consistent with earlier studies [10,11]. Unfortunately, the studies also confirmed the brittle nature of *E. pellita* and its tendency towards end-split formation. Solid wood recovery of *E. pellita* was reduced by as much as 50% of the viable log length due to longitudinal propagation of end-splits [9]. There were also anecdotal observations that there could be a provenance effect on end-split incidence, although insufficient samples did not allow for a statistically significant result [9].

Many studies have associated growth stress with an increase in the severity of end-split in logs [12,13]. Beltrame et al. [12] investigated the relationships between the level of longitudinal residual strain (DRL) and the longitudinal growth stresses (TCL) and their effects on the extent of log end-splitting (IRT) of *Eucalyptus* spp. They discovered that there were significant and positive correlations between DRL/TCL variables and IRT. Thus, it is possible to predict the trend of IRT by performing an evaluation of DRL in the field. Owing to that, this variable has become a reliable tool for the selection of clones less prone to splitting [14]. A high magnitude of longitudinal growth stress has a significant implication in recovery and processing of high-quality timber. Although longitudinal growth stresses are inherent in all trees, their magnitude varies from species to species and also within species. These stresses can cause ring shake and brittle heart in standing trees, end-splitting in logs within a short time span from harvest, severe splitting in timber immediately after sawing, and twisting and cracking in timber during drying [15,16]. Hence, growth stresses have become a major wood quality criterion in the selection of superior genetic material and also in assessing the economic values of logs. Addressing log end-splitting and distortion of timber due to growth stress is necessary if eucalypts are to succeed in solid wood or veneer markets [17]. This study evaluates the incidence and severity of end-splitting and possible effects of family and growth characteristics in *E. pellita* planted by the Asian Forestry Company Sabah (AFCS) in Northern Sabah.

2. Materials and Methods

2.1. Trial Site

The location of the trial site is shown in Figure 1. It is located at 260 m above sea level, has a mean slope of 24° , and high, unevenly distributed rainfall throughout the year ($>3000 \text{ mm}$), with drier summer months from March to October (ca. 200 mm per month) compared to more than 400 mm per month from November to February.

The soil type is classified as a Kumansi (red-yellow podzolic soil) with a clay content of about 50% and good drainage, but some seasonal waterlogging during the rainy season, and an effective rooting depth of 87 cm. Three soil pits were established on the upper, middle, and lower slopes. The soil type was classified by use of Sabah terminology (Figure 2, Table 1). The soil texture was assessed by use of a soil texture triangle to estimate clay, sand, and silt contents by the hand-feel test [18]. Effective rooting depth was measured to the last visible root in the soil profile. Other soil parameters such as soil structure, soil consistency, and stone and root abundance were assessed using The Food and Agriculture

Organization (FAO) Guidelines for Soil Description. Other aspects such as waterlogging or drainage characteristics were recorded. Details of the trial site are summarized in Table 1.



Figure 1. Location of the trial site at Asian Forestry Company (Sabah) Sdn Bhd (AFCS). Source: Google Earth.



Figure 2. Soil profile of the middle slope with Kumansi soil type and silty clay (50% clay) as soil texture.

2.2. Families and Trial Design

The 106 improved families used in the AFCS progeny trial originate from progeny tree breeding trials in China, Vietnam, and Papua New Guinea. These progeny trials were established with improved material from other breeding programs such as Ingham seedling seed orchard (SSO), Danbulla SSO, and Kairi SSO, and with material from Vietnam ex Bao Bang SSO. The trial also contained material from wild collections of individual mother

trees harvested in Queensland, Australia. The two improved bulk seed sources were from breeding programs in Sabah and Sarawak.

Table 1. Site Information.

