Genetic evaluation of growth and wood properties in new *Acacia mangium* × *A. auriculiformis* hybrid clones at Ba Vi, Hanoi, Vietnam

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Abstract

Acacia mangium × *A. auriculiformis* hybrids are widely deployed in tropical plantation forestry due to their rapid growth and versatile wood properties. This study evaluated growth, stem form, and wood properties in a clonal trial of 40 *Acacia* hybrid clones established at Ba Vi, northern Vietnam, with the objectives of quantifying clonal variation, estimating clonal-mean broad-sense heritability, examining relationships among traits, and identifying superior clones for potential deployment. The trial was assessed at age five using a randomized complete block design with four replications. Growth traits (diameter at breast height and total height), stem form traits (stem straightness and branch size), and wood properties (basic wood density and dynamic modulus of elasticity, MoEd) were analysed using linear mixed-effects models with spatially correlated residuals. Significant clonal variation was detected for all traits. Clonal-mean heritability was moderate for height (H^2 = 0.36 ± 0.06) and basic wood density (H^2 = 0.25 ± 0.06), and lower for MoEd (H^2 = 0.16 ± 0.05) and stem form traits. Genetic correlations indicated a strong positive association between height and diameter (rg = 0.90 ± 0.03) and moderate negative correlations between growth traits and basic wood density, indicating a trade-off between rapid growth and denser wood. Several clones outperformed certified control clones for stem volume while maintaining acceptable wood properties and survival, demonstrating substantial scope for phenotypic clonal selection and deployment of Acacia hybrids under Vietnamese plantation conditions.

Keywords: *Acacia* hybrids, clonal trial, basic wood density, modulus of elasticity, genetic parameters

1. Introduction

Acacia hybrids (*Acacia mangium* × *A. auriculiformis*) have emerged as pivotal genetic resources for industrial plantation forestry in tropical regions, combining rapid growth, environmental adaptability, and versatile wood properties (Kien et al. 2009; Harwood & Nambiar 2014). In Vietnam, these hybrids underpin national reforestation and timber production strategies and occupy more than 300,000 ha of plantations (Dong et al. 2014). Hybrid populations commonly exhibit heterosis, resulting in higher biomass production, improved stem form, and increased tolerance to several biotic stresses relative to their parental species (Nirsatmanto et al. 2014; Trang et al. 2017). Their wood is typically characterised by intermediate basic density (approximately 0.55–0.65 g cm^{-3}) and favourable fibre characteristics, making it suitable for pulp, paper and engineered wood products (Sunarti et al. 2016; Viet et al. 2020).

Ongoing genetic improvement of *Acacia* hybrids is required to sustain productivity and resilience under changing climatic conditions, increasing pest pressure and evolving industrial demands (Isik 2014). Although previous studies have documented growth performance and wood properties of *Acacia* hybrids (Hai et al. 2008b; Nambiar et al. 2015), important knowledge gaps remain in understanding the quantitative genetic basis of trait variation and in optimising selection strategies. In particular, the influence of parental (maternal) origin on growth and wood properties–well documented in other tropical hardwoods (Harwood & Williams 1992; Hai et al. 2015)-has received limited attention in *Acacia* hybrid breeding. In addition, quantitative assessments of heritability and genotypic variation (derived from variance components) for wood traits in Vietnamese *Acacia* hybrid clones remain scarce, despite their importance for predicting selection response (Hill & Mackay 2004). Furthermore, genetic relationships between growth traits (e.g. diameter at breast height), stem form traits, and wood quality attributes (e.g. basic density and dynamic modulus of elasticity) have not been comprehensively evaluated, constraining the development of balanced multi-trait selection criteria (Stamm 1964; Apiolaza 2009).

The present study addresses these gaps by: (1) evaluating maternal lineage effects on growth, stem form and wood properties; (2) estimating broad-sense heritability and genotypic variation for key traits; (3) analysing genetic relationships between growth performance and wood quality attributes; and (4) identifying superior clones for potential deployment. Using a clonal trial established at Ba Vi, northern Vietnam, and including certified commercial clones (BV16, BV33, BV73 and BV75) as references, within the scope of the present study, the results

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provide quantitative genetic information that may inform breeding and deployment decisions for *Acacia* hybrid clones under Vietnamese plantation conditions.

2. Materials and methods

2.1. Plant material.

The study was based on an extensive evaluation of 490 *Acacia* hybrid clones conducted across four major ecological zones of Vietnam (Northeast, North Central, South Central, and Southeast) during 2011–2014. From this initial screening, 68 superior clones were identified based primarily on growth performance and wood-related traits. Among these, 36 clones were successfully propagated by stem cuttings at the Ba Vi nursery and selected for further field evaluation.

The selected clones originated from two maternal lineages: *A. mangium* × *A. auriculiformis* (AM) and *A. auriculiformis* × *A. mangium* (AA). In addition, four officially registered *Acacia* hybrid clones (BV16, BV33, BV73 and BV75), all of AM maternal origin and widely deployed in Vietnam, were included as controls.

The trial comprised a total of 40 *Acacia* hybrid clones, including 36 newly selected clones (28 with *Acacia mangium* maternal origin and 8 with *Acacia auriculiformis* maternal origin) and four control clones listed in Vietnam's National Registry of Forest Plant Varieties. All control clones were of AM maternal origin.

The clonal field trial was established in August 2018 at Ba Vi district, Hanoi, Vietnam (21°06′N, 105°26′E; 66 m above sea level, a.s.l.), using a randomized complete block design (RCBD) with four replications. Each plot consisted of 25 trees, planted at 3 × 2 m spacing (1,660 trees ha^{-1}). Site characteristics, climatic conditions, soil properties, genetic materials, and the experimental layout are summarized in Table 1.

