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RESEARCH ARTICLE

Genetic Variation and Elite Clone Selection in *Gmelina arborea* for Seed Source Development in Northeast India

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Abstract

Gmelina arborea Roxb., a fast-growing timber species of tropical Asian origin, holds significant potential for industrial plantations in Northeast India. This study evaluates genetic variation among 70 clones maintained at the Naharoni gene bank in Golaghat, Assam, over 20 years (2000–2020). Quantitative traits, including height, diameter at breast height (DBH), collar diameter (CD) and stem straightness, were assessed using a comprehensive point-grading system. Significant variation occurred across all traits (p<0.01), with coefficients of variation (CV) from 14.35% (CD) to 24.91% (straightness). Twenty-four elite clones were selected, showing 15–25% superiority in combined growth traits over the population mean. Five clones exhibited low susceptibility to *Craspedonta leayana*, a major defoliator pest; four of these overlapped with elite growth performers. Phenotypic (PCV) and genotypic (GCV) coefficients of variation yielded high broad-sense heritability (h^2 = 0.62–0.89) for height and CD, indicating strong genetic control of economically important traits. These elite clones are recommended for second-generation clonal seed orchards (CSOs) to supply improved, genetically superior seed for commercial plantations, supporting restoration of 1.2 million hectares of degraded lands in Northeast India.

Keywords: Clonal seed orchard, Elite clone selection, Genetic variation, Germplasm conservation, Heritability, Point-grading, Pest resistance

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Introduction

Gmelina arborea Roxb. (Lamiaceae), commonly known as Gamhar or white teak in Indian forestry, represents a cornerstone species in tropical forestry due to its remarkable pioneer characteristics, rapid juvenile growth rates (mean annual increment 15–25 m^3/ha/yr) and highly versatile timber properties (Moya and Tomazello Filho, 2008; Orwa *et al.,* 2009). The wood exhibits a density of 450–650 kg m^3, straight grain, fine texture and excellent workability, making it ideal for plywood veneers, match splints, furniture production and pulp manufacturing (PROTA, 2016). The species is native to mixed deciduous forests throughout Indo-Malaya, with distribution spanning from Pakistan through India, Myanmar, Thailand and extending into Vietnam (Warrier *et al.,* 2019).

Ecologically, *G. arborea* exhibits wide amplitude across humid–subhumid tropical zones, thriving under mean annual temperatures of 24-28°C and annual rainfall regimes of 750–4,500 mm, with soil pH tolerance ranging from 5 to 8 (PROTA, 2016). The species demonstrates a clear preference for well-drained loamy soils while being intolerant of waterlogging and frost, characteristics that define its distribution limits (Warrier *et al.,* 2019). In India, *G. arborea* currently occupies approximately 100,000 hectares of

plantation area, with disproportionate concentration in Northeast states including Assam, Arunachal Pradesh and West Bengal, driven by monsoonal climate suitability, established agroforestry systems, rural livelihood integration and recognized carbon sequestration potential (FAO2020; FSI 2021).

Despite widespread cultivation, genetic improvement of *G. arborea* remains substantially underexploited in spite of the species exhibiting considerable intra-specific variation. Provenance trials conducted across tropical Asia have consistently documented variations of 20–30% in growth performance between superior and inferior provenances, exemplified by exceptional performance of the Sholayar and Baramura seed sources (Lauridsen and Kjaer, 2002). However, critical reproductive constraints severely limit the practical deployment of superior seed sources. The species exhibits protandrous dichogamy, resulting in erratic flowering cycles (biennial to quadrennial intervals), poor seed set (typically <20% viable seeds), dormancy-mediated germination problems (30–50% germination rate) and significant storage losses to fungal pathogens, including *Aspergillus* and *Penicillium* species (Okoro 1983; Luna 1996; Jantawong *et al.,* 2017).

Given these reproductive limitations, vegetative propagation via cuttings emerges as the only practical strategy to reliably capture, preserve and multiply genetically superior individuals exhibiting desirable phenotypes for height growth ($h^2 \approx$ 0.4–0.7), stem straightness, timber quality characteristics and ecological tolerance to recurrent defoliator pests. The most economically significant pest is *Craspedonta leayana* Distant (Coleoptera: Chrysomelidae), a leaf-feeding chrysomelid beetle that inflicts severe monsoon-season foliar damage, typically causing 20–50% defoliation across commercial plantations (Kumar *et al.,* 2003; Phukan *et al.,* 2022). Such defoliation stress directly impacts tree growth rates, wood quality parameters and long-term plantation productivity (Wellendorf 1989).

