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DIVERSITY ASSESSMENT AND SELECTION OF CANDIDATE PLUS TREES OF *ARTOCARPUS HIRSUTUS* LAM. IN CENTRAL KERALA INDIA

E.A. Niveditha*, Sreejith Babu, A.V. Santhoshkumar, N.K. Binu and R. Vishnu

Department of Forest Biology and Tree Improvement, College of Forestry, Kerala Agricultural University, Vellanikkara-680656, Thrissur, Kerala, India.

*Corresponding author E-mail: nivedithaea2018@gmail.com

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ABSTRACT

Artocarpus hirsutus Lam. is a valuable timber species endemic to the Western Ghats of India. A selection process was conducted in the districts of Thrissur, Ernakulam, and Malappuram in Kerala, identifying 30 candidates plus trees from a total of 225 trees evaluated for their phenotypic traits using baseline regression analysis, which assessed the relationship between trunk and crown volumes, along with qualitative scoring of traits such as branching habit, apical dominance, and self-pruning ability. Hierarchical cluster analysis was performed based on Squared Euclidean distances to categorize the candidate plus trees into distinct groups, highlighting the genetic relationships among the trees and facilitating targeted selection for breeding programs. The findings of this study underscore the importance of genetic variation in *A. hirsutus*, providing valuable insights for future tree improvement and sustainable management efforts.

Key words: *Artocarpus hirsutus* Lam., Plus tree selection, Genetic diversity, Cluster analysis.

Introduction

Artocarpus hirsutus commonly known as wild jack is a tropical evergreen tree species that is native to Kerala and Karnataka states of India. They are endemic to the Western Ghats and are found in evergreen forests. *A. hirsutus* belongs to family Moraceae and order Rosales. *A. hirsutus* is one of the most popular timber species along the Malabar coast. Better timber quality and lower cost may be the reasons for this. The most important use of wild jack wood timber has been in the production of ships and boats (Matthew *et al.*, 2006).

The recent rapid urbanization in several areas of the state has had a severe impact on the *A. hirsutus* species, with huge *A. hirsutus* trees being felled and nearby seedlings ruthlessly destroyed due to the construction of new buildings and widening of roads. Also, the current supply of *A. hirsutus* lags behind the demand, and the market price for wild jack timber remains high. However, no successful efforts have been made to consider the multiplication and cultivation of this highly demanded species. The selection of best seed source is essential

for the mass-scale multiplication of any tree species and the initial and formidable undertaking involves evaluating the naturally occurring population in order to choose the best planting material that will yield greater productivity.

The present study aimed to catalogue natural genetic diversity of *A. hirsutus* in Central Kerala and identify plus trees for genetic improvement.

Materials and Methods

The first step in the tree improvement programme is the identification and selection of candidate plus trees (CPTs) (DANEVA and Wilson 2014). Selection of suitable plus trees plays a vital role in tree breeding programs and can significantly impact the genetic improvement of forest stands. Studies have shown that by carefully selecting plus trees with favorable characteristics, genetic gains in height, diameter, and volume per unit area can be achieved (Roman *et al.*, 2020).

These gains can range up to 15% in height and diameter, and up to 35% in volume per unit area. Hazel

Table 1: Details of morphological characters of *Artocarpus hirsutus* Lam. from the Central Kerala.

	No. of trees	Height (m)			GBH			Crown width (m)			Clean bole height (m)		
		Min	Max	Avg	Min	Max	Avg	Min	Max	Avg	Min	Max	Avg
Engandiyoor	25	11	30	21.88	0.59	1.68	1.25	4.05	10.05	6.88	5	13	8.66
Thrikkoor	25	12	24	18.48	0.73	1.61	1.05	6	12.5	9.488	4	12	6.61
Vadanapilly	25	12	23	17.72	0.69	1.61	1.19	4.5	12	7.74	2	11	6.36
Edakkattuvalayal	25	9	22	15.2	0.72	2.21	1.17	3.5	12.5	7.24	3	9	5.52
Pindimana	25	9	21	14.88	0.76	1.76	1.16	3.5	9.25	6.01	2	13	5.96
Nayarambalam	25	13	22	17.56	1.07	1.66	1.42	3	11.5	6.26	2	10	6.44
Amarambalam	25	9	22	13.08	0.53	1.61	0.94	2.5	8	4.26	2	7	4.48
Ponnani	25	9	19	13.2	0.77	2.01	1.25	4	14.5	7.25	2	11	5.96
Maranchery	25	10	20	12.92	0.62	1.69	1.05	2.5	9	4.49	2	12	5.16