Table 1
Site characteristics and experimental design of the clonal trial at Ba Vi, Hanoi, Vietnam

Category	Description
Location	Ba Vi, Hanoi, Vietnam
Coordinates	21°06′N, 105°26′E; 66 m a.s.l.
Climate	Mean annual temperature: 23.1°C; Annual precipitation: 2,189 mm
Soil characteristics	Ferralitic loam; Soil depth: 80–100 cm
Site preparation	Slash-and-burn method followed by mechanical ploughing
Planting	Planting date: August 2018
Fertilization	2 kg cow dung + 0.3 kg NPK per tree
Experimental design	RCBD: 4 replications
Plot layout	25 trees per plot; 5 rows × 5 columns
Spacing	3 m × 2 m (1,660 trees ha^{-1})
Genetic Material	40 clones (36 new: AM = 28, AA = 8; 4 certified control clones)

2.2. Sampling method and data collection

Growth and stem-quality traits

Growth, stem form, and branching traits were assessed at Ba Vi at age five (2023). Diameter at breast height (DBH, cm) was measured at 1.3 m above ground using a diameter tape, and total tree height (HT, m) was determined with a Vertex hypsometer from the stem base to the apical meristem.

Stem form was visually evaluated by two trained assessors following a standardized protocol. Stem straightness (STR) was scored on a five-point scale: 1 = severely twisted stem (>2 major curves); 2 = two major curves; 3 = slightly curved stem (one major or multiple minor curves); 4 = nearly straight stem (1–2 minor curves); and 5 = completely straight stem.

Branching characteristics (BRA) were assessed based on relative branch diameter (RBD), defined as the ratio of branch diameter to trunk diameter. Branching was scored as: 1 = very thick (≥4 branches with RBD > 1/3); 2 = thick (2–3 branches with RBD > 1/3); 3 = moderate (2 branches with RBD > 1/3); 4 = thin (1 branch with RBD > 1/3); and 5 = very thin (no branches with RBD > 1/3).

Individual tree volume (VOL, dm^3 tree^{-1}) was calculated as:

$$VOL = \pi(DBH/2)^2 \times HT \times f$$

where: DBH is diameter at breast height (cm), HT is total height (m), π = 3.1416, and f is a form factor assumed to be 0.5, accounting for stem taper. All measurements were conducted during the dry season to minimize seasonal effects.

Wood sampling and measurements

Wood properties were assessed on a subset of trees sampled from the clonal field trial. Within each replicate, one tree per clone was sampled (4 trees per clone), giving a planned total of 160 trees (40 clones × 4 replicates) for wood-trait assessments before missing data.

To ensure a reproducible and unbiased sampling procedure, the sampled tree within each replicate was defined as the individual whose diameter at breast height (DBH) was closest to the plot mean for that clone. Border trees were excluded to avoid edge effects, and trees with severe stem defects, mechanical damage, or visible disease symptoms were not considered for wood sampling.

All selected trees were felled, and stem discs were collected at breast height (1.3 m). Basic wood density (DEN) was determined using standard gravimetric methods based on oven-dry mass and green volume. Acoustic velocity (Vel) was measured using a non-destructive time-of-flight method, and dynamic modulus of elasticity (MoEd) was calculated from DEN and Vel following established physical relationships.

Wood traits were measured on the same set of trees whenever possible. Due to occasional technical constraints or measurement failure, effective sample sizes varied slightly among traits. Final n for DEN, Vel and MoEd are given in the corresponding table footnotes. Missing observations were treated as missing at random and excluded from the analyses; no data imputation was applied.

Basic wood density (DEN)

Basic wood density (DEN) was determined following the water displacement method described by (Olesen 1971), using the standard definition applied in wood science and forest genetics, i.e. the ratio of oven-dry mass to green volume.

From each sampled tree, a 5-cm-thick disc was collected at breast height (1.3 m). Samples were fully saturated in water for 48 h to ensure complete hydration. The green volume (V_g) was determined by the volume of water displaced during immersion. Subsequently, samples were oven-dried at 105°C to constant mass to obtain oven-dry mass (M_0).

Basic wood density (DEN) was calculated as:

$$DEN = M_0 / V_g$$

where: DEN = basic wood density (g cm^{-3});
M_0 = oven-dry mass (g);
V_g = green volume determined by water displacement (cm^3).

Green density (DEN_{green})

Green density (DEN_{green}) was calculated as the ratio of fresh mass to green volume:

$$DEN_{green} = M_{green} / V_g$$

where: DEN_{green} = green density (kg m^{-3});
M_{green} = fresh (green) mass of the sample (kg);
V_g = green volume (m^3).

Green density was used exclusively for calculating the dynamic modulus of elasticity and was not interchangeable with basic density.

Acoustic velocity (Vel)

Acoustic measurements were conducted on standing trees using a Fakopp Microsecond Timer (FAKOPP Enterprise, Hungary). Stress waves were generated by tapping a transmitting probe positioned at 0.1 m above ground, with a receiving probe fixed at 1.5 m, resulting in a fixed propagation distance of 1.4 m along the stem.

Acoustic velocity was calculated explicitly as:

$$Vel = L / t$$

where: Vel = acoustic wave velocity (m s^{-1});
L = distance between probes (1.4 m);
t = measured wave transit time (s).

Velocity values were expressed in m s^{-1} for modulus calculations.

Dynamic modulus of elasticity (MoEd)

The dynamic modulus of elasticity (MoEd), an indicator of wood stiffness, was calculated using the acoustic velocity method:

$$MoEd = DEN_{green} \times Vel^2$$

where: MoEd = dynamic modulus of elasticity (Pa);
DEN_{green} = green density (DEN) (kg m^{-3});
Vel = acoustic velocity (m s^{-1}).

For reporting consistency, MoEd values were converted from pascals (Pa) to gigapascals (GPa) as:

$$\mathbf{1\ GPa = 10^9\ Pa}$$

Thus, all MoEd results are presented in GPa.