The Indian Council of Forestry Research and Education (ICFRE) initiated systematic genetic improvement programs for *G. arborea* through its Rain Forest Research Institute (RFRI) at Jorhat, Assam, commencing in 2000 under the All-India Coordinated Research Project (AICRP) framework. This program involved the identification and selection of 119 candidate plus trees (CPTs) from four Northeast Indian states using a weighted phenotypic selection index emphasizing height (40% weighting), DBH (30%), clear bole length (20%) and overall stem form (10%), which identified clones demonstrating 18–67% phenotypic superiority over regional population means (Kumar *et al.,*2003; Kumar and Matharoo, 2003). A first-generation gene bank was established at Naharoni Experimental Field Station in Golaghat, Assam, where selected clones were planted as replicated clonal ramets in a completely randomized block design with spacing of 4 × 4 meters. This facility enabled multi-decadal phenotyping under realistic rainfed conditions with minimal external inputs, receiving approximately 2,200 mm annual rainfall on Alfisol soils with pH ranging from 5.5 to 6.5. Earlier assessments documented heritable phenotypic variation (PCV 15–30%), confirming substantial breeding potential (Anandalakshmi *et al.,* 2016; Nautiyal *et al.,*2023).

Recent developments underscore the urgency of advancing *G. arborea* genetic improvement in Northeast India. Plantation forests face compound pressures from climate change-exacerbated pest and pathogen outbreaks, phenological shifts affecting growth dynamics, variable wood quality and market demands for genetically uniform, pest-resilient planting material (Khushi *et al.,* 2019; Mayanglambam *et al.,* 2022; Singh *et al.,* 2023; Rozar 2024). While international *G. arborea* improvement efforts emphasize genotype-by-environment (G×E) testing across diverse agroecological zones (exemplified by Central American programs managing 225,000 hectares, Costa Rican initiatives spanning 49,300 hectares), Indian breeding programs have lagged in second-generation clonal seed orchard (CSO) establishment and deployment (FAO, 2009).

The present investigation, part of the CAMPA-AICRP-30 research initiative (2019–2024), addresses this critical gap by conducting a comprehensive evaluation of multivariate growth traits across the Naharoni 70-clone germplasm and pest resistance in selected clones, base to rigorously identifying and characterising elite clones suitable for large-scale propagation and deployment. The specific objectives are to: (1) quantify genetic variation in growth traits (height, DBH, collar diameter, stem straightness) across the clone collection; (2) select elite clones demonstrating sustained growth superiority; (3) identify clones exhibiting enhanced resistance to the major defoliator pest *C. leayana*; and (4) recommend superior germplasm for second-generation CSO establishment in Northeast India.

Materials and Methods

Plant material and experimental site

The study utilized 70 clones of *Gmelina arborea* established at the Naharoni gene bank (26°35 N, 93°55 E; 110 m asl), Golaghat District, Assam, Northeast India. The clonal gene bank was established in 2000 using a completely randomized block design (CRBD) with 5 replications, 5 ramets/clone/replication, 4 m×4 m spacing. Site characteristics: red loamy Alfisol (pH 5.5–6.5), 2000–2500 mm annual rainfall, tropical humid climate. The 70 clones represent selections from 119 candidate plus trees (CPTs) identified during 2000 under ICFRE-AICRP from four Northeast Indian states: Assam (27 clones), Arunachal Pradesh (9 clones), West Bengal (24 clones), and Mizoram (10 clones) (Table 1).

Trait assessment and measurement protocols

Data were recorded in January 2020 on 20-year-old trees for four quantitative traits, conducted by trained field personnel using calibrated instruments:

Height (Ht): Total tree height was measured from ground level to the apex using a Suunto clinometer with measurement accuracy of ±0.5 m. Clinometer readings were taken from a standardized distance of 20 m perpendicular to the tree bole to minimize parallax error and ensure consistency across the clone population.

Diameter at breast height (DBH): Measured at standardized height of 1.37 m from the ground using a diameter tape with precision to ±0.1 cm. Measurements were taken on the north-facing side of the tree bole to reduce variation from bark texture irregularities. The mean of two perpendicular diameter measurements at DBH was recorded for each tree.

Collar diameter (CD): Stem diameter measured at 10 cm above the ground collar using diameter tape, recorded to ±0.1 cm. This trait reflects total above-ground biomass accumulation potential and serves as an important predictor of plantation productivity. Two perpendicular measurements were averaged to obtain the final CD value for each individual.

Stem straightness (S): Visual assessment using an ordinal scale where 1 = severely crooked/curved stem and 10 = perfectly straight stem. This trait was scored by the same trained evaluator across all ramets to minimize observer bias. Scoring was conducted by standing approximately 15 m from the tree at the base of the bole and assessing the visual deviation from a plumb line. Crooked trees with multiple stem curvatures in different directions received lower scores; trees with single minor deviations received intermediate scores; and trees approaching perfect verticality received scores approaching 10.

Pest susceptibility assessment: Visual scoring of *Craspedonta leayana* defoliation intensity was conducted on an ordinal scale (0 = no visible damage, 10 = severe complete defoliation) based on observations conducted during the active insect pressure period (monsoon months June–September) throughout the 2019–2024 period (five consecutive monsoon seasons). Clone susceptibility classification was based on cumulative damage assessments and frequency of defoliation events. Clones were classified into three categories: low susceptibility (mean damage score <3.5), moderate susceptibility (score 3.5–6.5) and high susceptibility (score >6.5).

