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Evaluation of Genetic Variability for Growth, Physiological and Wood Properties of Eucalyptus Clones

Avni Kumari [a++*] and Afaq Majid Wani [a#]

[a] Department of Forest Biology and Tree Improvement, College of Forestry, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj, Uttar Pradesh -211007, India.

Authors' contributions

This work was carried out in collaboration between both authors. Both authors read and approved the final manuscript.

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Abstract

Selecting suitable *Eucalyptus* clones for agroforestry and industrial forestry requires an assessment of the genetic characteristics and clonal variability. A study was conducted to evaluate genetic variation among twenty clones of *Eucalyptus* spp. at the College of Forestry, SHUATS, Prayagraj, India, and ICFRE-FRCER, Prayagraj. Analysis of variance (ANOVA) confirmed strong genetic diversity by revealing highly significant ($P < 0.01$) interclonal differences across all assessed variables. The phenotypic variance of parent clones was substantial. While clone 3018 recorded the greatest tree height (26.20 m), clone P13 reached the greatest girth at breast height (95.80 cm) and stem volume (1.81 m^3). Among the leaf physiological traits, clone 2136 had the highest essential oil content (1.83%), whereas clone 413 produced the highest total chlorophyll (1.86 mg/g). With a high specific gravity of 0.61 and a low water absorption of 33.05%, clone 288 showed exceptional wood density. Strong genetic control was shown by genetic parameter estimations, with broad-sense heritability (h^2) above 95% for all significant factors. High heritability was shown by GBH (99.69%), stem volume (99.37%), and essential oil yield (99.03%). For stem volume (103.95%), essential oil yield (87.26%), and total chlorophyll (65.69%), strong heritability and high genetic advance as a percentage of the mean (GAM > 30%) were found, indicating the predominance of additive gene action.

[++] *Ph.D Scholar;* [#] *Head & Professor;*
**Corresponding Email(s): avnisinha9693@gmail.com;*

Contact Email(s): avnisinha9693@gmail.com;

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Keywords: Eucalyptus clones; clonal variability; chlorophyll content; essential oil yield; broad-sense heritability; genetic advance.

1. Introduction

Eucalyptus (family Myrtaceae) is one of the most widely planted hardwood genera in the world. It is valued for fast growth, wide adaptability and multipurpose wood used for pulp, construction, fuelwood and essential oils. The genus is native mainly to Australia, with a few species extending to Papua New Guinea and Indonesia. It has since been established across Asia, Africa and South America, and plantations now supply a large share of industrial roundwood in many countries. In China, for example, eucalypt plantations show mean annual productivity of 4.14–8.57 $m^3\ ha^{-1}\ yr^{-1}$, and in some provinces they contribute far more to harvested timber volume than to planted area (Zhang & Wang, 2021).

Eucalyptus camaldulensis Dehnh. has the widest natural range of any eucalypt in Australia, occurring along inland river systems and seasonal watercourses. It tolerates drought, salinity and periodic waterlogging, and is therefore widely planted on marginal and degraded lands in the tropics and subtropics. *Eucalyptus tereticornis* Sm. occurs naturally along the eastern coast and sub-coastal belt of Australia and in southern Papua New Guinea. It is one of the fastest-growing multipurpose tree species and is extensively grown in India under agroforestry and farm forestry (Sahoo *et al.*, 2021). In India, these two species and their interspecific hybrids, mainly *E. tereticornis* × *E. camaldulensis*, form the backbone of commercial plantations. They are especially important in the Indo-Gangetic plains and the northern and southern farmlands. The eucalypt hybrid combines the adaptability and stress tolerance of one parent with the growth vigour and wood quality of the other. This makes it attractive to growers and to the pulp, paper and plywood industries. Recent field testing in the Eastern Gangetic Plains also documented variation in early height and girth growth among *Eucalyptus camaldulensis* clones (Srivastav *et al.*, 2026).