Description	Data
Type of Trial:	<i>Eucalyptus pellita</i> F. Muell. Progeny Trial
Trial Owner:	Asian Forestry Company (Sabah) Sdn Bhd (AFCS)
Trial Location:	Coupe 7, Block 1 & 2, Kota Marudu District, North Sabah
Latitude—Longitude:	6°30′8.82″ N 117°2′50.38″ E
Elevation:	260 m above sea level
Mean Annual Rainfall:	3140 mm
Mean Slope Degree:	24°
Soil Type:	Kumansi
Soil Texture:	Silty Clay (50% Clay)
Drainage:	Good with some periodic waterlogging in the rainy season
Effective Rooting Depth:	87 cm
Parent Material:	Sandstone
Planting Date:	May 2015
Assessment Date:	May 2020
Trial Age at Assessment:	5 years
Spacing:	3 m × 3 m

The AFCS trial was laid out using a randomized incomplete block design and was planted in May 2015 with nine replications. For every replication, there were 108 families that were planted in 18 blocks with six families in each block. Three trees per family were planted in line plot formation within each block (Table 2). Therefore, there were 27 trees planted for each family (3 trees × 9 replications) or 324 trees (18 blocks × 6 families × 3 trees) planted in one replication, with a total of 2916 trees altogether.

Table 2. Genetic material and trial design used in the AFCS *Eucalyptus pellita* F. Muell. progeny trial.

Origin of Seed Material	Papua New Guinea, China, Vietnam, Queensland, Sabah, Sarawak
Trial Design	Randomized Incomplete Block
Replications	9
No. of blocks per replication	18
Total no. of families	108
No. of families per block	6
Trees per families	3

2.3. Height and Diameter Measurements

The trial trees were first measured for height and diameter at breast height (DBH) together with a form assessment once they reached three years of age. After that measurement was taken, the first inferior tree per family in each replication was removed. When the trees were five years old, the second measurement of the height and DBH was carried out, at which stage the trial area was converted to a seed orchard (SSO) by removal of the second inferior tree per family per replication. Trees felled during this stage were denoted as second thinning and were used in this study.

2.4. End-Splitting Assessment

Trees felled during the second thinning operation were used to carry out the split assessment. The number of trees felled and assessed are varied between family as it depends on the suitability of the trees during thinning operation. Out of 2916 trees in the trial design, a total of 486 trees that are still alive and having over bark diameter more than 10 cm were sampled. Immediately after felling, the trees were cut into 1144 pieces of 2.2-m-long billets up to a small end over-bark diameter of 10 cm. Each log was labeled

with the treatment number at both ends with the use of a crayon. Seventy-two hours (three days) after felling and cross cutting, the incidence and severity of end-splitting were assessed for both large and small log ends using a modified Commonwealth Scientific and Industrial Research Organization Australia (CSIRO) Split Scoring System (Figure 3). Splits were classified according to the radial distance impacted by the split. The scores were determined according to Table 3.

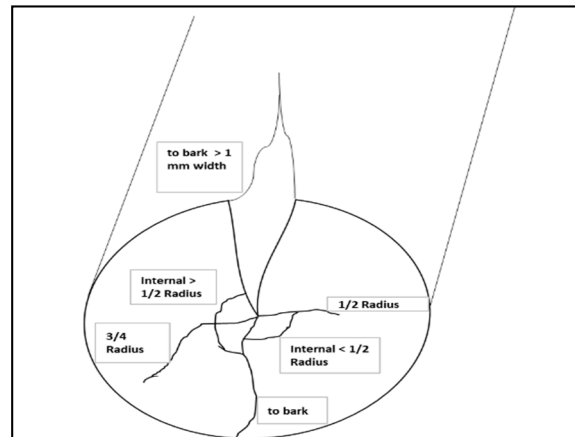


Figure 3. Modified CSIRO split scoring system showing type of splits in *Eucalyptus pellita* F. Muell. (Note: see Table 3 for Split Scoring Points assigned).

Table 3. Split scoring point assignment.

Description	Category (Split Type)	Scores
A split extending from the pith to half of the log radius	Half Radial Split (a)	1
A split extending from the pith to 70% of the log radius	Three Quarter Radial Split (b)	1.5
A split extending from the pith to the outer periphery of the log	Full Radius Split (c)	2
Pith to bark splits can open up at the outer circumference of the log and are measured in width by the use of an electronic caliper (Figure 4). Score is assessed for every 1 mm of gap ≥ 1 mm	Radial Split (d)	1 for every one millimeter (1/mm)
Internal splits tangentially connect the radial splits if they reach half the arc-circumferential length or part thereof	Internal Split (e)	1
If the internal split is longer than half of the log radius	Internal Split (f)	2



Figure 4. Measurement of split width for splits from pith to bark.

