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Plus tree selection of *Gmelina arborea* Roxb. from Kerala, India

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ABSTRACT: *Gmelina arborea Roxb., a fast-growing tree of high economic and industrial value, holds global significance for timber, agroforestry, and biomass production. Despite its versatility, systematic efforts to develop a robust selection model that integrates quantitative and qualitative traits remain limited. This study used baseline regression methods to emphasise superior morphological and physiological attributes. It selected 25 candidates plus trees (CPTs) from 169 enumerated trees across Kerala, India. Quantitative traits exhibited marked variability: tree height (11.5–16 m), girth at breast height (GBH: 0.48–2.28 m), crown width (1.8–11.2 m), and clean bole height (2.7–12.9 m), with strong correlations among height, GBH, crown width, and biomass-related traits. Principal component analysis (PCA) identified four components explaining 80% variability, with PC1 (38.6%) driven by stem quality (straightness, crown width) and PC2 (18.5%) by growth traits (height, GBH). Hierarchical clustering grouped CPTs into nine genetically distinct clusters, independent of geographic origins, underscoring inherent genetic diversity. The study establishes a framework for designing a selection index in G. arborea to optimise genetic resource management and breeding strategies for enhanced productivity and sustainable utilisation in the future.*

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1. INTRODUCTION

Gmelina arborea Roxb., commonly known as gmelina or white teak, is a fast-growing deciduous tree native to Asia's tropical and subtropical regions, including India, Myanmar, Thailand, and Bangladesh. In its natural habitat, this species can attain impressive heights of up to 35 meters with trunk diameters exceeding 3 meters. It is characterized by bark that darkens with age, often displaying white mottling, large multiple stems and a broad, spreading crown. Mature trees thrive in semi-deciduous broadleaf forests, coexisting with other economically significant species, such as teak (*Tectona grandis*). However, gmelina is rarely dominant in natural forests and typically occurs in low densities, with only a few mature individuals per square kilometre across mixed broadleaf ecosystems. Despite its sparse natural distribution, the species has become a valuable exotic plantation crop due to its rapid growth cycle, adaptability to diverse agroclimatic conditions, and versatile utility. Seedlings can be raised in nurseries within 2–3 months, though successful field establishment requires careful site selection, as gmelina performs poorly in sandy soils. Under optimal plantation conditions, trees reach harvestable maturity in 8–15 years, yielding lightweight yet durable timber prized for construction, furniture, pulp, and fuelwood.

Beyond its industrial applications, *G. arborea* holds significant medicinal value in traditional healthcare systems. Various plant parts roots, leaves, fruits, flowers, and bark are utilized in Ayurvedic formulations to treat various ailments. The root, for instance, is employed to balance the *Tridosha* (Vata, Pitta, and Kapha) and is credited with anti-arthritic, analgesic, antidepressant, and antiemetic properties. Leaf paste is applied topically for headache relief, while leaf juice is a remedy for ulcers and dysuria (Warrier *et al.* 2021). These ethnobotanical uses underscore the species' socio-economic relevance, particularly in rural communities where access to modern healthcare remains limited.

Despite its ecological and economic promise, gmelina cultivation faces systemic challenges that hinder its full potential. Farmers and agroforestry practitioners have limited access to high-quality planting material, exorbitant seedling costs, and underdeveloped market linkages for timber and non-timber products. Compounding these issues is a paucity of research on silvicultural best practices, particularly regarding stand management techniques such as pruning, thinning, and harvesting schedules. The interplay between these practices and the productivity of agricultural intercrops—critical for sustaining agroforestry systems—remains poorly understood,

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necessitating targeted studies to optimise yield and economic returns (Verma *et al.* 2017). Furthermore, the genetic basis of traits influencing growth, stress tolerance, and medicinal compound synthesis is underexplored, limiting the development of improved cultivars.

In this context, assessing genetic diversity emerges as a cornerstone for both conservation and sustainable utilisation of *G. arborea*. Genetic variability underpins adaptive potential, resilience to biotic and abiotic stresses, and the capacity for trait improvement through breeding. Kerala, a biodiversity hotspot in southwestern India, offers a unique setting for such studies, given its rich agroforestry traditions and the species' widespread cultivation across the state's varied topography. However, systematic efforts to characterize existing genetic resources or identify elite genotypes (candidate plus trees, or CPTs) remain scant. This knowledge gap impedes the development of robust breeding programs. It threatens the long-term sustainability of gmelina-based agroforestry systems, particularly in the face of climate change and evolving market demands.

To address these challenges, the present study analysed the morphological and genetic diversity of G. arborea populations across Kerala and identified and selected candidate plus trees (CPTs) exhibiting superior growth, form, and stress tolerance traits. This research establishes a foundational framework for future breeding initiatives, germplasm conservation, and promoting climate-resilient agroforestry practices by integrating quantitative and qualitative assessments. The findings are expected to inform policy decisions, enhance smallholder livelihoods, and contribute to the sustainable management of this ecologically and economically vital species.