and Lush emphasize the necessity of considering genetic variation, heritability of traits, and the correlation between traits in order to effectively select plus trees (Lalnunpuia *et al.*, 2021). These factors play a crucial role in successful phenotypic selection and the overall genetic improvement of tree populations. Furthermore, phenotypic selection has traditionally been the first step in breeding cycles for tree improvement programs (Kim *et al.*, 2020).

This study attempted to determine the genetic diversity and selection of candidate plus trees from various locations in selected districts of Central Kerala and to evaluate their progeny. A reconnaissance survey was carried out in the homesteads of selected districts of Central Kerala for assessing the population of *Artocarpus hirsutus* Lam. A total of 9 locations were selected from three districts, such that three locations from each district. These locations were categorized based on their altitudinal values into low land and mid land.

In Thrissur district, two lowland areas, Engandiyoor and Vadanapilly panchayats, and midland region Thrikkoor panchayats, were selected. In Malappuram, two low land areas, Ponnani Municipality and Maranchery panchayat and one mild land area, Amarambalam panchayat were chosen. Similarly, in Ernakulam, three panchayaths were selected: two midland areas, Edakkattuvalayal and Pindimana panchayats and one lowland area, Nayarambalam panchayat. The panchayats were thoroughly surveyed, and *Artocarpus hirsutus* Lam. trees located in homesteads were identified after the reconnaissance.

In this study, the selection of plus trees was carried out in two stages. The first stage involved using the baseline method to identify the more vigorous trees by evaluating the relationship between their crown volume and trunk volume. In the second stage, the trees were assessed and selected based on a scoring system that measured various qualitative traits. The trees were cataloged, and their locations were recorded using GPS. Only trees with a GBH greater than 45 cm were included

in the survey. The height of the trees was measured using a Laser Hypsometer and recorded in meters. The GBH was measured at 1.37 m using a tape. The crown diameter was calculated as the average of two measurements: the largest crown diameter and a second diameter measured perpendicular to the first. The bole length was measured from the ground to the first living branch, while the crown length was determined by subtracting the crown base height from the total tree height.

Preliminary screening was conducted before enumeration, focusing on bole straightness and roundness. Key qualitative traits observed included the branching habit, height of the first branch, apical dominance, forking, branch angle, branch thickness, and self-pruning ability. Additionally, foliar and stem damage were also recorded. The variations in these qualitative traits were assessed using the scoring method developed by Jayaraj (1997). A total of 225 trees were evaluated to assess genetic diversity.

The selection of 30 candidate plus trees from various locations was carried out using the base-line method (Rudolf 1956). This involved a regression analysis based on the relationship between crown diameter squared $\times$ crown length and DBH squared $\times$ height. Trees that appeared above the regression line were considered to exhibit higher vigor and were selected. If multiple trees were above the regression line, those with higher scores in various qualitative traits were chosen. The regression analysis was conducted individually for each location to ensure maximum diversity in the selected population. Additionally, it was guaranteed that at least three trees were selected from each locality.

The morphological data from the plus trees were subjected to hierarchical clustering analysis using Minitab software, based on squared Euclidean distance.

Results

Variations in general characteristics of the *Artocarpus hirsutus* Lam. Trees considered for selection

Table 2: Morphological characters of thirty CPTs of *Artocarpus hirsutus* Lam. from different locations.