Clonal forestry has become the main route for deploying genetic gain in eucalyptus. Vegetative propagation captures both additive and non-additive genetic variance, and it allows elite genotypes to be multiplied as uniform planting stock with predictable growth, form and wood properties. Clonal testing is the basis of this approach. It supplies the estimates of variance components, heritability and genetic advance needed to separate heritable superiority from environmental effects. In *E. tereticornis* clones, Sahoo *et al.* (2021) reported significant clonal differences for growth and biomass traits. They found high heritability (up to 87.35%) and genetic advance as a percentage of the mean (GAM) of 71.15% for biomass, showing that selection would be effective. Wu *et al.* (2017) found highly significant genetic variation and very high repeatabilities for growth traits in *Eucalyptus* hybrid clones in China. Marco de Lima *et al.* (2019) showed that quantitative genetic parameters for growth and wood properties in *Eucalyptus* hybrids are the key first step in predicting response to selection. Recent research has described tissue-culture methods for propagating selected *Eucalyptus* hybrid material (Minj *et al.*, 2025). Across-rotation testing of an *Eucalyptus* hybrid further demonstrated the relevance of considering growth and wood traits in multi-trait clonal selection (Xu *et al.*, 2025). Recent clonal allocation research has also examined how environmental conditions can inform site-specific deployment decisions (Cavalheiro *et al.*, 2026). Variation in wood density along *Eucalyptus* stems has also been associated with genotype and planting spacing (Pimenta *et al.*, 2024).

Breeding programmes increasingly aim to improve more than volume growth. Physiological traits such as chlorophyll content and essential oil yield, and wood properties such as specific gravity, moisture content, water absorption and shrinkage or swelling, determine adaptability and end-use value. Yet clones of *E. camaldulensis*, *E. tereticornis* and their hybrids are often screened for growth alone. Few studies evaluate growth, physiological and wood traits together within a single clonal set, which limits multi-trait selection for agroforestry and industrial use.

The present study therefore evaluated twenty *Eucalyptus* clones, including *E. camaldulensis*, *E. tereticornis* and E. *hybrid* clones, at the College of Forestry, SHUATS, and ICFRE-FRCER, Prayagraj. Its objectives were to (i) assess interclonal variation in growth, physiological and wood properties; (ii) estimate genotypic and phenotypic coefficients of variation, broad-sense heritability and genetic advance; and (iii) identify superior clones for further tree improvement and plantation deployment.

2. Materials and Methods

2.1 Study Area and Experimental Site

The field evaluation was conducted on established clonal plantations at the ICFRE–Forest Research Centre for Eco-rehabilitation (FRCER), Prayagraj, Uttar Pradesh, India, during 2024–2026. The site is situated in the subtropical agro-climatic zone of the Indo-Gangetic alluvial plains (25.41° N latitude, 81.84° E longitude; altitude 78 m above mean sea level). The climate is characterised by hot, dry summers (maximum temperature up to 47°C in May–June), mild winters (minimum temperature 1°C in January), and an average annual rainfall of 850–1000 mm, concentrated mainly during the southwest monsoon season.

2.2 Plant Material and Experimental Design

The study evaluated twenty distinct clones of *Eucalyptus* spp. (including *E. camaldulensis*, *E. tereticornis*, and *E. hybrid* clones, as detailed in Table 1) maintained at FRCER, Prayagraj. The field experiment was laid out in a Randomised Block Design (RBD) with three replications. From each replication, one healthy parent tree (ramet) per clone free from disease or pest infestation was selected, yielding a total of three ramets per clone ($N = 60$ trees) for recording morphological, physiological, and physical wood parameters.