Trait abbreviations used throughout the manuscript are: DBH (diameter at breast height), HT (total height), STR (stem straightness), BRA (branch size), VOL (individual tree volume), DEN (basic wood density), Vel (acoustic velocity), and MoEd (dynamic modulus of elasticity).

2.3. Statistical analysis.

Mixed model specification

All traits were analyzed using linear mixed-effects models fitted by restricted maximum likelihood (REML) to accommodate the randomized complete block design and unbalanced data. Analyses were conducted using Genstat 12.0 (VSN International) and ASReml 4.0 (Gilmour 2015), following standard procedures for forest genetic trials (Williams et al. 2002). Degrees of freedom were derived from the mixed-model structure and estimated using REML.

For growth, stem form, and branching traits measured at the individual-tree level, the following mixed model was applied:

$$y_{ijk} = \mu + B_i + C_j + {}_{\varepsilon ijk}$$

where: y_{ijk} is the observation of the k-th tree of the j-th clone in the i-th block; μ is the overall mean; B_i is the fixed effect of block (i = 1,…,4); C_j is the random effect of clone (j = 1,…,40); and $_{\varepsilon ijk}$ is the residual error term.

Replication was treated as a fixed effect because the number of blocks was small and they represent deliberate environmental stratification. Clone was treated as a random effect to allow inference on the genetic variance among clones.

Spatial modelling

To account for local environmental heterogeneity within replications, residuals were modelled using a two-dimensional first-order autoregressive structure across rows and columns:

$$e \sim AR1(\rho_r) \otimes AR1(\rho_c)$$

where: ρ_r and ρ_c represent spatial autocorrelation parameters along rows and columns, respectively. In this approach, explicit row and column effects were not included in the linear predictor, as their influence was modelled through the spatially correlated residual structure. Models with and without spatial residuals were compared using Akaike's Information Criterion (AIC).

Estimation of clonal-mean broad-sense heritability (clonal repeatability)

Wood properties, including basic density (DEN), acoustic velocity (Vel), and dynamic modulus of elasticity (MoEd), were analyzed using the same model structure, with a reduced number of observations because one tree per clone per replicate was sampled. Trait-specific differences in effective sample size were naturally accommodated within the REML framework.

Clone effects were treated as random to allow estimation of variance components and prediction of best linear unbiased predictors (BLUPs). The significance of random effects was assessed using likelihood ratio tests (LRT). For fixed effects and clone comparisons, Fpr denotes the probability value associated with the corresponding F-test.

Broad-sense heritability (clonal repeatability, H^2) was estimated on a clonal-mean basis (i.e. clonal repeatability), accounting for the number of replications and trees per clone following (Falconer & Mackay 1996):

$$H^2 = \sigma^2c / (\sigma^2c + \sigma^2e / (rn))$$

where: r is the number of replications and n is the number of trees per clone per replication.

Genotypic coefficient of variation

The genotypic coefficient of variation (CVG) was calculated as:

$$CVG = (\sqrt{\sigma^2_c} / \bar{x}) \times 100$$

where: $\bar{x}$ is the trait mean; σ^2_c is the clonal variance

Genetic and phenotypic correlations

Clonal (genotypic) correlations between traits x and y were estimated from clonal variance–covariance components as:

$$r_g = Cov_c(x, y) / \sqrt{(\sigma^2_{c,x}\, \sigma^2_{c,y})}$$

where: $Cov_c(x, y)$ is the clonal covariance between traits x and y, and $\sigma^2_{c,x}$ and $\sigma^2_{c,y}$ are the corresponding clonal variances.

Phenotypic correlations between traits x and y were calculated as:

$$r_p = Cov_p(x,y) / \sqrt{(\sigma^2_{p,x}\, \sigma^2_{p,y})}$$

where: Covp(x,y) is the phenotypic covariance between traits x and y, and $\sigma^2_{p,x}$ and $\sigma^2_{p,y}$ are the corresponding phenotypic variances.

Standard errors

Standard errors (±SE) for variance components, heritabilities, and genetic correlations were obtained directly from ASReml using the Delta method and are reported consistently throughout the Results section.

3. Results

3.1. Effects of maternal species on growth and some wood properties of Acacia hybrid clones at Ba Vi trial.

Significant differences among maternal lineages were detected for basic wood density (DEN) and dynamic modulus of elasticity (MoEd) at age five (Table 2).

Table 2
Variation in basic wood density (DEN) and dynamic modulus of elasticity (MoEd) among *Acacia* hybrid clones with different maternal origins at Ba Vi, Vietnam, at age five.

Clone type	Maternal lineage	Basic density (g cm^{-3})			Dynamic modulus of elasticity (GPa)		
		Mean	Fpr	CV (%)	Mean	Fpr	CV (%)
AA	*A. auriculiformis*	0.56	<0.001	12.93	15.25	<0.001	8.47
AM	*A. mangium*	0.57	<0.001	4.40	22.21	<0.001	15.11
Control	Certified	0.54	<0.001	4.09	16.98	<0.001	10.43
Mean		0.56	<0.001	8.34	18.15	<0.001	22.75

Note: AA: clones with *Acacia auriculiformis* maternal origin (n = 8 clones); AM: clones with *A. mangium* maternal origin (n = 28 clones); Control: certified commercial hybrid clones (n = 4); CV (%): phenotypic coefficient of variation within maternal groups; not a genetic parameter; Fpr: probability value associated with the F-test.

Clones with *Acacia mangium* maternal origin (AM) showed a higher mean DEN (0.57 g cm^{-3}) than clones with *A. auriculiformis* maternal origin (AA; 0.56 g cm^{-3}) and certified control clones (0.54 g cm^{-3}) (Fpr < 0.001). Phenotypic coefficients of variation (CV) for DEN differed among groups and were highest in AA clones (12.93 %), compared with AM clones (4.40 %) and control clones (4.09 %).