Table 1: Provenance distribution and site characteristics of candidate plus trees(CPTs) yielding 70 evaluated *Gmelina arborea* clones

State	Key Regions/ Sites	CPTs (n)	Selected Clones (n)	Elevation (m)	Rainfall (mm)
Assam	Lanka	50	17	50–400	2,200–3,000
	Langting		8		
	Lumding		2		
Arunachal Pradesh	Medo	30	8	200–800	3,000–4,500
	Chowkham		1		
West Bengal	Cooch Behar	27	15	100-500	2,000–2,800
	Kurseong		8		
	Buxa Tiger Reserve		1		
Mizoram	Bilkhawthlir	12	7	300-700	2,500–3,500
Kolasib		3			
Total		119	70		

Clone selection via point-grading system

Elite clones were identified using a comprehensive point-grading system that integrates the four growth traits with weighted importance assigned based on their economic significance in timber production and market demand:

Individual trait scores were normalized to a 0–1 scale using the formula:

$$Z_{ijk} = \frac{X_{ijk} - min\ (X)}{max\ (X) - min\ (X)}$$

where Z_{ijk} is the normalized score, X_{ijk} is the observed value and min(X) and max(X) are the minimum and maximum clone values observed.

The combined point-grade score was calculated as:

$$S_j = 0.4Z_{\text{Ht}} + 0.3Z_{\text{DBH}} + 0.2Z_{\text{CD}} + 0.1Z_{\text{S}}$$

where the weighting reflects: height (40%, primary growth indicator), DBH (30%, volume production), collar diameter (20%, biomass and vigour), and stem straightness (10%, wood quality). Clones scoring greater than one standard deviation above the population mean $S_j > \overline{S} + 1.SD_S$ were designated as elite clones, representing the top phenotypic performers (approximately 34–36% of germplasm collection). Additionally, Pearson correlation coefficients (r) were calculated among clone means for height (Ht), DBH, collar diameter (CD) and straightness (S) to evaluate trait interrelationships.

Statistical analysis and genetic parameter estimation

Analysis of variance (ANOVA) was performed using the CRBD statistical model:

$$Y_{ijk} = \mu + R_i + C_i + \epsilon_{k(ij)}$$

where Y_{ijk} is the observed value, μ is the grand mean, R_i is the replication effect, C_j is the clone effect and $\epsilon_{k(ij)}$ is the random error term. F-tests were used to determine significance of clone effects at $p = 0.01$ level.

Genetic parameters were estimated following standard quantitative genetics approaches for clonal trials (Lynch and Walsh, 1998). Variance components were partitioned using restricted maximum likelihood (REML) estimation in the R package 'lme4' (Bates *et al.*, 2015):

Phenotypic Coefficient of Variation (PCV):

"PCV"=($\sigma p \times 100$)/$\overline{X}$

Genotypic Coefficient of Variation (GCV):

"GCV"=($\sigma g \times 100$)/$\overline{X}$

where σ^2_p = phenotypic variance = $\sigma^2_g + \sigma^2_e$; σ^2_g = genotypic variance (among-clone variance component); σ^2_g ; = environmental variance (residual component).

Broad-sense Heritability (on clone mean basis):

$h^2 = \sigma^2_g / \sigma^2_p$

Genetic Advance (at 5% selection intensity):

$GA = k \times h \times \sigma p$

where k = 2.06 (selection differential at 5% selection intensity), h = square root of heritability and σp = phenotypic standard deviation.

For Genetic Variability Analysis: Hierarchical cluster analysis (Ward's method, squared Euclidean distances) was conducted on standardized clone means (Ht, DBH, CD, S) using R software to identify genetic variability patterns, reporting cluster composition, intra-and inter-cluster distances among elite selections.

Pest susceptibility scores were analyzed via one-way ANOVA, on the top nine (9) performing phenotypically superior clones, to test for significant differences among clones. Pairwise comparisons of elite clones with pest-resistant clones were conducted using Tukey's honest significant difference (HSD) test at α = 0.05 significance level.

All statistical analyses were performed using R statistical software (version 4.2.0; R Core Team, 2022) with custom scripts for variance component estimation, genetic parameter calculations and data visualization. Model diagnostics, including residual normality (Shapiro-Wilk test) and homogeneity of variance (Levene's test), were verified for all ANOVA models prior to before inference.

Results

Phenotypic variation in growth traits

Comprehensive analysis of phenotypic data across the 70-clone germplasm base revealed highly significant variation in all measured growth traits ($p<0.01$), demonstrating substantial genetic diversity within the *G. arborea* gene bank. The F-ratio values across traits ranged from 2.40 to 4.55, indicating significant clonal differentiation (Table 2).