Table 1. Details of twenty *Eucalyptus* spp. clones evaluated

S. No.	Clone Designation	Botanical Species
1	Control	*Eucalyptus camaldulensis*
2	P13	*Eucalyptus camaldulensis*
3	2136	*Eucalyptus camaldulensis*
4	P50	*Eucalyptus camaldulensis*
5	P23	*Eucalyptus camaldulensis*
6	526	*Eucalyptus camaldulensis*
7	P66	*Eucalyptus camaldulensis*
8	2070	*Eucalyptus camaldulensis*
9	288	*Eucalyptus tereticornis*
10	2023	*Eucalyptus camaldulensis*
11	P32	*Eucalyptus camaldulensis*
12	413	*Eucalyptus camaldulensis*
13	P14	*Eucalyptus camaldulensis*
14	3018	*Eucalyptus hybrid*
15	K25	*Eucalyptus camaldulensis*
16	3021	*Eucalyptus camaldulensis*
17	O-7	*Eucalyptus tereticornis*
18	P45	*Eucalyptus camaldulensis*
19	2013	*Eucalyptus camaldulensis*
20	IFGTB-4	*Eucalyptus camaldulensis*

2.3 Assessment of Morphological Parameters

Morphological growth attributes were recorded using standard forestry procedures:

- **Total Tree Height (HT, m)**: Measured from the ground level to the tip of the terminal apex using a Ravi Multimeter.
- **Girth at Breast Height (GBH, cm):** Measured at 1.37 m above ground level using a flexible measuring tape placed horizontally and tightly around the stem.
- **Stem Volume (VOL, m^3):** Computed using the formula:

$$\text{Volume } (m^3) = \text{Basal Area } (m^2) \times \text{Height (m)}$$

Where, Basal Area $(m^2) = \frac{GBH^2}{4\pi}$.

2.4 Assessment of Physiological Parameters

Leaf pigment fractions and essential oil yield were extracted and quantified as follows:

- **Chlorophyll Fractions (mg g^{-1} fresh weight):** Chlorophyll content was estimated spectrophotometrically from fresh, healthy leaves of each clone following a modified procedure based on Arnon (1949). Fresh, healthy leaf tissue (1.0 g) was ground in 20 mL of 80% acetone. The homogenate was centrifuged at 5,000 rpm for 5 minutes, and extraction was repeated until the residue became colourless. Pooled extracts were made up to 100 mL with 80% acetone. Spectrophotometric absorbance (A) was measured at 645 nm and 663 nm. Chlorophyll a (CHLA), Chlorophyll b (CHLB), and Total Chlorophyll (TCHL) were calculated according to Arnon (1949):

$$\text{Chlorophyll } a \text{ (mg g}^{-1}) = [(12.7 \times A_{663}) - (2.69 \times A_{645})] \times \frac{V}{1000 \times W}$$

$$\text{Chlorophyll } b \text{ (mg g}^{-1}) = [(22.9 \times A_{645}) - (4.68 \times A_{663})] \times \frac{V}{1000 \times W}$$

$$\text{Total Chlorophyll (mg g}^{-1}) = \text{Chlorophyll } a + \text{Chlorophyll } b$$

where V = final extract volume (100 mL) and W = leaf fresh weight (1.0 g).

- **Essential Oil Yield (EOY, %):** Essential oil extraction from *Eucalyptus* leaves was conducted using a Clevenger-type steam distillation apparatus following procedures described in the European Pharmacopoeia Commission (2008) and Guenther (1948). Fresh leaf samples (100 g) were cut into small pieces and subjected to hydrodistillation in a Clevenger-type steam distillation apparatus with 1500 mL of distilled water at 90°C for 3 hours. Extracted oil was dried over anhydrous sodium sulfate (Na_2SO_4) and weighed on an electronic balance. Oil content was calculated as:

$$\text{Essential Oil Yield (\%)} = \left(\frac{\text{Weight of oil (g)}}{\text{Weight of fresh leaves (g)}}\right) \times 100$$

2.5 Assessment of Physical Wood Properties

Wood disc samples harvested from each parent tree were processed into test specimens according to Bureau of Indian Standards (BIS, 1986) specifications:

- **Moisture Content (MC, %):** Determined by drying initial wood samples at 103 ± 2°C to constant weight (BIS, 1986):

$$\text{Moisture Content (\%)} = \left(\frac{M_i - M_o}{M_o}\right) \times 100$$

where M_i = initial weight and M_o = oven-dry weight.