Mean MoEd also differed significantly among maternal origins (Fpr < 0.001). AM clones exhibited the highest mean MoEd (22.21 GPa), followed by control clones (16.98 GPa) and AA clones (15.25 GPa). The phenotypic CV for MoEd was highest in AM clones (15.11 %), compared with AA clones (8.47 %) and control clones (10.43 %).
The distribution of DEN and MoEd across maternal lineages is shown in Figure 1.

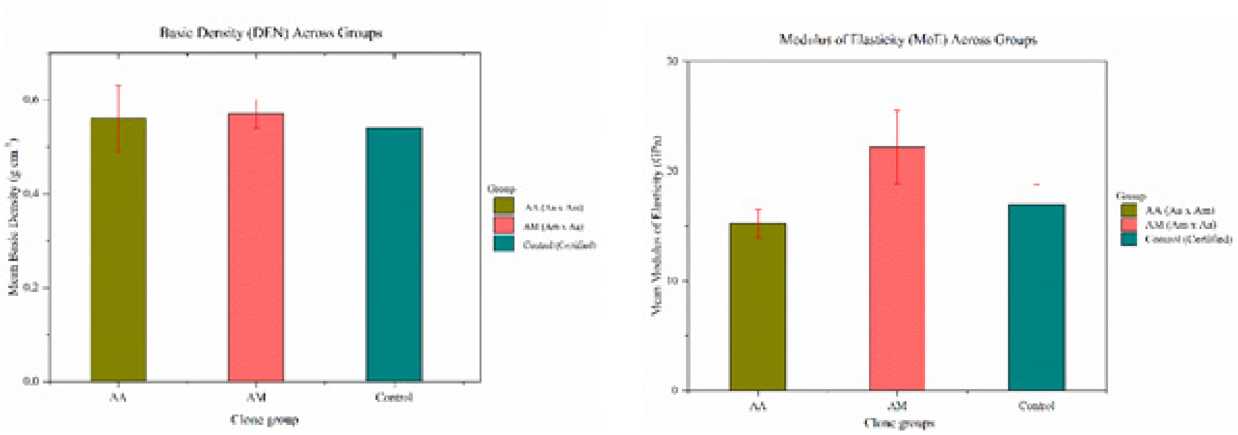

Figure 1
Variation in basic wood density (DEN, g cm^{-3}) and dynamic modulus of elasticity (MoEd, GPa) among *Acacia* clones with *A. mangium* (AM) and *A. auriculiformis* (AA) maternal origins.

Figure 1 illustrates the distribution and overlap of basic wood density and dynamic modulus of elasticity across maternal lineages, complementing the group means reported in Table 2.

3.2. Broad-sense heritability and genotypic coefficient of variation of wood properties traits at Ba Vi trial.

Broad-sense heritability (H^2) and genotypic coefficients of variation (CVG) for growth, form, and wood property traits are presented in Table 3.

Table 3
Clonal repeatability (H^2) and genotypic coefficient of variation (CVG) for growth and wood property traits of five-year-old *Acacia* hybrid clones at Ba Vi, Vietnam.

Category	Trait	Description	Unit	Mean	(H2)	CVG (%)
Growth traits	DBH	Diameter at breast height	cm	10.62	0.19 ± 0.04	9.66
	HT	Height	m	12.58	0.36 ± 0.06	6.67
Form traits	STR	Stem straightness	score	3.50	0.17 ± 0.04	6.81
	BRA	Branch size	score	3.40	0.15 ± 0.04	7.35
Wood properties	DEN	Basic density	g cm^{-3}	0.54	0.25 ± 0.06	5.28
	MoEd	Modulus of elasticity	GPa	17.16	0.16 ± 0.05	17.40

Note: Wood traits were assessed on four trees per clone (one per replicate); final sample size: n = 160 trees for DEN, Vel and MoEd.

Among growth traits, height (HT) showed the highest heritability (H^2 = 0.36 ± 0.06), followed by diameter at breast height (DBH; H^2 = 0.19 ± 0.04). Form traits exhibited lower heritability estimates, with H^2 values of 0.17 ± 0.04 for stem straightness (STR) and 0.15 ± 0.04 for branch size (BRA).

For wood properties, DEN exhibited moderate broad-sense heritability (H^2 = 0.25 ± 0.06) and a relatively low genotypic coefficient of variation (CVG = 5.28 %). In contrast, MoEd showed lower heritability (H^2 = 0.16 ± 0.05) but a higher CVG (17.40 %).

3.3. Correlation between growth traits and wood properties at Ba Vi trial.

Genotypic (rg) and phenotypic (rp) correlations among growth, form, and wood property traits are summarized in Table 4.

Table 4
Genotypic (upper) and phenotypic (lower) correlations (±SE) among traits in five-year-old *Acacia* hybrids.

Trait	HT (m)	DBH (cm)	STR (score)	BRA (score)	DEN (g cm^{-3})	MoEd (GPa)
HT	-	0.9 ± 0.03	0.77 ± 0.07	0.67 ± 0.09	-0.56 ± 0.13	0.34 ± 0.15
DBH	0.77 ± 0.02	-	0.56 ± 0.12	0.44 ± 0.14	-0.52 ± 0.14	0.34 ± 0.15
STR	0.38 ± 0.04	0.19 ± 0.04	-	0.95 ± 0.02		0.12 ± 0.17
BRA	0.37 ± 0.04	0.14 ± 0.04	0.65 ± 0.02	-		0.07 ± 0.17
DEN	-0.22 ± 0.07	-0.13 ± 0.07			-	0.42 ± 0.13
MoEd	0.19 ± 0.05	0.19 ± 0.04	0.05 ± 0.04	0.06 ± 0.04	0.31 ± 0.03	-

A strong positive genetic correlation was observed between HT and DBH (rg = 0.90 ± 0.03). Negative genetic correlations were detected between growth traits and basic wood density (HT-DEN: rg = -0.56 ± 0.13; DBH-DEN: rg = -0.52 ± 0.14).