During the field assessment, the number of splits, n , per split category (a–f) was recorded. The total score for each log section was calculated for large and small ends as

$$\text{Split score} = \Sigma [n_a(1) + n_b(1.5) + n_c(2) + n_e(1) + n_f(2) + \Sigma d] \quad (1)$$

where

n = the number of splits per split category

a, b, c, d, e, f = split category according to Table 3

Σd = sum of the width of the split (mm) at the outer circumference

value in () = scoring points according to categories of splits in Table 3

2.5. Determination of the Split Sample Size

Prior to the analysis, the required split sample size per family was determined by use of the Yamane formula [19].

$$n_{\text{Yamane}} = \frac{N}{1 + N(e^2)} \quad (2)$$

where

n = split sample number/size

N = population

e = confidence level

The Yamane formula is suitable to determine the sample numbers required for studies with a known population size. All families with a total split sample amount below the 80% confidence level were excluded from the statistical analysis.

2.6. Determination of Narrow Sense Heritability

Narrow sense heritability (h^2) for the trait log end-splitting was calculated for open pollinated half-sib families with increased relatedness as follows:

$$h^2 = \frac{3\sigma_f^2}{\sigma_p^2} \quad (3)$$

with σ_p^2 comprising $\sigma_f^2 + \sigma_{fr}^2 + \sigma_e^2$

where

σ_f^2 family component of variance

σ_p^2 phenotypic component of variance

σ_{fr}^2 family \times replication (block) component of variance

σ_e^2 error component of variance

2.7. Statistical Analysis

The statistical analysis incorporated the randomized incomplete block design of the progeny trial, with data organized according to replication, block, plot, and treatment/family. The Statgraphics Centurion 18 software package (Statgraphics Technologies, Inc., The Plains, VA, USA) and R version 4.0.3 (R Development Core Team, R Foundation for Statistical Computing, Vienna, Austria) were used for data analysis. Analysis of variance (ANOVA) was carried out to determine the effects of family by split and growth by split relationships at the 95% confidence level. Multiple range testing with 95% Tukey's honestly significant difference (HSD) procedure was used to determine significant differences in splitting between individual families. Regression analysis was conducted to further analyze the relationships between tree height and splits, as well as between DBH and splits. R statistical analysis software was used to calculate narrow-sense heritability estimates (h^2) for the trait log end-splitting in *E. pellita*. For this purpose, the bulk seed sources, comprising numerous unknown families, were excluded from the data set and only individual families

were analyzed. Best linear unbiased predictions (BLUP) were applied using R, predicting log end-splitting by family.

3. Results

3.1. Split Type and Occurrence

In this study, *E. pellita* showed a high tendency towards end-splitting which suggests the wood is brittle. About 99% of all logs showed some signs of splitting on their cross-sectional surface with an average of 2.7 splits per cut surface. Three-Quarter Radial Splits were the most frequently observed split types with a 54% occurrence rate, followed by Pith to Bark Splits, with 35%, and Half Radial Splits, with 11% (Figure 5). It appears that Internal Splits rarely occur in *E. pellita* and only amounted to 0.02% of all split types observed.

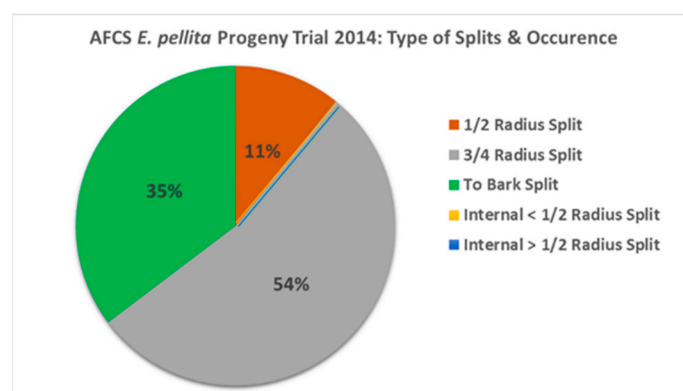


Figure 5. Split types and their occurrence rate (%) for *Eucalyptus pellita* F. Muell. in AFCS.