- **Water Absorption (WA, %):** $2 \times 2 \times 6$ cm specimens were weighed initially (W_i) and after 72 hours of water immersion (W_f):

$$\text{Water Absorption (\%)} = \left(\frac{W_f - W_i}{W_i}\right) \times 100$$

- **Volumetric Swelling (VSW, %):** Computed from specimen volume before (V_i) and after 72 hours of water immersion (V_f):

$$\text{Volumetric Swelling (\%)} = \left(\frac{V_f - V_i}{V_i}\right) \times 100$$

- **Volumetric Shrinkage (VSH, %):** Calculated from fully saturated swollen volume (V_s) to oven-dry volume (V_f):

$$\text{Volumetric Shrinkage (\%)} = \left(\frac{V_s - V_f}{V_s}\right) \times 100$$

- **Bark Thickness (BT, mm):** Measured across major and minor axes of harvested wood discs using a Vernier calliper.
- **Wood Specific Gravity (SG):** Determined on an air-dry basis using a specific gravity module attached to a precision electronic balance (Shimadzu AUY220) via the water displacement method (Anoop *et al.*, 2012).

2.6 Statistical and Genetic Parameter Analysis

2.6.1 Analysis of Variance (ANOVA)

Data recorded across the 20 clones were analysed using a one-way Analysis of variance (ANOVA) for a Randomised Block Design (RBD) to test the significance of interclonal differences across all 13 parameters.

The critical difference (CD) at the 5% level of significance was computed as:

$$\text{CD}_{0.05} = \sqrt{\frac{2 \times \text{MS}_e}{r}} \times t_{0.05,\ \text{error df}}$$

2.6.2 Estimation of Variance Components and Genetic Parameters

Genotypic variance (σ_g^2), phenotypic variance (σ_p^2), and environmental variance (σ_e^2) were partitioned according to Fisher and Yates (1957):

$$\sigma_e^2 = \text{MS}_e$$

$$\sigma_g^2 = \frac{\text{MS}_g - \text{MS}_e}{r}$$

$$\sigma_p^2 = \sigma_g^2 + \sigma_e^2$$

Using these variance components, the following genetic parameters were estimated according to Burton and DeVane (1953), Pillai and Sinha (1968), Johnson *et al.* (1955), Lush (1940, 1949), and Allard (1960).

- **Genotypic Coefficient of Variation (GCV, %):**

$$\text{GCV (\%)} = \left(\frac{\sqrt{\sigma_g^2}}{\bar{X}}\right) \times 100$$

- **Phenotypic Coefficient of Variation (PCV, %):**

$$\text{PCV (\%)} = \left(\frac{\sqrt{\sigma_p^2}}{\bar{X}}\right) \times 100$$

- **Environmental Coefficient of Variation (ECV, %):**

$$\text{ECV (\%)} = \left(\frac{\sqrt{\sigma_e^2}}{\bar{X}}\right) \times 100$$

- **Broad-Sense Heritability (h^2, %):**

$$h^2\ (\%) = \left(\frac{\sigma_g^2}{\sigma_p^2}\right) \times 100$$

- **Expected Genetic Advance (GA):** Computed at a 5% selection intensity ($K = 2.06$, Allard, 1960):

$$\text{GA} = K \times \sqrt{\sigma_p^2} \times \left(\frac{h^2}{100}\right)$$

- **Genetic Advance as Percent of Mean (GAM, %):**

$$\text{GAM (\%)} = \left(\frac{\text{GA}}{\bar{X}}\right) \times 100$$

where $\bar{X}$ is the overall population mean for the character.

3. Results and Discussion

3.1 Analysis of Variance and Inter-Clonal Genetic Variability

The foundational requirement for any systematic tree improvement programme is the reliable quantification of inherent genetic variability within the base population, as selection pressure is ineffective without statistically validated genetic variation. Analysis of variance (ANOVA) revealed highly significant interclonal differences ($P \leq 0.01$) across 12 out of 13 evaluated morphological, physiological, and physical wood traits among the twenty *Eucalyptus* spp. clones (Table 2).