Stem straightness (STR) and branch size (BRA) showed a strong positive genetic correlation (rg = 0.95 ± 0.02). Genetic correlations between form traits and MoEd were low and not statistically different from zero.

Phenotypic correlations were generally weaker than the corresponding genetic correlations.

3.4. Selection of elite Acacia hybrid clones to advance genetic improvement programs.

Highly significant clonal differences were detected for all measured traits (Fpr < 0.001; Table 5).

Clones BV340, BV333, BV102, BV566, and BV518 ranked highest for stem volume, exceeding the trial mean by 26–46 %. Clone BV340 showed the highest mean stem volume (85.16 dm^3 $tree^{-1}$), compared with the best-performing certified control clone (60.38 dm^3 $tree^{-1}$).

Survival rates of the top-ranked clones ranged from 84 % to 88 %. The distribution of stem volume for selected clones and certified controls is illustrated in Figure 2.

Table 5
Superior, inferior, and control *Acacia* hybrid clones ranked by growth at Ba Vi.

Rank	Clonal	Lineage	Growth traits			Quality traits		Wood properties		Survival (%)
			DBH (cm)	HT (m)	VOL (dm^3 $tree^{-1}$)	STR (score)	BRA (score)	DEN ($g\ cm^{-3}$)	MoEd (GPa)	
1	BV340	AM	12.33	13.64	85.16	3.96	3.84	0.51	16.83	88
2	BV333	AA	12.17	13.83	84.68	3.86	3.54	0.50	14.24	85
3	BV102	AM	12.34	13.68	84.61	3.65	3.39	0.47	17.42	85
4	BV566	AA	11.67	13.13	73.40	3.80	3.75	0.52	15.81	84
5	BV518	AM	11.27	13.56	72.00	3.92	3.86	0.55	17.08	74
18	BV16	Control	10.56	13.25	60.38	3.82	3.77	0.51	16.02	81
19	BV75	Control	10.58	12.74	59.93	3.57	3.20	0.52	15.07	77
20	BV33	Control	10.64	12.49	59.32	3.57	3.17	0.53	16.06	74
35	BV73	Control	9.63	11.53	47.65	3.65	3.51	0.49	17.32	68
36	BB001	AM	9.55	11.96	44.88	3.19	2.87	0.59	17.42	88
37	BV511	AM	8.86	11.85	40.71	3.50	3.44	0.55	17.28	82
38	BV012	AM	9.13	10.57	38.77	3.20	3.15	0.57	15.59	67
39	BV306	AA	8.12	11.89	34.05	3.82	3.75	0.56	18.56	86
40	BV316	AA	6.22	8.39	13.28	2.52	2.32	0.60	16.48	60
	Average		10.46	12.48	58.29	3.51	3.34	0.55	16.82	79.03
	Fpr		<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001
	LSD		1.11	0.93	15.10	0.32	0.45	0.02	1.50	15.75

Note: STR and BRA were scored on a 1–5 scale (1 = poor, 5 = excellent); Fpr: probability value of the F-test; LSD: least significant difference

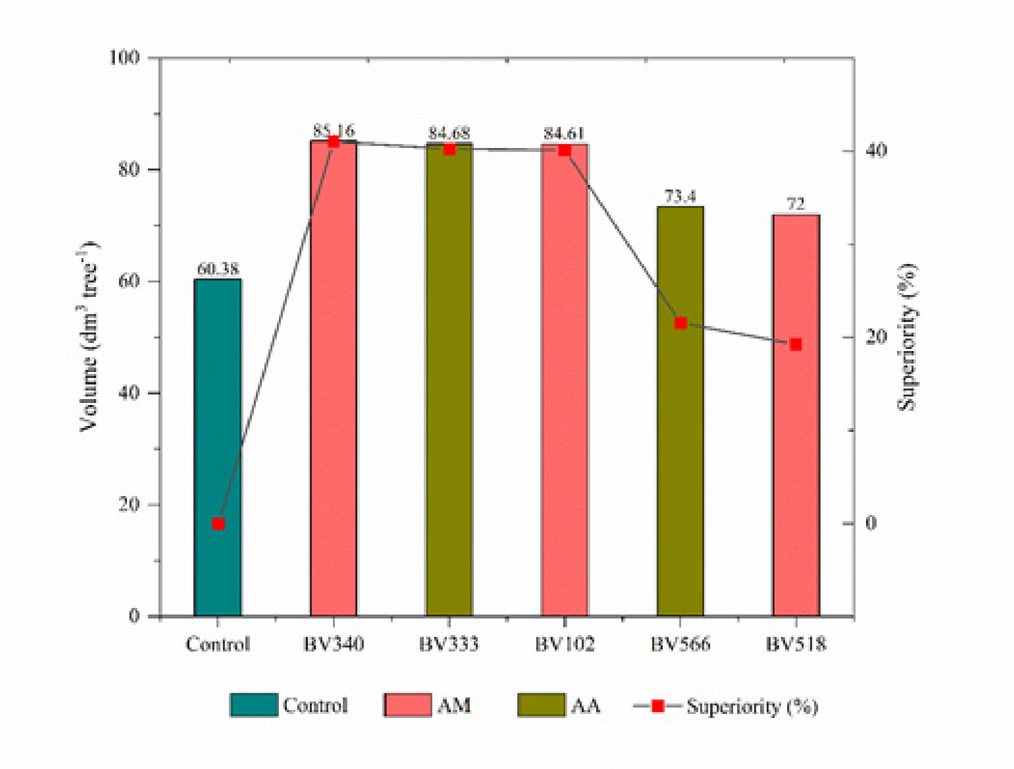

Figure 2
Volume comparison of top clones vs. certified varieties

Figure 2 summarizes the relative stem volume performance of selected top-ranked clones compared with certified control clones.