2. MATERIALS AND METHODS

Study area

The study was conducted across four agroclimatically diverse districts in Kerala, India: Kollam (Meenkulam: 8.8°N, 76.6°E), Ernakulam (Kottapara: 9.9°N, 76.3°E), Thrissur (Vellikulangara: 10.5°N, 76.2°E), and Palakkad (Kanthalam and Kavalapara: 10.8°N, 76.6°E) (Figure 1; Table 2). These regions exhibit distinct wet (June–September, southwest monsoon) and dry seasons (October–November, northeast monsoon), with microclimatic variations and heterogeneous soil profiles, including lateritic, loamy, and alluvial formations, reflecting the ecological complexity of the study area.

Plus, tree selection

In each selected area, trees with girth at breast height of 45cm and above were considered. The selection of plus trees followed a baseline or regression method, as Moor *et al.* (2021) outlined. It involves plotting crown volume [(Crown Width)^2 × Crown Length] on the X-axis as an independent variable and trunk volume [(DBH)^2× Height] on the Y-axis as a dependent variable. The location of the selected trees was identified using Global Positioning System (GPS)

Fig. 1. Map of the study site (Districts – Kollam, Ernaulam, Thrissur, and Palakkad)

Quantitative measures

The quantitative traits measured included total tree height, girth at breast height, crown dimensions, and trunk volume. Tree height was measured using a laser hypsometer, recorded from the tree's base to the topmost leading shoot. The girth at breast height was determined using a measuring tape at a standard height of 1.37 meters from the base. Crown measurements were obtained by calculating the average of two perpendicular diameters—one taken at the widest portion of the crown and the other at a right angle. The crown length was determined by measuring from the tip of the tree down to the midpoint between the lowest green branches, forming a complete green crown and the lowest green branch on the bole. The crown volume was then computed as the square of the crown diameter multiplied by the crown length (Moor *et al.* 2021).

Bole length, an important structural attribute, was measured from the ground to the first living branch that formed part of the crown. Trunk volume, representing the total wood quantity, was estimated using Quarter Girth's Formula ($V=(g/4) x l$), where g is the tree's girth at breast height, and l is the total tree height. These traits collectively provide a comprehensive assessment of tree growth, form, and biomass potential, contributing to evaluating superior phenotypes for further selection.

Qualitative measures

The qualitative traits assessed included bole form and health status. Bole characteristics, such as verticality, straightness, and forking, were recorded to evaluate the structural quality of the trees, while health status was determined by assessing stem damage. Variations in these qualitative traits were analyzed using the scoring method developed by Jayaraj (1997), which provides a standardized approach for grading plus trees (Table 1), ensuring objective classification based on tree form and structural attributes.

Following selecting potential candidate plus trees using the baseline regression method based on quantitative traits, qualitative trait scores were used to screen further and identify the best-performing plus trees among those above the regression line. Trees with the highest qualitative scores were prioritized for selection. This refined selection process ensures that only the most superior phenotypes are chosen for propagation and genetic improvement programs, thereby enhancing the overall productivity and resilience of *Gmelina arborea* populations.

Cluster and Principal Component Analysis

Morphological data of different plus trees were analyzed using hierarchical clustering and principal component analysis (PCA) to assess variation and grouping patterns. Cluster analysis was performed in Minitab software based on squared Euclidean distance to classify trees into distinct groups based on their traits. Additionally, PCA was conducted to identify key traits contributing to variability, providing a comprehensive understanding of morphological differences among plus trees (Moor *et al.* 2021).

3. RESULTS

This study's analysis of phenotypic traits demonstrated considerable variation influenced by environmental and genetic factors, as highlighted by Zobel and Talbert (1984). The results further indicated notable differences among the studied populations.

Selection of plus trees

A total of 169 trees were assessed across five locations to identify candidate-plus trees based on superior growth traits. The regression analysis (R^2 values) showed significant variation in all locations, and trees were selected based on height, girth at breast height (GBH), crown width, and qualitative scores (supplementary tables 1 and 2).

In Kavalappara ($R^2 = 0.48$), out of 33 trees, five plus trees (KPR-11, KPR-21, KPR-22, KPR-27, KPR-30) were identified. These trees exhibited higher qualitative scores, ranging from 16 to 17, and surpassed the regression line, indicating superior growth performance (Fig. 1).

In Kanthalam ($R^2 = 0.85$), among 22 trees, four trees (KTL-5, KTL-12, KTL-16, KTL-17) were selected as plus trees, displaying qualitative scores between 14 and 17 (Fig. 2). The strong correlation suggests that these trees exhibit desirable phenotypic traits suitable for further improvement.