Table 2: Growth parameters of 70 *Gmelina arborea* clones at 20 years (CRBD, n=5 reps × 5 ramets/clone)

Clone	Ht m	CD mm	DBH cm	S
RFRI/GA/002	16.07	56.07	49.00	2.27
RFRI/GA/004	16.44	48.17	41.92	2.60
RFRI/GA/005	14.33	51.43	44.35	3.05
RFRI/GA/006	20.52	53.80	48.23	3.62
RFRI/GA/007	16.67	50.53	43.60	2.87
RFRI/GA/008	17.60	62.93	52.20	2.40
RFRI/GA/009	15.20	50.25	43.05	2.33
RFRI/GA/011	18.80	60.80	51.40	2.73
RFRI/GA/014	16.68	52.45	47.20	1.93
RFRI/GA/015	16.22	51.18	48.33	2.07
RFRI/GA/016	15.80	52.67	45.93	2.47
RFRI/GA/017	22.13	67.07	62.22	3.33
RFRI/GA/019	14.23	50.77	42.85	2.40
RFRI/GA/020	13.27	43.23	35.62	1.97
RFRI/GA/021	19.60	54.27	47.07	3.60
RFRI/GA/022	10.81	42.28	36.13	1.90
RFRI/GA/023	14.69	38.13	33.91	1.91
RFRI/GA/025	17.80	57.42	51.27	2.70
RFRI/GA/026	12.03	45.25	38.47	2.18
RFRI/GA/027	18.33	65.33	58.33	2.53
RFRI/GA/028	16.17	48.87	42.33	3.20
RFRI/GA/029	12.07	38.20	32.20	2.07
RFRI/GA/030	13.73	47.07	39.87	2.47
RFRI/GA/031	16.97	42.20	36.33	1.93
RFRI/GA/033	14.98	56.10	49.38	2.78
RFRI/GA/034	17.73	59.13	51.80	2.93
RFRI/GA/036	12.62	42.03	37.55	2.47
RFRI/GA/037	14.03	49.20	41.53	2.73
RFRI/GA/038	17.67	50.40	44.87	3.07
RFRI/GA/039	22.13	63.93	54.87	4.03
RFRI/GA/040	20.87	59.60	51.48	1.80
RFRI/GA/042	16.95	45.08	40.32	2.08
RFRI/GA/043	11.92	50.50	46.33	1.67
RFRI/GA/045	17.57	55.98	48.95	2.67
RFRI/GA/046	10.80	50.23	44.03	2.33
RFRI/GA/071	14.93	51.93	42.07	2.67
RFRI/GA/072	8.86	33.10	28.21	1.90
RFRI/GA/073	11.13	43.90	38.93	2.73R
FRI/GA/075	17.37	34.35	28.83	2.52
RFRI/GA/077	16.13	45.67	39.16	2.80
RFRI/GA/079	14.27	44.43	37.08	2.35
RFRI/GA/081	10.81	43.83	36.05	2.25
RFRI/GA/085	14.53	50.20	42.07	2.53
RFRI/GA/086	15.35	56.10	49.40	2.75
Clone	Ht m	CD mm	DBH cm	S
RFRI/GA/088	17.07	43.42	39.24	2.40
RFRI/GA/093	15.33	51.18	44.40	2.24
RFRI/GA/094	19.46	47.80	40.96	2.01
RFRI/GA/095	14.30	50.23	43.10	1.63
RFRI/GA/096	18.20	65.57	57.47	2.53
RFRI/GA/097	19.00	51.68	45.32	2.52
RFRI/GA/098	16.32	54.65	45.23	1.83
RFRI/GA/099	19.15	66.67	58.82	2.50
RFRI/GA/100	15.65	57.78	47.80	2.22
RFRI/GA/101	15.55	56.97	49.20	1.93
RFRI/GA/102	17.80	64.45	52.73	2.95
RFRI/GA/103	17.27	58.40	48.27	2.15
RFRI/GA/104	13.02	53.72	47.90	1.55
RFRI/GA/105	16.28	50.16	42.60	2.18
RFRI/GA/106	14.45	68.42	59.77	2.72
RFRI/GA/107	21.56	63.14	57.11	1.44
RFRI/GA/108	15.77	52.70	43.13	3.03
RFRI/GA/109	16.58	59.83	54.83	3.15
RFRI/GA/110	8.12	41.78	31.00	1.57
RFRI/GA/111	16.77	48.60	41.93	2.67
RFRI/GA/111	9.80	42.60	36.85	1.92
RFRI/GA/112	17.53	59.78	50.75	2.58
RFRI/GA/113	10.40	43.89	38.04	1.47
RFRI/GA/114	9.06	39.58	33.06	1.67
RFRI/GA/115	18.33	31.67	22.44	1.44
RFRI/GA/116	16.20	60.33	52.40	2.40
Mean ± SE	15.42 ± 0.32	52.75 ± 1.26	45.63 ± 1.13	2.47 ± 0.10
Range (Low–High)	8.12–22.13	31.67–68.42	22.44–62.22	1.44–4.03
F ratio	2.62	4.09	4.55	2.40
C.V. (%)	24.13	14.35	14.94	24.91

Note: All F-ratios are significant at $p<0.01$. CV = phenotypic coefficient of variation.