4. Discussion

4.1. Maternal effects on wood properties in Acacia hybrid clones.

The present study provides clear evidence of maternal-origin effects on basic wood density (DEN) and dynamic modulus of elasticity (MoEd) in five-year-old *Acacia mangium* × *A. auriculiformis* hybrid clones grown at Ba Vi. Clones with *A. mangium* maternal origin exhibited higher mean MoEd, whereas clones with *A. auriculiformis* maternal origin showed greater phenotypic variation for DEN. These results are consistent with earlier studies reporting significant parental and maternal influences on growth and wood properties in *Acacia* hybrids and other tropical hardwoods (Harwood & Williams 1992; Kien et al. 2009).

Maternal effects on wood traits in *Acacia* hybrids have been attributed to differences in growth rhythm, cambial activity, and wood formation patterns inherited from the maternal parent (Lopez et al. 2003; Chi et al. 2020; Nirsatmanto et al. 2014). The higher MoEd observed in clones with *A. mangium* maternal origin is in agreement with previous reports of superior mechanical performance in this species and its hybrids (Hai et al. 2015; Viet et al. 2020). Conversely, the larger phenotypic dispersion in DEN among *A. auriculiformis* maternal clones suggests greater within-group variability for this trait, which has also been documented in earlier provenance and hybrid studies (Kien et al. 2009; Hai et al. 2008a).

Importantly, phenotypic coefficients of variation reported here should not be interpreted as indicators of genetic diversity. Genetic variability was evaluated explicitly through genotypic coefficients of variation (CVG) derived from variance components. This distinction is critical in quantitative genetics and aligns with recommendations for reporting genetic parameters in forest tree breeding studies (Falconer & Mackay 1996; Apiolaza 2009).

4.2. Heritability, genotypic variation, and implications for selection.

Broad-sense heritability estimates revealed contrasting genetic architectures among growth, form, and wood property traits. Height exhibited the highest heritability, suggesting that height may be suitable for early selection in clonal breeding populations, whereas diameter and form traits showed lower heritability, consistent with their more complex genetic control and stronger environmental sensitivity (Wei & Borralho 1998; Resende et al. 2012).

For wood properties, basic wood density displayed moderate heritability but low genotypic variation, indicating a potentially limited scope for rapid genetic gain through direct phenotypic selection. Similar patterns have been reported in *Acacia* and *Eucalyptus*, where density often shows moderate genetic control but relatively narrow genetic variance within breeding populations (Zobel & Jett 1995; Hai et al. 2008c).

In contrast, MoEd exhibited lower heritability but substantially higher CVG, reflecting a trait with greater genetic dispersion but stronger environmental influence. Such a combination is typical of mechanically complex traits in forest trees and has been reported in *Acacia mangium*, *Eucalyptus globulus*, and other fast-growing species (Raymond 2002; Hai et al. 2015). However, low heritability alone does not imply that genomic prediction or marker-assisted selection would necessarily be effective. Prediction accuracy depends on factors such as training population size, genetic relatedness, marker density, genetic architecture, and genotype-by-environment interaction, none of which were evaluated in the present study (Grattapaglia & Resende 2011; Isik 2014). Consequently, no inference regarding the performance of genomic-assisted selection can be drawn from the current dataset.

The comparatively lower heritability estimates observed in this five-year-old trial, relative to older *Acacia* progeny tests (Hai et al. 2008c), are consistent with age-dependent expression of genetic control in perennial species. Wood properties, in particular, often stabilize later in rotation, as cambial maturation progresses and environmental noise is reduced (Apiolaza 2009; Viet et al. 2020).

4.3. Genetic correlations and growth-wood trade-offs.

The strong positive genetic correlation between height and diameter confirms that these growth traits are largely under shared genetic control, a pattern commonly observed in forest trees and indicative of coordinated carbon allocation to stem growth (Wei & Borralho 1998; Raymond 2002).

In contrast, the negative genetic correlations detected between growth traits and basic wood density highlight a well-documented trade-off between rapid biomass accumulation and wood densification. Similar antagonistic relationships have been widely reported in *Acacia, Eucalyptus*, and other fast-growing hardwoods (Zobel & Jett 1995; Hai et al. 2008c). These trade-offs reflect fundamental physiological constraints, whereby increased growth rate may be associated with reduced investment in secondary wall thickening and lignification.

The positive genetic correlation observed between basic wood density and MoEd indicates that denser wood tends to be stiffer in this hybrid population, although the relationship is moderate. This finding agrees with previous studies showing that density explains only part of the genetic variation in stiffness, as MoEd is also influenced by microfibril angle and cell-wall architecture (Raymond et al. 2001; Viet et al. 2020). Consequently, indirect selection for stiffness based solely on density is unlikely to be efficient.

The near-perfect genetic correlation between stem straightness and branch size suggests tight genetic linkage or pleiotropic control of stem form traits, as previously reported in *Acacia* and *Eucalyptus* breeding programs (Apiolaza 2009; Hollender & Dardick 2015). The weak genetic associations between form traits and MoEd indicate that improvement of stem form is unlikely to compromise wood stiffness, which is favorable for multi-trait selection.

4.4. Methodological considerations and trait assessment.

Several methodological considerations are relevant when interpreting these results. Dynamic modulus of elasticity was assessed using acoustic tools, which are widely adopted in forest genetic and tree breeding studies due to their non-destructive nature, rapid measurement, and suitability for large field trials (Greaves et al. 1996; Proto et al. 2017). Although static bending tests remain the reference method for mechanical characterization, their destructive nature and logistical constraints limit their routine application in breeding populations.