	Locality	Tree ID	Accession No.	Location	H	GBH	CW	CBH	CB: TH	TS
Low lands (below 20m)	Engandiyoor	EN-16	FCV AH-1	10° 29' 45.36" N 076° 04' 45.36" E	25	1.67	9	7.5	0.296	47
		EN-21	FCV AH-2	10° 29' 44.28" N 076° 04' 46.08" E	30	1.6	8.25	9	0.3	45
		EN-23	FCV AH-3	10° 29' 44.34" N 076° 04' 46.20" E	23	1.38	4.05	10	0.434	48
	Vadanapilly	VA-01	FCV AH-4	10° 27' 45.66" N 076° 04' 7.32" E	21	1.26	6	10	0.476	46
		VA-09	FCV AH-5	10° 29' 43.62" N 076° 04' 3.54" E	23	1.46	9	8	0.347	45
		VA-21	FCV AH-6	10° 29' 55.26" N 076° 04' 8.76" E	18	1.28	7.5	11	0.611	47
	Nayarambalam	NA-13	FCV AH-7	10° 3' 45.18" N 076° 12' 9.18" E	18	1.24	5.5	7	0.388	47
		NA-17	FCV AH-8	10° 3' 36.42" N 076° 12' 57.66" E	20	1.51	5	10	0.5	48
		NA-22	FCV AH-9	10° 3' 4.86" N 076° 12' 36.00" E	18	1.25	8	8	0.444	48
	Ponnani	PO-02	FCV AH-10	10° 46' 1.86" N 075° 56' 12.30" E	16	1.31	8.5	10	0.625	50
		PO-09	FCV AH-11	10° 46' 6.30" N 075° 56' 8.34" E	15	1.6	9	6	0.4	49
		PO-19	FCV AH-12	10° 46' 9.30" N 075° 56' 2.76" E	14	1.16	5	9	0.642	48
		PO-25	FCV AH-13	10° 46' 11.16" N 075° 56' 1.56" E	16	1.39	7	9	0.562	47
	Maranchery	MA-06	FCV AH-14	10° 45' 42.54" N 075° 57' 55.56" E	20	1.68	2.5	12	0.6	44
		MA-15	FCV AH-15	10° 45' 43.68" N 075° 57' 54.48" E	18	1.21	4	7	0.388	42
		MA-22	FCV AH-16	10° 45' 44.58" N 075° 57' 37.56" E	13	1.37	3.5	6	0.461	45
		MA-25	FCV AH-17	10° 45' 36.36" N 075° 57' 59.82" E	20	1.69	5.5	10	0.5	46
Mid lands (20m-100m)	Thrikkoor	TH-01	FCV AH-18	10° 27' 17.64" N 076° 19' 17.46" E	19	1.27	12.5	9	0.473	42
		TH-02	FCV AH-19	10° 27' 16.92" N 076° 19' 17.88" E	23	1.45	6.3	12	0.521	46
		TH-03	FCV AH-20	10° 27' 18.96" N 076° 19' 17.34" E	24	1.61	10.25	9	0.375	47
	Edakkattuvayal	ED-01	FCV AH-21	09° 52' 40.80" N 076° 27' 40.68" E	18	2.21	10.5	9	0.5	45
		ED-10	FCV AH-22	09° 52' 18.78" N 076° 27' 1.50" E	21	1.36	9	7	0.3333	44
		ED-18	FCV AH-23	09° 52' 19.20" N 076° 27' 18.12" E	22	1.46	11	9	0.4091	47
	Pindimana	PI-02	FCV AH-24	10° 8' 9.90" N 076° 39' 26.76" E	20	1.48	7.5	12	0.6	47
		PI-08	FCV AH-25	10° 8' 11.58" N 076° 39' 9.66" E	15	1.18	5.5	10	0.6666	47
		PI-09	FCV AH-26	10° 8' 11.64" N 076° 39' 9.36" E	20	1.36	5	13	0.65	46
		PI-24	FCV AH-27	10° 8' 9.78" N 076° 39' 10.38" E	16	1.28	4	8	0.5	47
	Amarambalam	AM-07	FCV AH-28	11° 15' 54.84" N 076° 18' 31.44" E	13	1.15	5	7	0.538	47
		AM-22	FCV AH-29	11° 13' 41.76" N 076° 16' 27.96" E	20	1.41	5	5	0.25	45
		AM-23	FCV AH-30	11° 13' 54.84" N 076° 16' 27.96" E	22	1.52	4	6	0.272	42
			Mean		19.37	1.43	6.76	8.85	0.469	
			SD		3.8	0.22	2.53	2	0.12	
			CV		19.63	15.22	37.37	22.65	25.39	

H: Height; CW: Crown width; CBH: Clean Bole Height; TS: Total score

Considerable differences in growth characteristics were found among 225 trees enumerated from different locations (Table 1). The trees had average tree height of 16.19 m, mean GBH of 1.17 m and clean bole height of 6.02 m. GBH values ranged from 0.53 m to 2.21m, tree heights from 9 m to 30 m, and clear bole height from 2 m to 13 m. Crown width varied between 2.5 m and 14.5 m.