3.2. Family Effects and End-Splitting

Table 4 shows that end-splitting among the families is significantly different (at $p \leq 0.01$), which infers that end-splitting in *E. pellita* is, to some extent, under genetic control. This is further evidenced by the end-splitting score for different families of *E. pellita* in the AFCS plantation (Figure 6), which shows a near four-fold difference in the incidence of splitting between the families with the most severe splitting and those families with the least. The bar chart is arranged based on the occurrence of end splitting as denoted by different letters according to Tukey's test.

Table 4. Analysis of variance for the effects of family on log end-splitting.

Source	Sum of Squares	df	Mean Square	SD	F-Ratio	p-Value
Between groups	1744.63	86	20.2864	1.541	3.86	0.0000 ***
Within groups	5280.31	1006	5.24882			
Total (Corr.)	7024.94	1092				

*** Significant at $p \leq 0.01$.

Table 5 lists five families with high (having split scores of >7.0) and low (having split scores of <2.8) occurrence of end-splitting. In the AFCS progeny trial, there was a significant variation of 78% between the highest and lowest split score. The Sabah 129 family had the highest split occurrence, as well as severity, whereas Queensland 126 had the lowest (Figure 6). Based on these performances, about 3.4% (three families—Sabah 129, PNG 88, and Vietnam 43) in the AFCS breeding population had notably higher split occurrence and severity. In addition, families Queensland 126, Vietnam 41, China 3, Queensland 120, and China 21 all showed a low incidence and severity of end-split. It may be possible that careful selection of second-generation genetic material could select against end-splitting.

The narrow-sense heritability estimate (h^2) for the log end-splitting trait in *E. pellita* within the 106 families within the progeny trial was 0.24, indicating a reasonably high

genetic heritability for this trait. The best linear unbiased prediction (BLUP) for log end-splitting in *E. pellita* predicted split by family with results very similar to those of the actual split assessment, although some of the families changed with regard to the sequence of the severity ranking (Figure 7).