Height (Ht): Tree height measurements ranged from a minimum of 8.12 m (clone RFRI/GA/110) to a maximum of 22.13 m (clones RFRI/GA/017 and RFRI/GA/039), with a population mean height of 15.42 ± 0.32 m (±SE). The coefficient of variation (CV) for height was 24.13%, reflecting substantial phenotypic diversity. F-ratio for clonal effect = 2.62 ($p<0.01$), confirming significant genetic differentiation for height growth. The superior performers exceeded the population mean by up to 43.5%, indicating substantial opportunity for genetic gain through clone selection.

Collar Diameter diameter (CD): Collar diameter exhibited a range of 31.67 cm (clone RFRI/GA/115) to 68.42 cm (clone RFRI/GA/106), with a population mean of 52.75 ± 1.26 cm. Coefficient The coefficient of variation was 14.35%, the lowest among traits measured, suggesting relatively strong genetic control with constrained environmental effects. F-ratio = 4.09 ($p<0.01$), indicating highly significant clonal differentiation. The superior clones exceeded the population mean by up to 29.6%, demonstrating strong potential for selecting high-biomass phenotypes.

Diameter at breast height (DBH): DBH measurements ranged from 22.44 cm (clone RFRI/GA/115) to 62.22 cm (clone RFRI/GA/017), with a population mean DBH of 45.63 ± 1.13 cm. Coefficient The coefficient of variation was 14.94%, consistent with collar diameter variation. F-ratio = 4.55 ($p < 0.01$), representing the highest F-value among measured traits, indicating particularly strong genetic control of diameter growth. Superior clones demonstrated 36.3% superiority over the population mean in DBH, reflecting the strong heritable basis of this commercially important trait.

Stem Straightness straightness (S): Straightness scores ranged from 1.44 (clones RFRI/GA/115 and RFRI/GA/113) to 4.03 (clone RFRI/GA/039), with a population mean of 2.47 ± 0.10. The coefficient of variation (24.91%) was the highest among all traits, suggesting this character exhibits substantial environmental influence in addition to genetic determination. F-ratio = 2.40 ($p<0.01$), confirming significant clonal variation. The top performers achieved 63% superiority in straightness scores relative to the population mean, demonstrating appreciable genetic variation for this economically important wood quality trait.

The superior-performing clones merit specific mention: Clone RFRI/GA/017 demonstrated exceptional performance across multiple traits, recording height of 22.13 m, collar diameter of 67.07 cm and DBH of 62.22 cm. Clone RFRI/GA/039 similarly achieved a height of 22.13 m with the highest straightness score of 4.03 and DBH of 54.87 cm. Clone RFRI/GA/106, while demonstrating moderate height (14.45 m), exhibited the maximum collar diameter of 68.42 cm and exceptionally high DBH of 59.77 cm, indicating efficient volume production. These top performers were consistently identified through the point-grading system as elite candidates.

Performance of selected elite clones

Twenty-four elite clones were selected from the 70-clone population (34.3% selection rate) using an integrated point-grading system ($Sj = 0.4, Z_{Ht} + 0.3, Z_{DBH} + 0.2, Z_{CD} + 0.1, Z_S$), Clones scoring >1 SD above the population mean S_j were designated elite. These clones demonstrated 7.3–20.4% superiority across growth traits compared to population means (Table 3). Elite clones originated from diverse provenances, ensuring adaptation across Northeast India's agroecological gradient. The substantial superiority of elite clones, particularly in height (20.4%) and DBH (9.6%), demonstrates strong potential for genetic gain through clonal deployment in second-generation seed orchards. Top 24 performers included: RFRI/GA/017, RFRI/GA/039, RFRI/GA/107, RFRI/GA/006, RFRI/GA/040, RFRI/GA/021, RFRI/GA/099, RFRI/GA/097, RFRI/GA/094, RFRI/GA/096, RFRI/GA/011, RFRI/GA/102, RFRIGA025, RFRI/GA/034, RFRI/GA/038, RFRI/GA/045, RFRI/GA/109, RFRI/GA/007, RFRI/GA/014, RFRI/GA/008, RFRI/GA/103, RFRI/GA/112, RFRI/GA/105 and RFRI/GA/031.

Table 3: Mean performance of 24 elite clones versus population means (70 clones), Naharoni gene bank, Golaghat, Assam (20 years)

Trait	Population Mean ± SE	Elite Mean ± SE	% Superiority	Elite Range
Height (m)	15.42 ± 0.32	18.57 ± 0.36	20.4	16.28–22.13
DBH (cm)	45.63 ± 1.13	50.01 ± 1.23	9.6	36.33–62.22
Collar Diameter (cm)	52.75 ± 1.26	57.42 ± 1.34	8.8	42.20–67.07
Straightness	2.47 ± 0.10	3.18 ± 0.12	28.7	1.44–4.03
Point-grade (S_j)	0.00 ± 0.15	2.65 ± 0.13	-	1.12–1.89

Note: Means based on clone averages from CRBD analysis (n=5 reps × 5 ramets/clone/rep). % Superiority = [(Elite mean - Population mean)/Population mean] × 100.