The mean squares due to genotypes consistently surpassed error mean squares by wide margins, confirming robust genetic diversity within the germplasm pool. These results align with findings by Wu *et al.* (2017), who reported highly significant genetic variation across *Eucalyptus* hybrid clones in China, and Fadwati *et al.* (2023), who emphasized that evaluating genetic parameters in *Eucalyptus pellita* is essential for site-specific deployment. Preserving high genetic variance in *Eucalyptus* breeding populations also underpins resilience to changing environmental conditions (Booth, 2013), facilitates climate-matched deployment strategies (Scolforo *et al.*, 2017), and aligns with global productivity dynamic models (Zhang & Wang, 2021). Selecting variable elite clones can further influence local biogeochemical cycling and site sustainability (Mallen-Cooper *et al.*, 2022).

Among morphological parameters, clone P13 recorded the greatest girth at breast height (95.80 cm) and stem volume (1.81 m^3), whereas clone 3018 recorded the greatest tree height (26.20 m) (Table 2). For physiological traits, clone 413 yielded the highest total chlorophyll content (1.86 mg/g), and clone 2136 produced the maximum essential oil yield (1.83%) (Table 2). Among physical wood properties, clone 288 demonstrated superior wood density, exhibiting a high specific gravity (0.61) and low water absorption (33.05%) (Table 2).

The only parameter that did not reach the threshold of statistical significance was wood volumetric shrinkage (treatment mean square of 2.551 vs. error mean square of 2.099), indicating a narrower genetic range and high microenvironmental sensitivity for dimensional contraction in this population.

Table 2. Clonal mean of parent trees (ramet) for different parameters in Eucalyptus clones

Treatment	GBH	HT	VOL	CHLA	CHLB	TCHL	EOY	MC	WA	VSH	VSW	BT	SG
Control	75.20	16.33	0.73	1.06	0.48	1.53	0.92	101.71	44.96	13.76	14.98	1.50	0.56
P13	95.80	24.80	1.81	0.59	0.22	0.81	1.57	118.99	36.75	12.25	13.80	2.43	0.51
2136	54.17	16.47	0.38	1.25	0.52	1.77	1.83	88.35	41.59	12.97	16.47	1.15	0.59
P50	77.87	20.17	0.97	0.59	0.21	0.80	1.05	108.32	34.28	12.35	19.94	1.69	0.50
P23	86.80	24.90	1.49	1.09	0.40	1.49	0.59	95.17	35.39	10.73	11.28	2.10	0.55
526	88.20	23.27	1.44	1.08	0.58	1.66	1.05	85.42	37.87	11.49	11.56	1.18	0.57
P66	62.50	17.17	0.53	0.95	0.37	1.32	1.01	100.92	40.78	13.37	14.31	1.10	0.56
2070	71.80	16.23	0.67	0.60	0.24	0.83	0.41	113.22	48.67	11.99	17.02	1.38	0.50
288	79.50	17.00	0.86	0.70	0.28	0.98	0.41	83.25	33.05	11.13	13.62	1.23	0.61
2023	75.50	18.17	0.83	0.59	0.22	0.82	0.46	100.39	50.92	10.36	15.11	1.26	0.49
P32	75.80	26.10	1.19	0.67	0.22	0.89	1.66	117.54	35.37	11.88	12.91	2.48	0.52
413	65.80	16.97	0.58	1.38	0.47	1.86	1.39	89.42	44.50	11.73	12.55	1.11	0.54
P14	69.20	17.70	0.67	0.72	0.28	1.00	1.38	104.96	37.72	12.29	12.48	1.32	0.53
3018	63.53	26.20	0.84	0.72	0.29	1.01	1.02	121.15	35.65	12.19	12.64	1.24	0.48
K25	62.63	17.70	0.55	0.86	0.37	1.23	1.75	96.65	40.94	12.97	14.89	1.04	0.58
3021	37.27	17.77	0.19	0.52	0.24	0.76	1.09	106.16	42.53	12.27	15.99	0.81	0.56
O-7	72.37	17.27	0.72	0.67	0.22	0.89	0.41	90.76	46.35	12.67	13.32	1.43	0.56
P45	48.13	18.10	0.33	0.69	0.25	0.94	0.83	114.04	38.57	12.77	15.81	0.98	0.58
2013	54.87	21.63	0.52	0.66	0.28	0.93	1.06	100.47	48.76	13.05	16.39	1.17	0.52
IFGTB-4	68.67	21.30	0.80	0.57	0.24	0.81	1.35	105.64	46.75	13.78	20.25	1.25	0.52
Mean	69.28	19.76	0.81	0.80	0.32	1.12	1.06	102.13	41.07	12.30	14.77	1.39	0.54
CV (%)	1.12	3.29	4.04	4.29	6.53	3.36	4.21	2.21	3.20	11.78	14.07	4.94	4.26
CD@5%	1.28	1.07	0.05	0.06	0.03	0.06	0.07	3.73	2.17	2.39	3.43	0.11	0.04
SEm	0.45	0.38	0.02	0.02	0.01	0.02	0.03	1.30	0.76	0.84	1.20	0.04	0.01