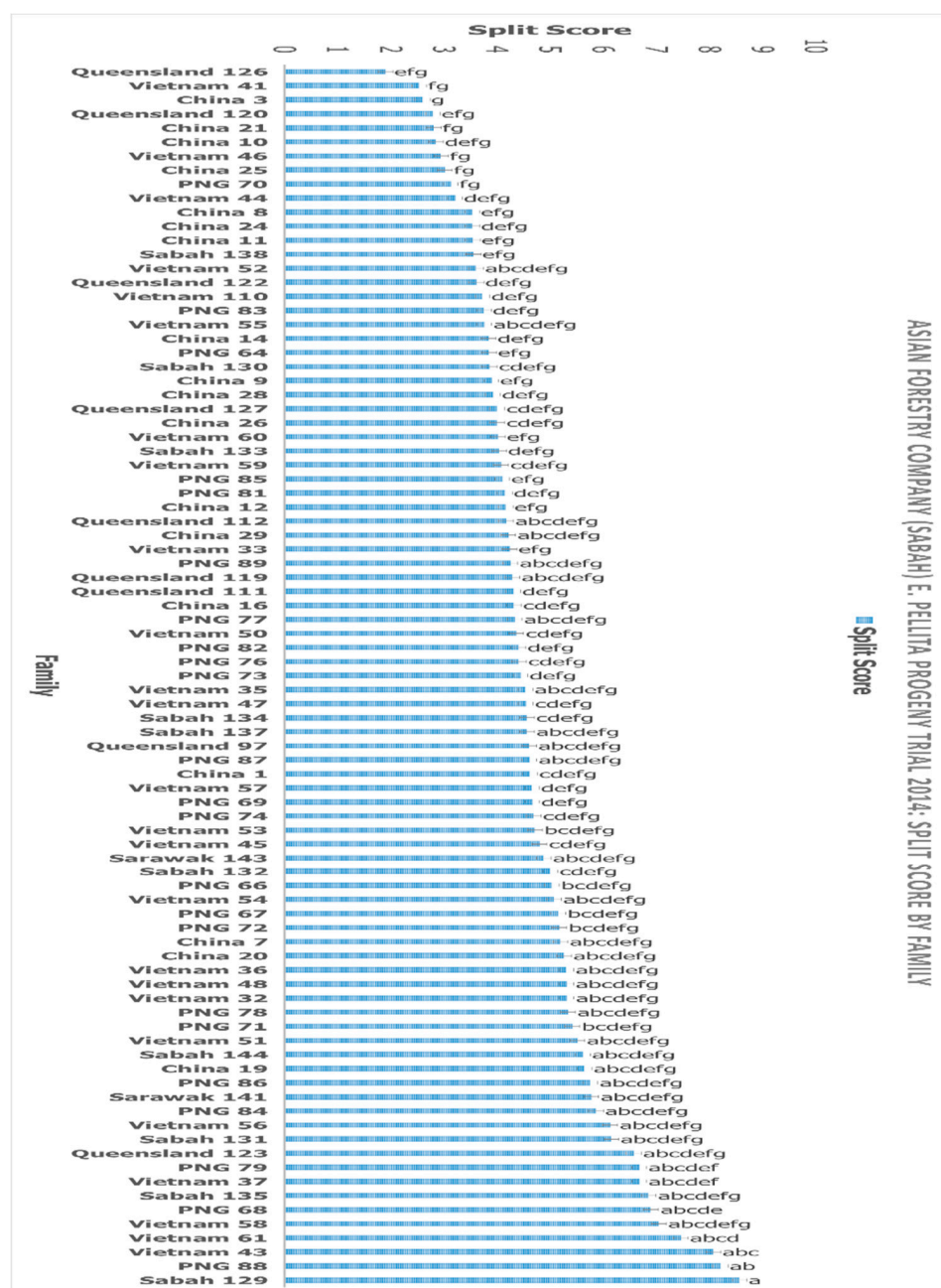


Figure 6. Mean split scores of *E. pellita* logs of different families obtained from the AFCS plantation site. (Note: Means followed by the same letters a, b, c, d, e, f, g are not significantly different at $p \leq 0.05$ according to Tukey's test).

3.3. Growth Effects and End-Splitting

Figure 8 illustrates the relationship between height and the occurrence of end-splitting in *E. pellita*. Based on the ANOVA (Table 6), tree height was statistically significant ($p \leq 0.01$) in relation to log end-splitting. A similar result was obtained for the relationship between DBH and end-splits, but at a lower significance level, i.e., $p \leq 0.05$ (Figure 9 and Table 7). Since the growth of a tree or a certain family is dependent on the site conditions, especially

soil characteristics, it can be construed that environmental factors in interaction with family genetics contribute significantly to log end-splitting in *E. pellita*.

Table 5. List of families with high (>7.0 score) and low (<2.8 score) occurrence of end-splitting.

High Occurrence of Splitting	Low Occurrence of Splitting
Sabah 129	Queensland 126
PNG 88	Vietnam 41
Vietnam 43	China 3
Vietnam 61	Queensland 120
Vietnam 58	China 21