The variations in the tree height recorded within the location and between the locations is illustrated in Fig. 1. According to the analysis, the boxplot of the trees in the Engandiyoor region was larger, indicating a wider range of values. The trees in Maranchery, on the other hand, showed a narrower boxplot, indicating that the data was not as dispersed. On average, the tallest trees are found

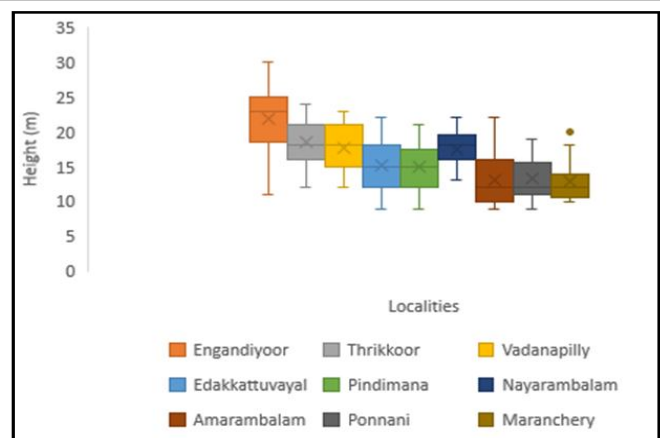


Fig. 1: Box and whisker plot illustrating the variations in the height (m) of *Artocarpus hirsutus* Lam. trees.

Table- 3. Correlation matrix of qualitative characters of CPTs of *Artocarpus hirsutus* Lam.

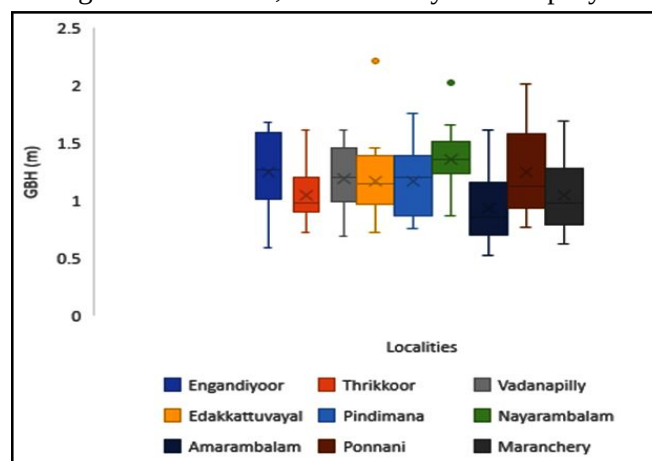
	Height	GBH	CW	CBE
Height	1			
GBH	0.388*	1		
CW	0.275	0.295	1	
CBE	0.193	0.084	-0.014	1

* Correlation is significant at 0.05 level;
CW: Crown width; **CBE:** Clean bole eight

in Engandiyoor (21.88 meters), Thrikkoor (18.48 meters), and Vadanapilly (17.72 meters), while the lowest average height is found in Maranchery (12.92 meters).

Variations in the GBH were observed among the trees within the location and between the locations. Figure.2 as evident from box plot size difference. Nayarambalam stands out with the largest average GBH at 1.42 meters, followed by Edakkattuvayal and Engandiyoor. Meanwhile, Amarambalam (0.94 meters) and Thrikkoor (1.05 meters) display the smallest GBH measurements. Larger GBH could indicate older or more robust trees, while smaller values might point to younger trees or less favorable growing conditions. There were noticeable variations in clean bole height among trees both within the location and between the locations (Fig. 4) which was evident from the size of the box plot. The longest clear trunks are found in Engandiyoor (8.66 meters), Thrikkoor (6.61 meters), and Vadanapilly (6.36 meters), indicating that trees in these places may be competing for light or profiting from certain management practices. Maranchery, with the lowest clear bole height at 3.56 meters, may indicate younger or differently managed trees.