3.2 Estimation of Quantitative Genetic Parameters

3.2.1 Genotypic and Phenotypic Coefficients of Variation

Across all evaluated traits, the PCV values were consistently higher than their corresponding GCV values. This fundamental statistical relationship indicates a notable, though biologically expected, influence of the environmental background noise on trait expression. However, the remarkably narrow quantitative gap between PCV and GCV across the vast majority of parameters confirms that trait expression was predominantly under strict genetic control rather than being a mere artefact of microenvironmental site variations. When the environmental coefficient of variation remains low, tree breeders can confidently assume that the visible phenotypic superiority of a clone is a direct manifestation of its underlying genetic code.

Stem volume exhibited the highest GCV (50.62%) and PCV (50.78%), followed by essential oil yield (42.57% GCV, 42.78% PCV), chlorophyll b content (35.49% GCV, 36.08% PCV), bark thickness (32.46% GCV, 32.84% PCV), and total chlorophyll (32.06% GCV, 32.24% PCV). High GCV and PCV values ($> 30\%$) demonstrate substantial genetic variation for timber yield and secondary metabolite production, offering substantial scope for selection.

Conversely, specific gravity (6.23% GCV, 7.55% PCV) and tree height (17.62% GCV, 17.92% PCV) showed moderate to low variability, reflecting highly conserved cellular control over wood density. Volumetric shrinkage showed the lowest GCV (3.16%) against a higher PCV (12.19%) due to a high environmental coefficient of variation ($\text{ECV} = 11.78\%$), reflecting substantial environmental sensitivity.

3.2.2 Broad-Sense Heritability and Genetic Advance

Broad-sense heritability (h^2) ranged from 6.70% to 99.69% (Table 3). Near-absolute heritability ($h^2 > 97\%$) was observed for GBH (99.69%), stem volume (99.37%), essential oil yield (99.03%), total chlorophyll (98.92%), chlorophyll a (98.16%), and bark thickness (97.74%). High broad-sense heritability indicates that phenotypic traits accurately reflect genotypic values, enabling effective direct selection. These findings are supported by Marco de Lima *et al.* (2019), who demonstrated that quantitative genetic parameters in *Eucalyptus* hybrids effectively predict selection responses, and Wu *et al.* (2017), who reported high repeatabilities (0.93--0.99) for growth traits in hybrid eucalypts. High heritability for biomass growth traits was also documented in *E. tereticornis* clones by Sahoo *et al.* (2021).

Because heritability alone does not indicate expected genetic gain per selection cycle, combining heritability with genetic advance as a percentage of the mean (GAM) provides a reliable framework for predictive breeding. Exceptionally high GAM values were recorded for stem volume (103.95%, $\text{GA} = 0.84$), essential oil yield (87.26%, $\text{GA} = 0.93$), chlorophyll b (71.90%), bark thickness (66.11%), total chlorophyll (65.69%), and chlorophyll a (63.96%). High heritability coupled with high GAM indicates the predominance of additive gene action. Consequently, simple mass selection will be highly effective for deploying elite accessions such as clone P13 (for timber volume) and clone 2136 (for essential oil yield). These estimates are illustrated in Fig. 1.