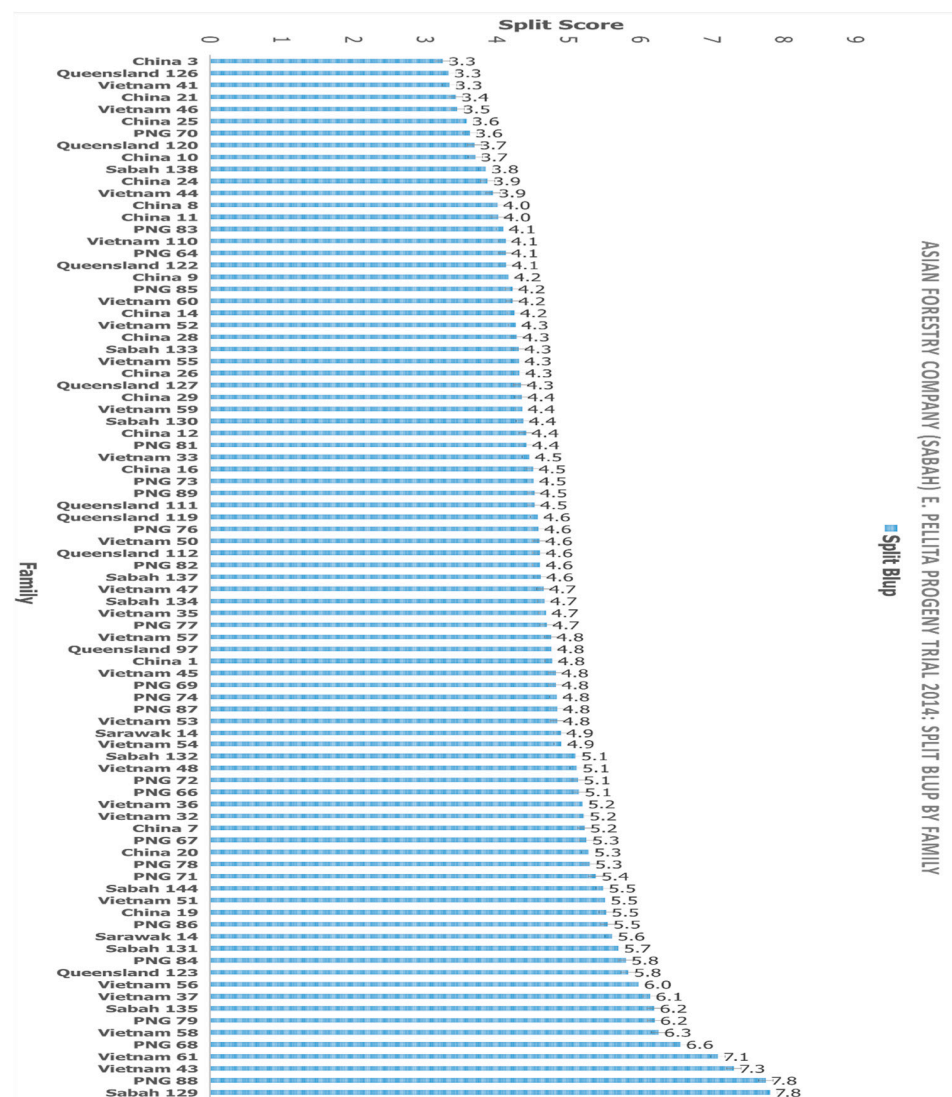


Figure 7. Best linear unbiased prediction (BLUP) for log end-splitting by family in *E. pellita*.

Table 6. Analysis of variance between log end-splitting and tree height.

Source	Sum of Squares	df	Mean Square	F-ratio	p-Value
Between groups	783.577	120	6.5298	1.8	0.0000 ***
Within groups	1035.89	285	3.63471		
Total (Corr)	1819.47	405			

*** Significant at $p \leq 0.01$.

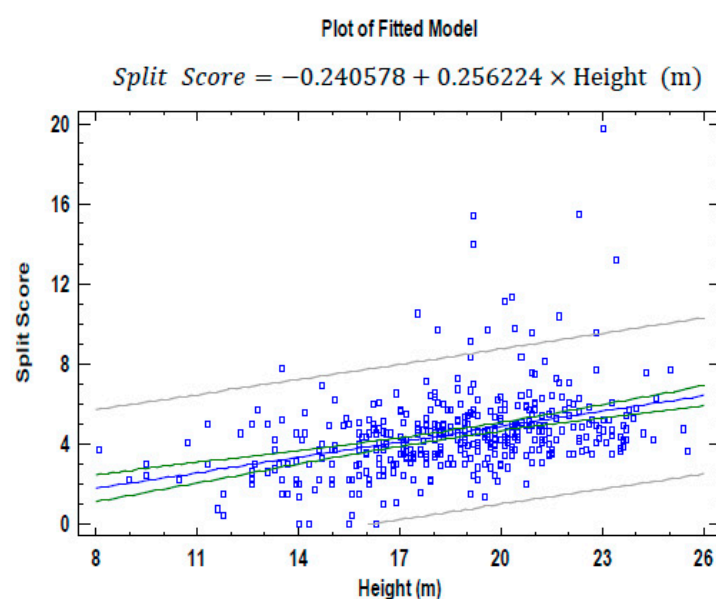


Figure 8. Simple regression for log end-splitting in relation to tree height.