Near-infrared spectroscopy (NIR) represents a complementary high-throughput tool for predicting wood density and chemical properties such as lignin and cellulose content, but it does not directly measure mechanical stiffness (Raymond et al. 2001; Schimleck 2008). Consequently, NIR is most effective for density-related traits, whereas acoustic methods remain more appropriate for assessing stiffness proxies such as MoEd.

The relatively large standard errors associated with some genetic correlation estimates likely reflect limitations related to sample size, clone number, and the young age of the trial. Such uncertainty is common in early-stage clonal evaluations and underscores the importance of validation across ages and environments (Tan et al. 2017).

4.5. Implications for Acacia hybrid breeding.

Taken together, the results provide quantitative information that may be useful for designing balanced selection strategies in *Acacia* hybrid breeding. Growth traits can be improved efficiently through early selection, whereas wood density and stiffness require more cautious approaches due to genetic trade-offs and age-dependent expression. Maternal origin emerges as an important source of structured variation that may be considered in breeding population design.

Future work should focus on extended-age assessments and multi-environment trials to confirm the stability of genetic parameters and clonal rankings. The feasibility of genomic prediction may be evaluated in the future once suitably sized training populations, replicated trials, and genome-wide marker data become available. Within the scope of the present study, however, conclusions are restricted to phenotypic and quantitative-genetic inference based on a single-site clonal trial.

5. Conclusions

This study quantified clonal variation, clonal-mean broad-sense heritability, and trait relationships for growth, stem form, and wood properties in *Acacia mangium* × *A. auriculiformis* hybrid clones at age five in a single-site clonal trial in northern Vietnam. Clear differences among clones and maternal lineages were observed for growth performance and wood properties, particularly basic wood density and dynamic modulus of elasticity.

Moderate negative genetic correlations between growth traits and basic wood density indicate an inherent trade-off that may constrain simultaneous improvement of these traits through univariate selection. Consequently, balanced phenotypic selection approaches that consider both growth and wood properties are likely to be required.

Several clones outperformed certified control clones in stem volume while maintaining acceptable wood properties and survival, highlighting their potential for further testing and possible deployment.

All genetic parameter estimates reported here are derived from phenotypic data collected at a single site and at an early age. Accordingly, inferences should be interpreted with caution and are restricted to the conditions examined. Validation across ages and environments will be necessary to confirm the stability of genetic parameters and clonal rankings. Within the scope of the present study, the results provide quantitative genetic information that may inform breeding and deployment decisions for *Acacia* hybrid clones under Vietnamese plantation conditions.

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References

Apiolaza, LA (2009) Very early selection for solid wood quality: screening for early winners. Annals of Forest Science, 66: 1–10. https://doi.org/10.1051/forest/2009047

Chi NQ, Harwood CE, Griffin R, Harbard JL, Son DH, Chinh, NV (2020) Are maternal and reciprocal effects important in breeding the inter-specific hybrid between *Acacia auriculiformis* and *A. mangium*? Euphytica, 216: 176. https://doi.org/10.1007/s10681-020-02711-w

Dong TL, Doyle R, Beadle CL, Corkrey R, Quang NX (2014) Impact of short-rotation *Acacia* hybrid plantations on soil properties of degraded lands in Central Vietnam. Soil Research, 52: 271–281. https://doi.org/10.1071/sr13166

Falconer DS, Mackay, T.F.C. (1996) Introduction to Quantitative Genetics. 4th edn. Pearson Education Limited, Harlow, England.

Gilmour AR (2015) ASReml user guide release 4.1 Structural specification. VSN International Ltd, Hemel Hempstead, UK.

Grattapaglia D, Resende MD (2011) Genomic selection in forest tree breeding. Tree Genetics & Genomes, 7: 241–255. https://doi.org/10.1007/s11295-010-0328-4

Greaves BL, Borralh, NMG, Raymond CA, Farrington A (1996) Use of a Pilodyn for the indirect selection of basic density in *Eucalyptus* nitens. Canadian Journal of Forest Research, 26: 1643–1650. https://doi.org/10.1139/x26-185

Hai PH, Duong LA, Toan NQ, Ha TTT (2015) Genetic variation in growth, stem straightness, pilodyn and dynamic modulus of elasticity in second-generation progeny tests of *Acacia mangium* at three sites in Vietnam. New Forests, 46: 577–591. https://doi.org/10.1007/s11056-015-9484-6

Hai PH, Harwood CE, Kha LD, Pinyopusarerk K, Thinh HH (2008a) Genetic gain from breeding *Acacia auriculiformis* in Vietnam. Journal of Tropical Forest Science, 20: 313–327.

Hai PH, Jansson G, Harwood CE, Hannrup B, Thinh HH (2008b) Genetic variation in growth, stem straightness and branch thickness in clonal trials of *Acacia auriculiformis* at three contrasting sites in Vietnam. Forest Ecology and Management, 255: 156–167. https://doi.org/10.1016/j.foreco.2007.09.017

Hai, P.H., Jansson, G., Harwood, C.E., Hannrup, B., Thinh, H.H. & Pinyopusarerk, K. (2008c) Genetic variation in basic wood density and knot index and their relationship with growth traits for *Acacia auriculiformis* in northern Vietnam. New Zealand Journal of Forestry Science, 38: 176–193.

Harwood, C.E. & Nambiar, E.K.S. (2014) Productivity of *Acacia* and *Eucalypt* plantations in Southeast Asia. II. Trends and variations. International Forestry Review, 16: 249–260.