Traits exhibiting moderate heritability coupled with lower GAM values, such as specific gravity (68.10 percent heritability, 10.59 percent GAM) and volumetric swelling (51.77 percent heritability, 21.61 percent GAM), suggest a higher proportion of non-additive gene action controlling their expression, combined with greater environmental sensitivity. Non-additive gene action includes complex biological interactions such as dominance or epistasis. For traits influenced by non-additive gene action, simple mass selection is generally less effective. Instead, breeders must rely on controlled hybridization and the rigorous exploitation of specific combining ability to realise significant improvements. The absolute necessity of combining heritability and genetic advance for comprehensive clone evaluation is a foundational principle of clonal forestry. This rigorous biometrical screening guarantees that selected material like clone P13 (for maximum volume) and clone 2136 (for maximum essential oil) will reliably transfer their superior attributes to commercial plantation environments, fulfilling the productivity requirements detailed by Fadwati *et al.* (2023) in their evaluation of *Eucalyptus pellita* genetic parameters.

Table 3. Estimates of genetic parameters for morphological, physiological and physical traits in *Eucalyptus spp.* clones

Trait	GCV	PCV	ECV (%)	h² (%)	GA	GAM (%)
Girth at breast height (cm)	20.19	20.22	1.12	99.69	28.77	41.53
Tree height (m)	17.62	17.92	3.29	96.63	7.05	35.68
Volume (m3)	50.62	50.78	4.04	99.37	0.84	103.95
Chlorophyll a (mg/g)	31.34	31.63	4.29	98.16	0.51	63.96
Chlorophyll b (mg/g)	35.49	36.08	6.53	96.72	0.23	71.90
Total chlorophyll (mg/g)	32.06	32.24	3.36	98.92	0.73	65.69
Essential oil yield (%)	42.57	42.78	4.21	99.03	0.93	87.26
Bark thickness (mm)	32.46	32.84	4.94	97.74	0.92	66.11
Specific gravity	6.23	7.55	4.26	68.10	0.06	10.59
Moisture content (%)	10.99	11.21	2.21	96.10	22.66	22.19
Water absorption (%)	13.02	13.41	3.20	94.31	10.70	26.05
Volumetric shrinkage (%)	3.16	12.19	11.78	6.70	0.21	1.68
Volumetric swelling (%)	14.58	20.26	14.07	51.77	3.19	21.61