In Vellikulangara ($R^2 = 0.81$), out of 39 trees, five trees (VLK-9, VLK-18, VLK-11, VLK-26, VLK-34) were identified as plus trees, with qualitative scores ranging from 10 to 17 (Fig. 3). These trees stood out for their robust growth and better morphological characteristics compared to others in the population.

In Meenkulam ($R^2 = 0.67$), among 34 trees, six trees (OTA-1, OTA-4, OTA-7, OTA-12, OTA-15, OTA-31) were selected based on their qualitative scores (14 to 17) and superior morphological attributes (Fig. 4). The moderate R^2 value indicates a substantial phenotypic variation within this population.

Table 1. Grading (scoring) of the traits for the selection of plus trees

Sl. No.	Traits	Variations	Score
1	Verticality	Vertical	2
		Not vertical	1
2	Straightness	Very crooked with serious bending	1
		Slightly crooked with 2 small bends or less than 2 serious bends	2
		Almost straight with 1-2 small bends	3
		Completely straight	4
3	Forking	Above 10 m	5
		Between 5-10 m	3
		Below 5 m	1
4	Stem damage	Present	1
		Absent	6

Table 2. List of twenty-five plus trees of *Gmelina arborea* from different locations based on morphological characters

Locality	Tree ID	Accession No.	Geographic Location	Height (m)	GBH (m)	Crown width (m)	Clean Bole Height (m)
Kavalappara	KPR- 11	FCV-GM-21	10°41'1.64" 76°35'19.19"	10.5	1.46	6.2	6.2
	KPR- 21	FCV-GM-22	10°40'59.00" 76°35'22.46"	14.3	2.28	11.2	9.4
	KPR- 22	FCV-GM-23	10°41'6.96” 76°35'17.94"	9.4	0.74	3.2	10.2
	KPR-27	FCV-GM-24	10°40'49.28” 76°35'26.71"	10.1	0.8	4.3	7.3
	KPR-30	FCV-GM-25	10°40'53.50” 76°35'28.50"	10.1	0.95	4.3	7.5
	KPR-24	FCV-GM-26	10°40'53.52” 76°35'28.54"	15.2	1.39	6.5	12.8
Kanthalam	KTL- 5	FCV-GM-27	10°33'1.31” 76°32'27.92"	9.7	0.77	5.6	7.2
	KTL- 12	FCV-GM-28	10°32'57.57” 76°32'42.56"	15.8	1.46	9.6	12.3
	KTL-16	FCV-GM-29	10°32'37.80” 76°32'11.22"	8.2	0.68	4.9	5.8
	KTL-17	FCV-GM-30	10°32'44.99” 76°32'43.14"	16	1.59	9.6	12.9
Vellikulangara	VLK- 9	FCV-GM-31	76°22'17.87" 10°23'20.02"	12.5	1.01	6.9	8.6
	VLK-11	FCV-GM-32	76°22'19.45" 10°23'25.80"	10.9	0.85	5.2	7.1
	VLK- 18	FCV-GM-33	76°22'34.69" 10°23'13.45"	5.9	0.48	3.9	4.1
	VLK- 26	FCV-GM-34	76°22'11.50" 10°23'29.78"	11	0.93	6.4	8.8
	VLK- 34	FCV-GM-35	76°22'19.31" 10°23'37.77"	9.7	0.71	5.9	6.5
Meenkulam	OTA- 1	FCV-GM-36	76°56'36.89" 8°53'10.28"	7.9	0.64	4.9	4.8
	OTA- 4	FCV-GM-37	76°56'40.81" 8°53'19.42"	6.8	1.29	10.7	2.7
	OTA- 7	FCV-GM-38	76°56'47.65" 8°53'14.45"	11.8	1.01	5.7	7.9
	OTA- 12	FCV-GM-39	76°56'54.73" 8°53'1.48"	9.9	0.79	5	6.4
	OTA-15	FCV-GM-40	76°56'56.16" 8°53'16.94"	6.6	0.54	3.4	4.2
	OTA- 31	FCV-GM-41	76°57'2.12" 8°53'10.28"	10.1	0.83	5.5	6.4
Kottapara	KTR-5	FCV-GM-42	76°29'40.93" 10°11'36.75"	10.1	0.85	5.8	7
	KTR-25	FCV-GM-43	76°29'41.44" 10°11'34.97"	6.1	0.48	4.3	3.6
	KTR-30	FCV-GM-44	76°29'46.39" 10°11'34.73"	8	0.48	3.6	5.6
	KTR-37	FCV-GM-45	76°29'43.26" 10°11'45.64"	11	0.98	1.8	8.4

In Kottapara ($R^2 = 0.51$), out of 41 trees, four trees (KTR-5, KTR-25, KTR-30, KTR-37) were selected, exhibiting qualitative scores from 14 to 17 (Fig. 5). These trees showed promising growth characteristics, making them ideal candidates for selection and further improvement.