Further, Inter-trait relationships among growth parameters were assessed via Pearson correlation analysis (Table 4). Height showed moderate positive correlations with DBH ($r = 0.68$) and collar diameter ($r = 0.65$), while DBH and CD exhibited strong correlation ($r = 0.78$; all $p<0.01$). These relationships validate the weighted multi-trait selection index used for elite clone identification.

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Table 4: Pearson correlation matrix among growth traits of 70 *Gmelina arborea* clones (clone means, df = 68)

	Height	DBH	CD	Straightness
Height	1.00			
DBH	0.68	1.00		
CD	0.65	0.78	1.00	
Straightness	0.22	0.35	0.28	1.00

All correlations are significant at p<0.01 (df = 68) except Straightness (p<0.05). Strong size trait relationships (r = 0.65-0.78) support a multi-trait selection index.

Genetic parameters

The genetic parameters derived from variance component analysis (Table 5) revealed the genetic basis of observed phenotypic variation. High broad-sense heritability estimates were obtained for height (h^2 = 0.82) and collar diameter (h^2 = 0.62), indicating that 62–82% of the phenotypic variance is of genetic origin, substantially heritable and responsive to selection. Diameter at breast height showed intermediate heritability (h^2 = 0.70), while straightness exhibited high heritability (h^2 = 0.78). These heritability estimates are consistent with literature values for *G. arborea* and similar tropical timber species, confirming strong genetic control of economically important traits.

Phenotypic and genotypic coefficients of variation were similar in magnitude for most traits (Table 5), reflecting the substantial genotypic variance. The close correspondence between PCV and GCV indicates that environmental variance contributes proportionally less than genetic variance to total phenotypic variation, particularly for diameter traits. Genetic advance at 5% selection intensity ranged from 0.72 units (straightness) to 9.87 cm (collar diameter), indicating the expected progress from selection of the top 5% of clones. For height, selecting the top 5% of clones would yield a genetic advance of 4.21 m, representing approximately 27% increase over the population mean.

The phenotypic coefficients of variation (14.35–24.91%) were proportionally consistent with genetic advances, confirming substantial breeding potential. The high heritability estimates combined with appreciable genetic advances suggest that these traits are suitable targets for a clone-based breeding strategy, where gains achieved through current elite clone selection will be fully captured in offspring through vegetative propagation.

Table 5: Genetic parameters for four growth traits in 70 clones of *G. arborea*.

Trait	σ^2g	σ^2p	PCV (%)	GCV (%)	h^2	GA (5%)
Height (m)	12.40	15.12	24.13	22.87	0.82	4.21
CD (cm)	45.20	73.00	14.35	11.52	0.62	9.87
DBH (cm)	78.50	112.40	14.94	12.89	0.70	8.45
Straightness	0.32	0.41	24.91	22.94	0.78	0.72

Genetic parameters based on CRBD analysis of 70 clones (k = 2.06 for 5% selection intensity); σ^2g = genotypic variance; σ^2p = phenotypic variance; PCV = phenotypic coefficient of variation; GCV = genotypic coefficient of variation; h^2 = broad-sense heritability; GA = genetic advance at 5% selection intensity.

Table 6: Hierarchical clustering analysis of 24 elite Gmelina arborea clones: cluster composition and distance parameters

Cluster	No. Clones	Key Characteristics	Composition (Key Clones)	Intra-cluster D^2	Inter-cluster D^2 (I-II, I-III, II-III)
Cluster I (High Growth)	8	Tallest, largest DBH/CD	RFRIGA017,039,107, 040,021,099,094,096	12.45	28.67, 35.42,22.18
Cluster II (Moderate Growth)	10	Balanced traits	RFRIGA011,102,025, 034,038,045,109,007,014,008	15.23	28.67, 19.85
Cluster III (Stem Quality)	6	Superior straightness	RFRIGA103,112,105, 031,097,006	10.89	35.42, 19.85

Note: Clusters represent distinct genetic variability patterns among elite selections.

Cluster analysis and genetic variability

Hierarchical cluster analysis using Ward's method and squared Euclidean distances partitioned the 24 elite clones into three phenotypic groups based on growth traits (Table 6). Cluster I (n=8) represented high-growth genotypes with the lowest intra-cluster variation (D^2=12.45), while Cluster III (n=6) showed superior stem quality with tight clustering (D^2=10.89). Substantial inter-cluster distances (19.85-35.42) confirmed genetic distinctiveness among clusters, supporting diverse clonal deployment strategies across Northeast India's agroecological zones.

Pest resistance and agronomic concordance

Pest susceptibility scores across the 9 top phenotypically superior clones showed significant variation (one-way ANOVA: F = 4.56, p<0.01; population mean: 4.8 ± 0.1 cm^2/larva). Three clones exhibited low susceptibility (damage ⩽ 3.5 cm^2/larva): RFRI/GA/031, 034, 039 and four clones were reported to be moderately susceptible, i.e. RFRI/GA/075, 088, 095 and 107 (Table 7). Notably, from low-susceptibility clones, two clones (RFRI/GA/034, GA/039) were also reported to be elite performers in the point-grading system, which in turn demonstrates favourable concordance between superior growth and pest resistance. Clone RFRI/GA/039 exemplified this dual superiority with the highest straightness (S=4.03) and least leaf damage (3.01 ± 0.01 cm^2/larva). This multi-trait excellence positions these elite clones for deployment in pest-prone Northeast India plantations.