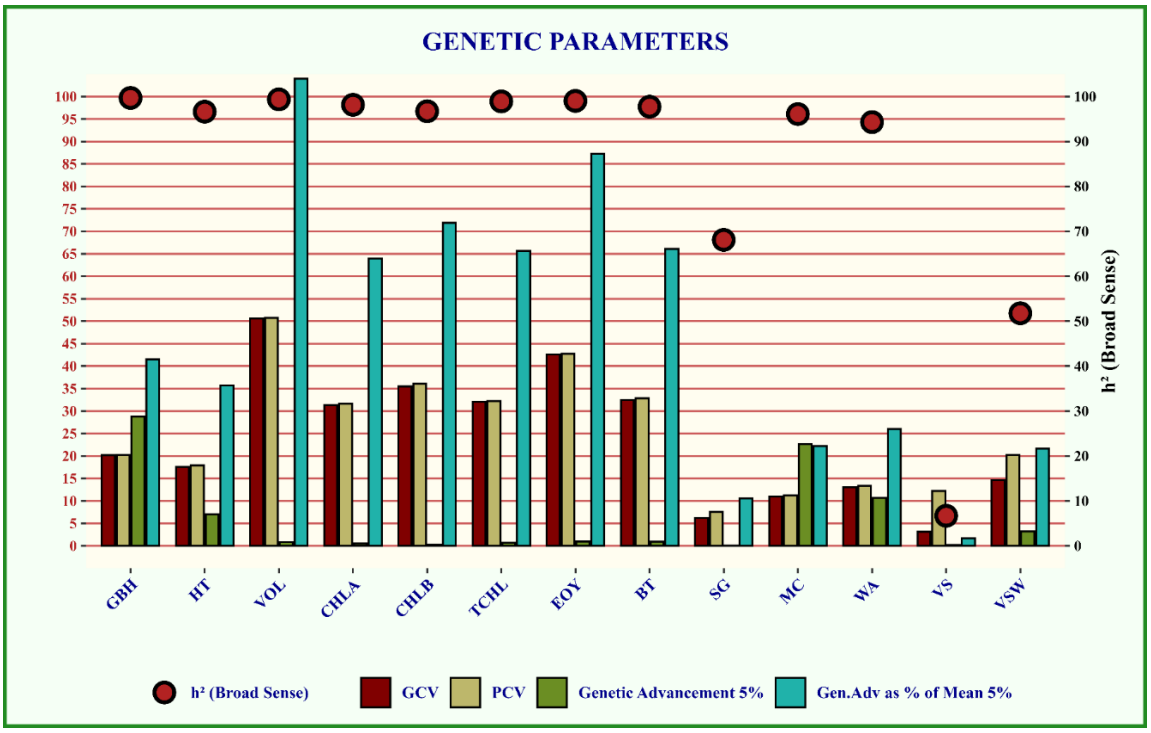


Fig. 1. Graphical representation of genetic parameters including coefficient of variation, heritability and genetic advance for morphological parameters

4. Conclusion

The comprehensive evaluation of twenty *Eucalyptus* clones demonstrated substantial genetic variability across morphological, physiological, and physical wood properties. The Analysis of variance (ANOVA) revealed highly significant differences ($P \leq 0.01$) for nearly all evaluated traits, confirming a robust genetic base that provides an exceptional foundation for clonal selection and tree improvement programmes. Significant performance variation identified elite clones tailored for specific commercial objectives. Clone P13 proved superior for volumetric timber production, recording the highest girth at breast height (95.80 cm) and stem

volume (1.81 m^3), whereas clone 3018 achieved the maximum tree height (26.20 m). For physiological traits, clone 2136 exhibited the highest essential oil content (1.83%), and clone 413 produced the maximum total chlorophyll content (1.86 mg/g). Clone 288 demonstrated exceptional wood physical properties with a high specific gravity (0.61) and low water absorption (33.05%).

Broad-sense heritability estimates exceeding 95% for key parameters indicate strict genetic regulation and minimal environmental modification, ensuring that phenotypic selections accurately reflect true breeding values. Traits such as stem volume (GAM = 103.95%), essential oil yield (GAM = 87.26%), total chlorophyll (65.69%), and bark thickness (66.11%) combined high heritability with high genetic advance as a percentage of the mean (GAM > 30%). This demonstrates the predominance of additive gene action, indicating that direct phenotypic selection will yield rapid and reliable genetic gains over successive rotations.

Overall, the identified elite clones offer valuable genetic resources for multi-trait selection, making them highly promising candidates for commercial plantation forestry, agroforestry, and industrial applications.

5. Limitations

The experiment assessed only 20 clones at one site, with three ramets per clone. This limits the extent to which the rankings can be generalised to other soils, climates and management conditions. The study did not report multi-location or across-rotation validation. Reported broad-sense heritability estimates do not separate additive and non-additive genetic effects. The identified clones should therefore be considered candidates for further evaluation rather than definitive selections.

Declaration of AI Use

This manuscript was prepared through the intellectual contributions of the author(s) to the study design, data analysis, interpretation of results, and scholarly content. ChatGPT, Claude and Perplexity were used solely to assist with grammatical refinement and reference formatting during manuscript revision. The author(s) accept full responsibility for the accuracy, integrity, and final content of the manuscript

Competing Interests

Authors have declared that they have no known competing financial interests or non-financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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