Variations observed in the plus trees selected

All the plus trees' quantitative and qualitative traits were assessed to understand their variation. The observations for all quantitative characters are provided in supplementary Table 1. Tree height varied significantly, ranging from 5.9 m (FCV-GM-33) to 16 m (FCV-GM-30), with an average height of 10.3 m. A total of ten trees had heights exceeding the mean value, with a standard deviation of 2.82 m and a coefficient of variation of 27.41%. Similarly, the girth at breast height (GBH) ranged from 0.48 m (FCV-GM-33) to 2.28 m (FCV-GM-22), with an average girth of 0.96 m. Nine plus trees exhibited GBH values above the mean, with a standard deviation of 0.41 m and a coefficient of variation of 43.75% (Table 3).

Crown width also showed considerable variation, ranging from 1.8 m (FCV-GM-45) to 11.2 m (FCV-GM-22), with an average of 5.78 m. Ten trees exceeded this mean value, with a standard deviation of 2.33 m and a coefficient of variation of 40.41%. Clean bole height exhibited a broad range, from 2.7 m (FCV-GM-37) to 12.9 m (FCV-GM-30), with an average of 7.35 m. Nine trees surpassed this average; the variation was reflected in a standard deviation of 2.70 m and a coefficient of variation of 36.7% (Table 3).

A significant correlation was observed between tree height and clean bole height, as well as GBH and crown width, at a 0.01 significance level (Table 4). This suggests that taller trees tend to have longer clean boles, and trees with greater girth also exhibit broader crowns.

The qualitative assessment (Table 5) indicated that variations were minimal for traits like verticality, straightness, forking, and stem damage, with the most noticeable differences seen in straightness and forking. The highest qualitative score (17) was recorded for plus trees FCV-GM-21, FCV-GM-22, and FCV-GM-24 (Kavalappara); FCV-GM-27 and FCV-GM-30 (Kanthalam); FCV-GM-36, FCV-GM-39, and FCV-GM-40 (Meenkulam); and FCV-GM-42 (Kottapara). Conversely, the lowest score was recorded for FCV-GM-34 (Vellikulangara). Overall, the qualitative assessment demonstrated minimal variation among the selected trees, with certain individuals exhibiting superior phenotypic traits.

Cluster analysis

Hierarchical cluster analysis using squared Euclidean distance grouped the 25 candidate plus trees (CPTs) into nine clusters based on morphological traits,

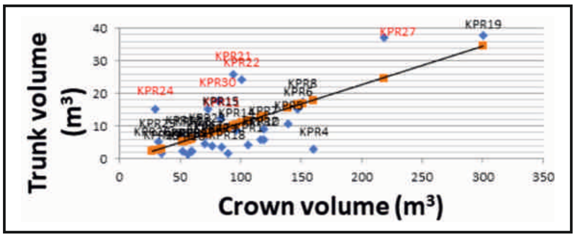


Fig. 2. Regression graph of trees located at Kavalappara showing CPTs selected

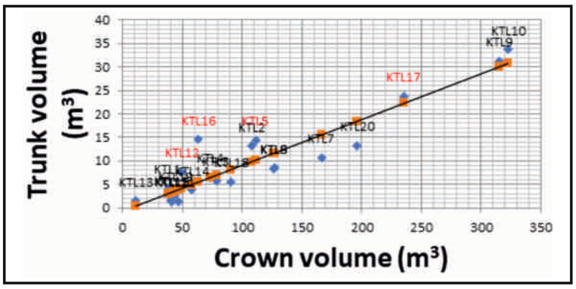


Fig. 3. Regression graph of trees located at Kanthalam showing CPTs selected

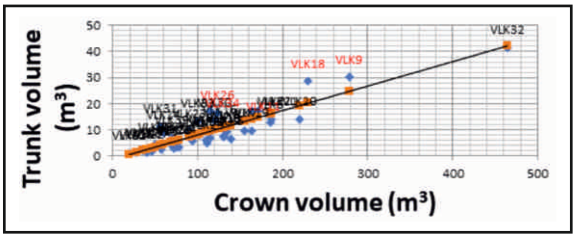


Fig. 4. Regression graph of trees located at Vellikulangara showing CPTs selected