Table 7: Leaf area damage by *Craspedonta leayana* on selected *Gmelina arborea* clones (mean ± SE, n=5 reps)

Clone	Category	Area Fed (cm^2/larva)	Tukey HSD Group
GA034	Less susceptible	3.11 ± 0.07	A
GA039	Less susceptible	3.01 ± 0.01	A
GA031	Less susceptible	3.50±0.20	A
GA075	Moderately susceptible	5.89 ± 0.09	B
GA088	Moderately susceptible	5.73 ± 0.02	B
GA095	Moderately susceptible	5.45 ± 0.05	B
GA107	Moderately susceptible	5.73 ±0.02	C
GA006	Most susceptible	7.22 ±0.20	C
GA017	Most susceptible	6.04 ±0.05	B
	Mean ± SE	4.85 ± 0.105	

Means within same HSD group (α=0.05) not significantly different. Population mean: 4.85 ± 0.105 cm^2/larva (F =4.56, p<0.01).

Discussion

Magnitude and significance of genetic variation

The substantial genetic variation documented across all four quantitative traits confirms the substantial breeding potential of the *G. arborea* germplasm base maintained at Naharoni. The coefficients of variation (14.35–24.91%) exceed those reported in earlier assessments of the same gene bank (PCV 15–30%, Anandalakshmi *et al.,* 2016) and are comparable to global variation documented for *G. arborea* and related tropical hardwoods (CVs 12–28%, Lauridsen and Kjaer, 2002). The particularly high variation for height (CV 24.13%) and straightness (CV 24.91%) reflects both substantial genetic differentiation among clones and environmental responsiveness of these traits across the heterogeneous soil and microclimate conditions of the Naharoni site.

The F-ratio values (2.40–4.55) indicate strong clonal differentiation, with the highest F-value for DBH (4.55) suggesting particularly strong genetic control of this commercially important trait. This strong heritability of diameter growth is ecologically and economically significant, as DBH directly determines merchantable timber volume and plantation profitability. The exceptional phenotypic superiority of leading clones (up to 20.4% above mean for height, 9.6% for DBH) (Table 3) demonstrates that substantial productivity gains are achievable through clone selection alone, without requiring hybridization or advanced breeding protocols.

Heritability and breeding response

The high broad-sense heritability estimates (h^2 = 0.62–0.82) confirm that the observed phenotypic variation is predominantly genetic in origin, with strong potential for capture through vegetative propagation (Table 5). These heritability estimates align with published values for *G. arborea* (Nautiyal *et al.,* 2023) and tropical timber species generally. Height heritability of 0.82 indicates that 82% of phenotypic variance reflects genetic effects, suggesting that superior height performance will be consistently maintained in clonal progeny. Similarly, the heritability of 0.70 for DBH and 0.78 for straightness indicates that these economically important traits will respond predictably to selection and preservation through vegetative propagation.

The genetic advance calculations indicate substantial expected gains from the deployment of elite clones. For height, selecting the top 5% of clones

achieves an expected genetic advance of 4.21 m, representing approximately 27% increase over the population mean. For DBH, the expected genetic advance of 8.45 cm represents a 18.5% increase-a substantial improvement that directly translates to increased timber volume and plantation revenue. These gains are fully heritable and will be maintained in all vegetative descendants, making clonal propagation economically justified for commercial plantation establishment.

The close correspondence between PCV and GCV (ratios 1.06–1.24) indicates that environmental variance comprises a relatively small proportion of total phenotypic variance. This finding suggests that environmental heterogeneity within the Naharoni experimental site is modest relative to genetic differentiation, or that the traits measured are intrinsically stable across varying environmental conditions. This stability enhances the predictability of clone performance across diverse plantation sites within the Northeast region.

Clone selection strategy and practical utility

The point-grading system successfully identified 24 elite clones representing the top 34.3% of the germplasm collection. This selection rate aligns with international guidelines for CSO establishment, which recommend inclusion of 20–50 elite clones to balance genetic gain with maintenance of reproductive and genetic diversity (EUFORGEN, 2013). The 15–25% superiority of elite clones over population mean is economically meaningful; for example, the 20.4 % superiority in Height translates directly to approximately 20% increase in merchantable timber at rotation and correspondingly increases in DBH (assuming volume scales approximately with DBH^2). The geographic diversity of selected elite clones (distributed across four Northeast Indian states) is strategically advantageous for several reasons. First, it ensures that the selected germplasm represents adaptation to regionally variable climatic and edaphic conditions, reducing the risk of maladaptation if CSOs are established across diverse sites. Second, geographic diversity limits risk from pest and pathogen outbreaks, as clones of common origin might share susceptibility to locally prevalent pests or diseases. Third, the provenance diversity reflects evolutionary adaptation to local monsoon patterns, soil conditions and temperature regimes accumulated over generations, enhancing long-term plantation resilience.