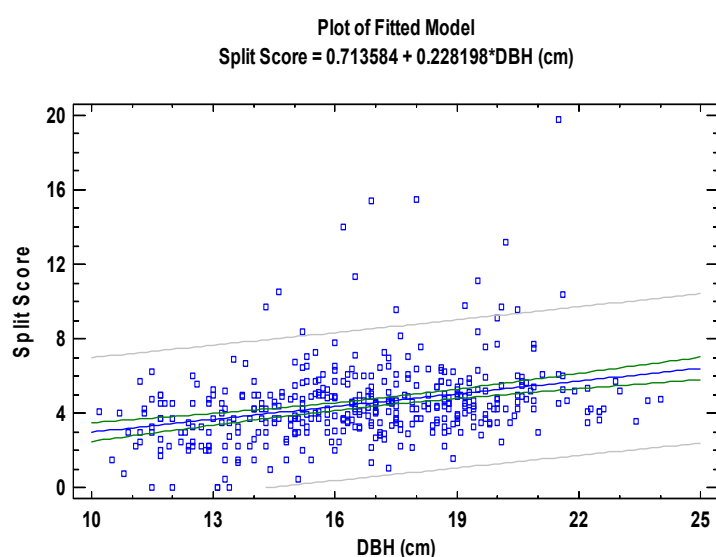


Figure 9. Simple regression for log end-splitting in relation to DBH.

Table 7. Analysis of variance between log end-splitting and DBH.

Source	Sum of Squares	df	Mean Square	F-Ratio	p-Value
Between groups	631.942	115	5.49515	1.34	0.0259 **
Within groups	1187.53	290	4.09492		
Total (Corr)	1819.47	405			

** Significant at $p \leq 0.05$.

4. Discussion

This study has shown that both family and growth characteristics (tree height and DBH) are the main factors related to end-splitting in five-year-old plantation-grown *E. pellita*. The AFCS progeny trial results revealed a significant and heritable influence of family variation on the end-splitting severity of *E. pellita* for the 106 families. The buildup and

release of growth strain (stress), which leads to wood split, vary based on the genetic makeup of the individual tree and the family it originates from. The narrow-sense heritability of 0.24 suggests that end-splitting is under some degree of genetic control, so strategic genetic selection could be used to breed against high incidence of end-splitting in *E. pellita*. It is therefore an important criterion that should be incorporated into *E. pellita* breeding programs. The results of this study are supported by research findings of other fast-growing *Eucalyptus* species in different countries. For instance, the end-splitting trait in South African *E. grandis* is moderately heritable, which allows its reduction by genotype selection [20]. A study in Sri Lanka suggested heritability estimates for end-splitting of 0.16 to 0.15 for *E. grandis* [21]. Higher heritability estimates for end-splitting of 0.31 were reported for *E. grandis* in Brazil [22]. An assessment of nine-year-old *E. dunnii* Maiden. plantation trees in Australia reported a heritability of 0.3–0.5 for longitudinal growth strain [23]. These reported heritability estimates indicate that growth stress levels can be genetically altered via selection.

In the South African breeding program for *E. grandis*, only genotypes with low end-splitting were accepted to form a part of the breeding population [20]. Within the New Zealand *Pinus radiata* breeding program, prior focus on volume production alone has in some instances led to a decrease in wood properties and overall economic returns [24]. This suggests that the traditional approach to selection of genetic material for breeding purposes based only on phenotypic expression (mainly form and volume) is insufficient and therefore requires additional incorporation of wood property traits [25–27].