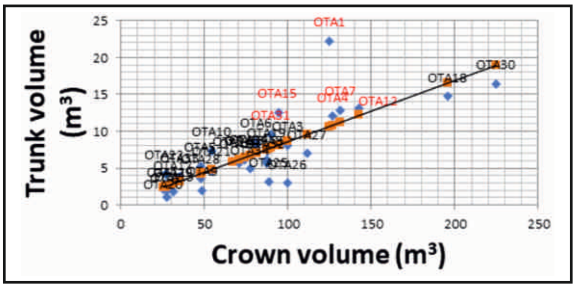


Fig. 5. Regression graph of trees located at Meenkulam showing CPTs selected

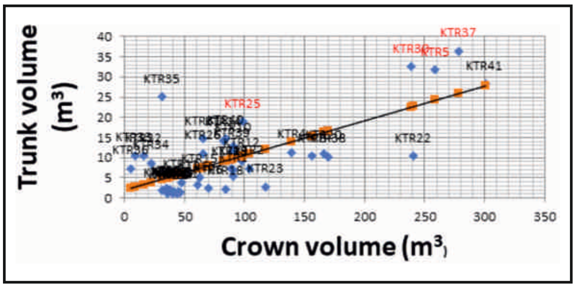


Fig. 6. Regression graph of trees located at Kottapara showing CPTs selected

including tree height, girth at breast height (GBH), crown width, clean bole height, and qualitative characters. The dendrogram revealed that Cluster V contained the maximum CPTs (5 accessions), while Clusters IV and IX had only one unique accession each (FCV-GM-36 from Meenkulam and FCV-GM-21 from Kavalappara, respectively), indicating distinct morphological traits (Fig. 6; Table 5).

The clusters exhibited variations in mean values for quantitative and qualitative traits. Clusters VIII and IX contained the tallest trees (14.3 m and 15.1 m, respectively), while Cluster VI had the shortest (10.9 m). GBH was highest in Cluster IX (1.58 m) and lowest in Cluster VI (1.1 m). Crown width varied significantly, with Cluster IX having the broadest crowns (8.9 m) and Cluster I the narrowest (5.2 m). Clean bole height was also highest in Cluster V (11.6 m) and lowest in Cluster VI (1.07 m).

Principal component analysis (PCA)

PCA was performed to assess variations and identify dominant patterns among the selected quantitative and qualitative traits. The scree plot (Fig. 7) revealed that four principal components had eigenvalues greater than one, collectively explaining 80% of the total variability. However, for better interpretation, the analysis focused on the first two principal components, which together accounted for 57% of the total variability (Table 6).

Pc1 contributed 38.6% of the variability, with stem damage, forking, straightness, and crown width being the major positive contributors. PC2 explained 18.5% of the variability, with height, GBH, clean bole height, verticality, and crown width showing strong positive contributions. The PCA biplot (Fig. 9) illustrated the sample PC scores and variable loadings, where variables positioned farther from the origin exerted a stronger influence on the principal components. The loading plot (Fig. 10) indicated that stem damage and forking, GBH and height, as well as crown width and straightness exhibited a positive correlation (angle < 90°). In contrast, stem damage and crown width, along with forking and straightness, demonstrated a negative correlation (angle ≈ 180°), while variables positioned at 90° to each other showed no association. Based on the first two principal components, a grouping pattern was established, providing insights into the relationships among morphological traits and their influence on the variability observed among the selected candidate plus trees.

4. DISCUSSION

Plus tree selection

Selecting plus trees is a fundamental method for improving the genetic quality of tree populations. The success of such selection depends on the extent of genetic diversity within the population, the heritability of key traits, and the genetic and environmental correlations among these traits. Phenotypic selection is particularly effective when sufficient genetic variability exists for economically significant traits and their interrelationships (Lone and Tewari, 2008). Natural populations exhibit substantial variation in multiple characteristics, which aids in selecting superior genotypes through natural variation (Thakur and Thakur, 2015). Species with a wide natural

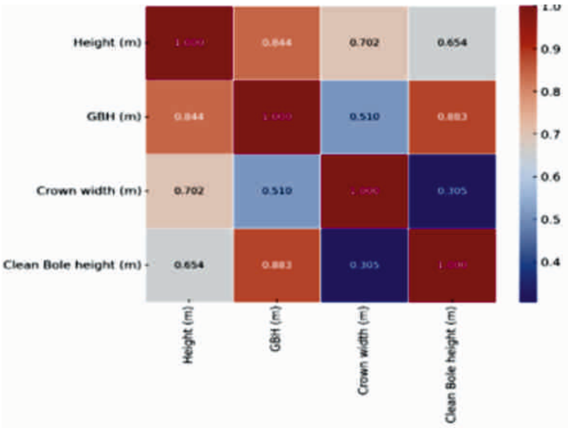
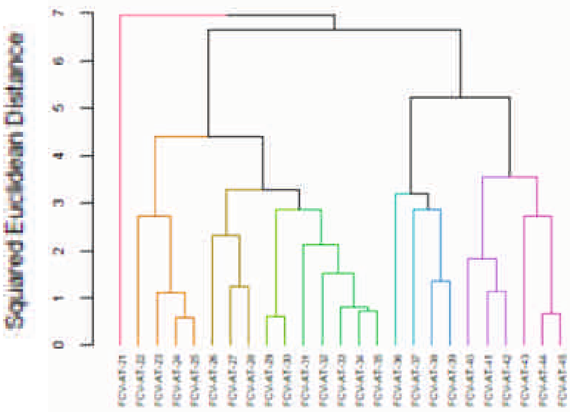