Integration of pest resistance and growth performance

The identification of pest-resistant clones with low *Craspedonta leayana* susceptibility (Table 7) provides critical additional value. *C. leayana* defoliation stress is estimated to reduce annual tree growth rates by 15–30% and plantation productivity by 20–25% if unmanaged (Kumar *et al.,* 2003; Phukan *et al.,* 2022). The fortunate concordance of three pest-resistant clones with elite growth phenotypes (RFRI/GA/031, 034, 039) suggests that resistance mechanisms do not incur growth trade-offs-a finding of substantial practical importance for plantation managers. These clones merit priority consideration for CSO deployment in regions with endemic *C. leayana* populations.

The absence of comprehensive pest resistance data across all 70 clones represents a limitation of the present study, as only 2019–2023 pest pressure observations were available. Pest susceptibility can be highly dependent on environmental conditions, pest population dynamics and insect phenology. Expanded monitoring across multiple seasons and diverse environmental conditions would provide more robust quantification of clone resistance. However, the clones identified as low-susceptibility performers represent good candidates for further evaluation in targeted pest-prone plantations.

Genetic gain and CSO productivity projections

The established elite clones, when deployed through second-generation CSOs, will produce improved planting material with predictable genetic superiority over current commercial seed sources. Conservative estimates suggest that clonal seed from elite clones will deliver:

- Height advantage: ~3.5 m additional height at 20 years (20% above current population mean)
- Strainghtness (Clear bole length): ~28-30% additional merchantable timber volume per hectare at rotation (compound effect of height and diameter improvements)

These productivity gains translate directly to enhanced economic returns for plantation growers. At commercial timber prices (₹8,000–12,000 per m^3 for sawn timber), the improved productivity from elite clonal seed justifies the higher costs of establishing and maintaining CSOs compared to conventional seed orchards or seed-source plantations.

Alignment with land degradation neutrality goals

India has committed to restoring 26 million hectares of degraded lands by 2030 under the United Nations Convention to Combat Desertification (UNCCD) and complementary national pledges. Northeast India, with substantial areas of degraded tea, agricultural and ravine lands, represents a primary target for restoration activities. *G. arborea* plantations, particularly when established with genetically superior, locally adapted clones, contribute substantially to achieving Land Degradation Neutrality (LDN) targets while generating livelihood benefits through timber production.

The 24 elite clones identified in this study, when deployed across an estimated 1.2 million hectares of Northeast India where *G. arborea* is suited, could generate approximately 30–40% higher biomass productivity compared to current seed-source plantations. This enhanced productivity translates to: (i) more rapid vegetation cover establishment, (ii) enhanced soil carbon sequestration, (iii) improved hydrological function and erosion control and (iv) increased livelihood income for smallholder farmers engaged in agroforestry systems. The convergence of genetic improvement, restoration goals and rural development objectives makes CSO deployment strategically important for Northeast India's sustainable development agenda.

Limitations and Future Directions

Several limitations of the present investigation warrant acknowledgement. First, the evaluation was conducted at a single site (Naharoni) under specific environmental conditions (tropical humid monsoon, Alfisol soils, 2,200 mm rainfall). Genotype-by-environment (G×E) interactions could affect clone performance across diverse plantation sites with different rainfall patterns, soil types, or elevations. Validation of elite clones through multi-site trials across representative agroecological zones of Northeast India would strengthen confidence in recommendations for regional deployment.

Second, the study assessed phenotypic performance at a single time point (20 years post-establishment). Long-term phenotypic stability, age-related growth trends and age-related changes in pest resistance have not been evaluated. Continued monitoring of these clones through subsequent decades would reveal whether superior early growth performance is sustained or diverges over longer rotations.

Third, while four economically important traits were measured, other quality attributes, including wood density, grain characteristics, fibre properties and end-use suitability, were not assessed. Comprehensive wood quality evaluation would strengthen the case for CSO deployment and provide species-specific recommendations to timber processors and end-users.

Fourth, comprehensive molecular genetic characterization of the elite clones has not been conducted. Genomic analysis would elucidate the genetic basis of trait variation, reveal linkages between traits and provide tools for molecular marker-assisted selection in future breeding generations. Application of genome-wide association studies (GWAS) and genomic prediction could accelerate breeding gains in subsequent improvement cycles.

Despite these limitations, the present study provides a solid empirical foundation for CSO establishment and deployment of genetically improved *G. arborea* germplasm in Northeast India.

Conclusion

This comprehensive 20-year evaluation of the Naharoni 70-clone *G. arborea* germplasm base documents substantial genetic variation in growth traits and pest resistance, confirming the breeding potential of this strategically important tropical timber species. The identification of 24 elite clones demonstrating 15–25% phenotypic superiority over the population mean, combined with high broad-sense heritability estimates (0.62–0.82) for economically important traits, provides a robust scientific basis for the establishment of second-generation clonal seed orchards in Northeast India.

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