Economic losses due to end-splitting are not restricted to round log production only but occur at all stages of downstream processing. Maree and Malan [28] estimated the losses due to splitting amounted for up to 10% of the sawn timber production for *E. grandis* in South Africa whilst Yang [16] reported losses of 6% due to the need to remove the curved edges in the slabs of *E. globulus* Labill. Similarly, with veneer recovery, assessment of a number of different eucalypts in Australia showed 28% of the veneers were down-graded to low-value D-grade quality due to veneer splits [29], whilst peeling and sawing trials in Sarawak [8] and Sabah [9] states in Malaysia identified end-splits as the greatest source of recovery loss with up to 50% loss of viable log length. A similar result was observed in veneer recovery of New Zealand-grown *E. globoides* Blakely., where recovery per log varied from 23.6% to 74.5% with the loss of recovery due to split formation [30]. In China [31], the use of *E. urophylla* × *E. grandis* hybrids was able to increase recovery of higher value veneer grades, as well as reduce losses. Yang and Pongracic [32] developed a method to quantify the overall severity of log end-splitting using split indices. They also reported on methods to determine the loss of sawn timber recovery associated with growth stress release by estimating the volume of the curved-edge off-cuts.

This study has also proven that, apart from the family component, growth characteristics such as tree height and DBH play an important role in influencing the end-splitting of *E. pellita*. In comparison to DBH, tree height exerted a more prominent effect as tall trees commonly exhibit increased split occurrence and higher split severity. On the other hand, although the influence has proven to be statistically moderate, *E. pellita* with larger DBH does exhibit increased end-splitting. In plantation-grown *E. nitens* Deane & Maiden., splitting was observed to increase with tree diameter and with increased storage time [33]. In another study, Nascimento et al. [34] revealed that density did not have any notable influence on the end-splitting and surface cracks of *E. urophylla* logs; instead, the log diameter significantly contributed to the extent of end splits. Due to this unfavorable relation of wood splitting and growth in *E. pellita*, tree breeders need to carry out genetic selections of high volume and low-splitting genetic material and to exclude high growth strain individuals/families from the breeding program. These findings are in agreement with several reported studies. A study on *Acacia auriculiformis* Cunn. ex Benth. showed that growth strain (stress) development, which is responsible for wood splits, is dynamic and varies significantly during the development of a tree with increased age and tree height increment [35]. The same study with *A. auriculiformis* concluded a moderate relationship of

DBH and growth strain [35]. For *E. nitens* plantation-grown trees in Chile, growth strain changes significantly with increased age and tree height and slenderness (height–diameter ratio) [36]. Soil chemical and physical characteristics have a significant impact on growth and therefore on growth strain level development. In relation to this, end-splitting in South African *E. grandis* logs increases with growth rate, resulting in higher split occurrence for fast-grown trees [37]. Similarly, end-splitting in *E. grandis* on good-quality sites is increased by about 50% in comparison to low-quality sites in South Africa [20]. For *E. pellita* and other tree species, growth is an expression of genotype by environment interaction. Good or poor growth of a certain genotype/family is dependent on the site conditions, and therefore growth strain development is partly environmentally controlled. Together with growth, wood property traits have to be improved simultaneously in order to assure the long-term productivity and optimization of higher grade recovery and thus higher economic returns.

5. Conclusions

E. pellita planted in Sabah, North Borneo, has up to 99% occurrence of end-splitting in logs. The main split type was that of ‘Three-Quarter Radial Splits’ followed by ‘Pith to Bark Splits’ and ‘Half Radial Splits’. Internal splits were very rare. Both family and growth characteristics (tree height and DBH) were the main factors associated with end-splitting. Compared to DBH, tree height had a more significant influence on the occurrence of end-splitting. The study has shown that end-splitting is heritable ($h^2 = 0.24$) and is associated with family–growth–environment interactions and is not the result of a single factor. Significant family-by-growth variation exists for end-splitting in *E. pellita* logs. The reduction of growth stress levels via genetic selection is seen as a crucial element to be incorporated in the *E. pellita* breeding strategy. Simultaneous improvement of growth and wood property traits is crucial for the long-term productivity and economic returns of *E. pellita* plantations in North Borneo.

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