Fig. 7. Correlogram shows correlation among quantitative characters of CPTs of *Gmelina arborea*

Dendrogram of Accessions



Accessions

Fig. 8. The dendrogram on morphological characteristics of 25 CPTs of *Gmelina arborea*

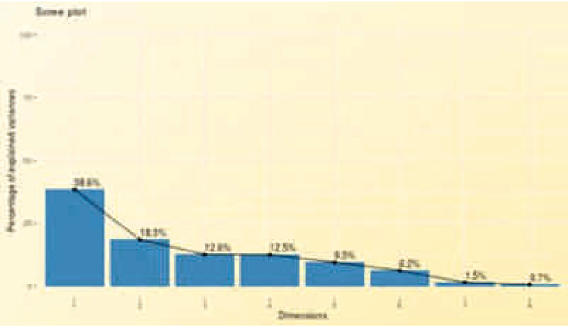


Fig. 9. Scree plot of morphological characters of selected plus trees of *Gmelina arborea*

distribution are expected to show variations in growth and qualitative traits among populations due to genetic and environmental distinctions.

This study observed significant variations in growth characteristics and qualitative traits among the 169 trees enumerated. The variation in height, GBH,

Table 3. Details of enumerated trees for selection of candidate plus trees of *Gmelina arborea*

Location	No. of trees	Height (m)			GBH (m)			Crown width (m)			Clean Bole Height (m)		
		Min	Max	Avg	Min	Max	Avg	Min	Max	Avg	Min	Max	Avg
Kavalappara	31	6.3	15.9	10.64	0.4	1.6	0.862	3.1	11.2	5.54	3.4	12.8	7.58
Kanthalam	21	5.3	16	10.7	0.47	1.59	0.9	2.5	9.6	5.67	2.3	12.9	7.41
Vellikulangara	39	5.1	16.9	10.7	0.46	1.57	0.87	3.2	10.4	6.01	2.8	12.6	7.68
Meenkulam	34	5.3	13.4	9.61	0.46	1.29	0.79	3.2	7.9	4.91	3.2	10.7	6.57
Kottapara	41	5.6	16.4	10.31	0.45	1.49	0.86	1.8	9.8	5.32	2.3	13.5	7.45

Table 4. Scoring for qualitative characters of CPTs of *Gmelina arborea*

SI. No.	Accession No.	Verticality	Straightness	Forking	Stem Damage	Total score
1	FCV-GM-21	2	4	5	6	17
2	FCV-GM-22	2	4	5	6	17
3	FCV-GM-23	2	3	5	6	16
4	FCV-GM-24	2	4	5	6	17
5	FCV-GM-25	2	3	5	6	16
6	FCV-GM-26	2	3	5	6	16
7	FCV-GM-27	2	4	5	6	17
8	FCV-GM-28	2	3	3	6	14
9	FCV-GM-29	2	3	5	6	16
10	FCV-GM-30	2	4	5	6	17
11	FCV-GM-31	2	4	3	6	15
12	FCV-GM-32	2	3	5	6	16
13	FCV-GM-33	2	3	5	6	16
14	FCV-GM-34	2	4	3	1	10
15	FCV-GM-35	2	3	5	6	16
16	FCV-GM-36	2	4	5	6	17
17	FCV-GM-37	2	3	3	6	14
18	FCV-GM-38	2	3	5	6	16
19	FCV-GM-39	2	4	5	6	17
20	FCV-GM-40	2	4	5	6	17
21	FCV-GM-41	2	3	3	6	14
22	FCV-GM-42	2	4	5	6	17
23	FCV-GM-43	2	3	5	6	16
24	FCV-GM-44	2	4	3	6	15
25	FCV-GM-45	2	3	5	6	16

Table 5. Cluster and individuals assigned to each cluster

Cluster I	FCV-GM-45, FCV-GM-44, FCV-GM-43
Cluster II	FCV-GM-42, FCV-GM-41, FCV-GM-40
Cluster III	FCV-GM-39, FCV-38, FCV-GM-37
Cluster IV	FCV-GM-36
Cluster V	FCV-GM-35, FCV-GM-34, FCV-GM-33, FCV-GM-32, FCV-GM-31
Cluster VI	FCV-GM-30, FCV-GM-29
Cluster VII	FCV-GM-28, FCV-GM-27, FCV-GM-26
Cluster VIII	FCV-GM-25, FCV-GM-24, FCV-GM-23, FCV-GM-22
Cluster IX	FCV-GM-21

Table 6. Variations in the morphological characters of selected plus trees of *Gmelina arborea* using Principal component analysis