Harwood, C.E. & Williams, E.R. (1992) A review of provenance variation in growth of *Acacia mangium*. In: Carron, L.T. & Aken, K.M. (eds.) Breeding Technologies for Tropical Acacias: Proceedings of a Workshop held in Tawau, Sabah, Malaysia, 1–4 July 1991. ACIAR Proceedings 37, Canberra, pp. 22–30.

Hill, W.G. & Mackay, T.F.C. (2004) D. S. Falconer and Introduction to Quantitative Genetics. Genetics, 167: 1529–1536. https://doi.org/10.1093/genetics/167.4.1529

Hollender, C.A. & Dardick, C. (2015) Molecular basis of angiosperm tree architecture. New Phytologist, 206: 541–556. https://doi.org/10.1111/nph.13204

Isik, F. (2014) Genomic selection in forest tree breeding: the concept and an outlook to the future. New Forests, 45: 379–401. https://doi.org/10.1007/s11056-014-9422-z

Kien, N.D., Harwood, C.E., Kha, L.D. & Baltunis, B.S. (2009) Genetic variation in growth, basic wood density and pilodyn penetration in *Acacia auriculiformis, A. mangium* and their F1 hybrids in Vietnam. Agroforestry Systems, 76: 389–396. https://doi.org/10.1007/s11056-011-9263-y

Lopez, G.A., Potts, B.M., Vaillancourt, R.E. & Apiolaza, L.A. (2003) Maternal and carryover effects on early growth of *Eucalyptus* globulus. Canadian Journal of Forest Research, 33: 2108–2115. https://doi.org/10.1139/x03-132

Nambiar, E.K.S., Harwood, C.E. & Kien, N.D. (2015) *Acacia* plantations in Vietnam: research and knowledge application to secure a sustainable future. Southern Forests, 77: 1–10. https://doi.org/10.2989/20702620.2014.999301

Nirsatmanto, A., Setyaji, T. & Wahyuningtyas, R.S. (2014) Realized genetic gain and seed source × site interaction on stand volume productivity of *Acacia mangium*. Indonesian Journal of Forestry Research, 1: 21–32. https://doi.org/10.20886/ijfr.2014.1.1.21-32

Olesen, P.O. (1971) The water displacement method: a fast and accurate method of determining the green volume of wood samples. Forest tree improvement, 3. Akademisk Forlag, København. 57pp.

Proto, A., Macri, G., Bernardini, V., Russo, D. & Zimbalatti, G. (2017) Acoustic evaluation of wood quality with a non-destructive method in standing trees: a first survey in Italy. iForest - Biogeosciences and Forestry, 10: 700–706. https://doi.org/10.3832/ifor2065-010

Raymond, C.A. (2002) Genetics of *Eucalyptus* wood properties. Annals of Forest Science, 59: 525–531. https://doi.org/10.1051/forest:2002037

Raymond, C.A., Schimleck, L.R., Muneri, A. & Michell, A.J. (2001) Genetic parameters and genotype-by-environment interactions for pulp-yield predicted using near infrared reflectance analysis and pulp productivity in *Eucalyptus globulus*. International Journal of Forest Genetics, 8: 213–224.

Resende, M.D., Resende, M.F.J., Sansaloni, C.P., Petroli, C.D., Missiaggia, A.A., Aguiar, A.M., Abad, J.M., Takahashi, E.K., Rosado, A.M. & Faria, D.A. (2012) Genomic selection for growth and wood quality in *Eucalyptus*: capturing the missing heritability and accelerating breeding for complex traits in forest trees. New Phytologist, 194: 116–128. https://doi.org/10.1111/j.1469-8137.2011.04038.x

Schimleck, L.R. (2008) Near-infrared spectroscopy: a rapid non-destructive method for measuring wood properties and its application to tree breeding. New Zealand Journal of Forestry Science, 38: 14–35.

Stamm, A.J. (1964) Wood and Cellulose Science. Ronald Press Company, New York.

Sunarti, S., Praptoyo, H. & Nirsatmanto, A. (2016) Characteristics of fiber from the wood of *Acacia auriculiformis* × *Acacia mangium* hybrid with regard to pulp. Jurnal Pemuliaan Tanaman Hutan, 10: 135–143.

Tan, B., Grattapaglia, D., Martins, G.S., Ferreira, K.Z., Sundberg, B. & Ingvarsson, P.K. (2017) Evaluating the accuracy of genomic prediction of growth and wood traits in two *Eucalyptus* species and their F1 hybrids. BMC Plant Biology, 17: 1–15. https://doi.org/10.1186/s12870-017-1059-6

Trang, T.T., Glen, M., Eyles, A., Ratkowsky, D., Beadle, C.L. & Mohammed, C. (2017) Quantifying stem discoloration and decay following pruning and thinning an *Acacia* hybrid plantation. Forest Pathology, 47: e12312. https://doi.org/10.1111/efp.12312

Viet, D.D., Te, M., Itoh, T., Kim, N.T., Chi, N.Q. & Tsubomura, S. (2020) Physical and mechanical properties of fast growing polyploid *Acacia* hybrids (*A. auriculiformis* × *A. mangium*) from Vietnam. Forests, 11: 717. https://doi.org/10.3390/f11070717

Wei, X. & Borralho, N.M.G. (1998) Genetic control of growth traits of *Eucalyptus urophylla* S.T. Blake in south-east China. Silvae Genetica, 47: 158–165.

Williams, E.R., Matheson, A.C. & Harwood, C.E. (2002) Experimental Design and Analysis for Tree Improvement. CSIRO Publishing, Collingwood. https://doi.org/10.1071/9780643090132

Zobel, B.J. & Jett, J.B. (1995) The importance of wood density (specific gravity) and its component parts. In: Zobel, B.J. & van Buijtenen, J.P. (eds.) Genetics of Wood Production. Springer, Berlin–Heidelberg, pp. 78–97. https://doi.org/10.1007/978-3-642-79514-5_4