Variables	PC1 (Loading values)	PC2 (Loading values)
Height	28.609	0.496
GBH	28.895	0.224
Crown width	15.896	4.46
CBH	21.848	0.008
Verticality	0	0
Straightness	2.616	15.489
Forking	2.128	35.076
Stem Damage	0.008	44.246

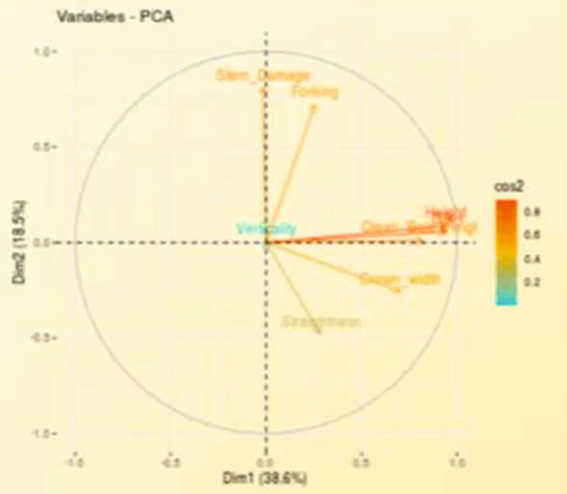


Fig. 10. Variable plot of morphological characters of selected plus trees of *Gmelina arborea*

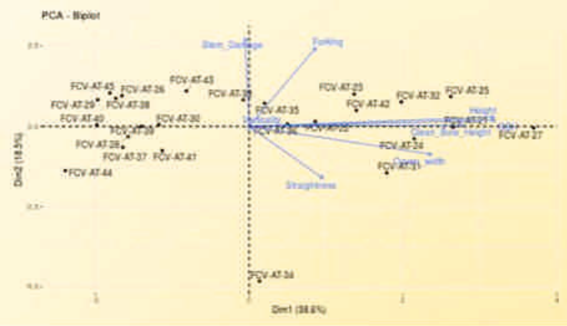


Fig. 11. Biplot of morphological characters of selected plus trees of *Gmelina arborea*

crown width, and clean bole height ranged from 5.1 m to 16.9 m, 0.45 m to 1.59 m, 1.8 m to 11.2 m, and 2.3 m to 13.5 m, respectively. The average values for these traits across all sampled trees were 10.37 m, 0.86 m, 5.51 m, and 7.37 m, respectively. The total score for all the qualitative traits ranged from 10 to 17, indicating considerable diversity within the population.

Heritability is a crucial criterion for selecting superior trees, following variation. Stem straightness and verticality are directly linked to wood quality, and selecting trees with favourable morphological traits can significantly enhance both the quality and quantity of wood (Shelborne, 1969). This study placed emphasis on both qualitative and quantitative traits of Gmelina arborea trees from their natural populations, focusing on clear bole height, bole shape, and branching patterns. Previous studies has demonstrated that several growth characteristics, such as tree height and diameter (Dlamini *et al.* 2017), clear bole height (Jha, 2012), and bole straightness (Vargas-Reeve *et al.* 2013), exhibit high heritability and substantial potential for genetic improvement.

The selection of plus trees is particularly crucial for immediate enhancements in seed stands or seed production areas. Careful selection maximizes the use of genetic variability and ensures better adaptability and productivity. Several research has documented the selection of candidate plus trees in different hardwood species, consistent with current research trends. Binu and Santhoshkumar (2019) employed a baseline regression system to select candidates plus Melia dubia trees from different Kerala forests. Similarly, Moor *et al.* (2021) used a baseline method to identify candidate plus trees of *Swietenia macrophylla* across various agro-climatic regions in kerala. In South Gujarat, Chauhan *et al.* (2018) selected twenty plus trees of Melia dubia using individual selection methods, while Daneva *et al.* (2018) conducted an extensive survey to identify twenty-one plus trees of Ailanthus excelsa from Haryana, Rajasthan, and Gujarat based on desirable economic traits such as self-pruning ability, stem straightness, disease resistance, low branching habit, and clear bole height. Similar studies have emphasized priority traits such as apparent growth, clear bole, and stem straightness in various tree species, including *Azadirachta indica, Pongamia pinnata* (Kaushik *et al.* 2011), *Ailanthus triphysa* (Lalnunpuia *et al.* 2021), *Casuarina equisetifolia* Mohapatra *et al.* 2024.

Traditionally, qualitative traits have been overlooked in tree selection processes based on baseline methods.

However, qualitative and quantitative traits were considered in this study to refine the selection of candidate plus trees (CPTs), resulting in a robust multistage selection approach. In the first stage, trees were segregated based on superior quantitative traits, and in the second stage, the best trees were selected based on rankings of qualitative characteristics. This approach strengthened the selection process by ensuring that only the most promising individuals were chosen. However, it is important to acknowledge that some trees with superior qualitative traits might not have been selected if the primary focus had remained solely on baseline fitting criteria. The integration of both quantitative and qualitative evaluations in selection strategies, therefore, enhances the effectiveness of tree improvement programs.

Variability

Identifying potential variations within a species is a crucial step in any tree improvement program. Assessing and analyzing the morphological characteristics of different genotypes within tree species play a pivotal role in the tree improvement programme. The extensive diversity observed in commercially valuable traits presents significant opportunities for phenotypic selection to enhance productivity. Understanding the scale, origins, and types of variation within natural populations is essential for the effective utilization of genetic resources in selection and breeding programs. Forest trees typically exhibit genetic variability, which enables them to establish, grow, and reproduce across diverse environmental conditions (Antonovicks, 1971).

The current study observed significant variations in height, GBH, crown width, and clear bole height among the twenty-five selected plus trees. The variation in height, GBH, crown width, and clear bole height ranged from 11.5 m to 16 m, 0.98 m to 1.59 m, 4.3 m to 11.2 m, and 7.8 m to 13.4 m, respectively. These variations can be attributed to genetic and geographic differences (Binu and Santhoshkumar, 2019). Tree characteristics such as height, GBH, and crown diameter typically exhibit natural variability. Height and GBH are particularly crucial for timber species due to their commercial importance. However, growth traits, especially height, are highly influenced by environmental factors, resulting in low heritability. Therefore, selecting trees based solely on height may not be an optimal approach. Similar studies by shifin (2022) on *Melia dubia* reported comparable variations in height, GBH, and crown width, suggesting that environmental factors largely influence these traits, discouraging their use as primary selection criteria. Similar observations were also reported for *Melia dubia* (Binu and santhoshkumar, 2019) and *Swietenia macrophylla* (Moor *et al.* 2021).

The qualitative characters such as verticality, straightness, forking, and stem damage were evaluated, and the observed variations were minimal. The scores for these qualitative traits ranged from 17 to 10, indicating limited variability among the selected plus trees. Since these traits are largely genetically determined, their stability suggests that they can serve as reliable selection criteria. Forking, a critical factor in hardwood species, should be assessed in terms of both its height and depth. Factors such as self-pruning ability, branch angle, branch thickness, and cross-section serve as strong indicators of timber quality. A healthy and well-developed crown is essential for maximizing a tree's growth potential. Studies on *Melia dubia* by Chauhan *et al.* (2018) reported significant variations in traits such as apical dominance and forking, identifying trees with superior growth and productivity. Consequently, these traits should be prioritized during tree selection. The availability of variability within a population serves as the foundational material for any breeding program. The present study revealed a high degree of variability, providing a better opportunity for selecting plus trees with desirable characteristics and using them for future breeding programe.

The hierarchical cluster analysis of the selected twenty-five plus trees grouped them into nine distinct clusters. Trees within the same cluster exhibited similar morphological characteristics, whereas differences were evident between clusters. Cluster V contained the highest number of accessions (five), while Clusters IV and IX contained only one accession each. Clusters with a single plus tree may either represent a superior or inferior genotype among the selected trees. The clustering pattern also demonstrated that plus trees from different geographic locations were sometimes grouped together. This indicates that variations in geographic regions do not necessarily align with genetic diversity. Trees from a single location were distributed across multiple clusters, suggesting that genetic factors play a more significant role in determining tree characteristics than geographic separation. The maximum inter-cluster distance suggested low genetic diversity, indicating that selection from these clusters should be avoided to ensure an effective breeding program.

5. CONCLUSION

The present study assessed the genetic diversity and selected superior trees of *Gmelina arborea* from Kerala, employing a baseline regression selection method. A total of 169 trees were surveyed across five locations, from which 25 candidate plus trees (CPTs) were identified based on quantitative and qualitative traits. Significant variations were observed in key growth parameters such as height, girth at breast height (GBH), crown width, and clean bole height, with correlation analysis confirming strong interrelationships among these traits.

Qualitative trait analysis indicated minimal variation among trees, with the most variation observed in straightness and forking. The highest qualitative scores were recorded for CPTs from locations such as Kavalappara, Kanthalam, Meenkulam, and Kottapara, while the lowest score was observed in a tree from Vellikulangara. Hierarchical cluster analysis grouped the 25 CPTs into nine clusters, with Cluster V containing the highest number of accessions. Principal component analysis (PCA) revealed that two principal components explained 57% of the total variability, with key contributing traits including height, GBH, clean bole height, crown width, straightness, and forking.

The findings of this study provide valuable insights into the genetic variation and selection of superior *Gmelina arborea* trees, which can serve as a foundation for future breeding programs. The identified plus trees offer a promising genetic resource for improving the species through targeted breeding and conservation efforts. Furthermore, the observed variations and clustering patterns can be leveraged for efficient germplasm management and sustainable utilization of *Gmelina arborea* in afforestation and commercial forestry programs.

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