Variations in the crown width were observed among the trees within the location and between the locations (Fig. 3) as evident from box plot size difference. The box plots shows that Thrikkoor (9.488 meters) has the largest average crown width, followed by Vadanapilly and

**Fig. 2:** Box and whisker plot illustrating the variations in the GBH (m) of *Artocarpus hirsutus* Lam. trees.**Table 4:** Clusters of *Artocarpus hirsutus* Lam. based on morphological characters.

Cluster 1	FCVAH-01, FCVAH-05, FCVAH-20, FCVAH-22, FCVAH-23
Cluster 2	FCVAH-03, FCVAH-04, FCVAH-06, FCVAH-08, FCVAH-14, FCVAH-17, FCVAH-19, FCVAH-24, FCVAH-26
Cluster 3	FCVAH-29, FCVAH-30
Cluster 4	FCVAH-02, FCVAH-09, FCVAH-10, FCVAH-11, FCVAH-12, FCVAH-13, FCVAH-15, FCVAH-16, FCVAH-18, FCVAH-21, FCVAH-25, FCVAH-26, FCVAH-28
Cluster 5	FCVAH-02

Engandiyoor. Amarambalam and Maranchery exhibit reduced crown widths, possibly due to competition for resources or less optimal conditions.

The CB:TH provides insights into tree shape and timber potential. While Nayarambalam exhibits lower ratios, indicating trees that may be spread out and have less potential for timber, Engandiyoor consistently displays a higher ratio, indicating longer trunks devoid of branches (Fig. 5).

Plus, tree selection

Thirty candidates plus trees of *Artocarpus hirsutus* Lam. were selected from various locations using a baseline regression system and qualitative trait scoring and assigned accession numbers from FCV-AH-01 to FCV-AH-30 (Table 2). The variation in height, GBH, crown width, and clean bole height among the selected CPTs indicates significant genetic diversity, which is essential for tree improvement programs.

The qualitative traits assessed in the study, such as verticality, straightness, cross-section, forking, foliar and stem damage, branch angle, and self-pruning ability, exhibited minimal variation across trees, suggesting these characteristics are largely genetically determined.

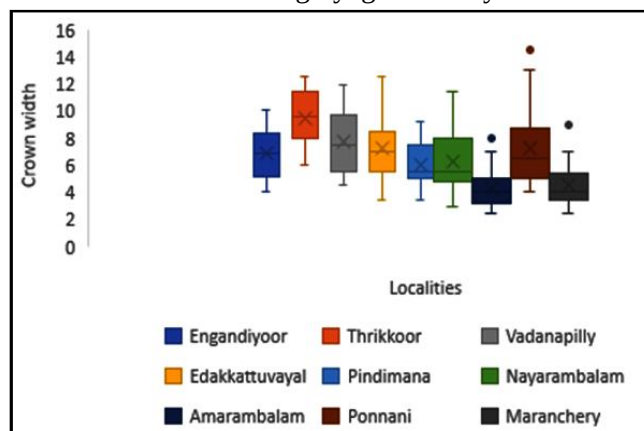
**Fig. 3:** Box and whisker plot illustrating the variations in the crown width (m) of *Artocarpus hirsutus* Lam. trees.

Table 5: Cluster modes of quantitative characters of *Artocarpus hirsutus* Lam.

Variable	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Mean	SD	CV (%)
Height	23	30	20.5556	16.0769	21	19.3667	5.0766	26.21%
GBH	1.512	1.6	1.4544	1.3554	1.465	1.4267	0.0892	6.25%
Crown width	9.65	8.25	5.4833	6.7692	4.5	6.7617	2.0715	30.64%
Clean bole height	8.1	9	11.1111	8.0769	5.5	8.85	2.019	22.81%
CB:TH	0.3522	0.3	0.5437	0.5071	0.2613	0.469	0.1259	26.84%

Important indicators of timber quality included self-pruning ability, cross-section, branch angle, and crown size, with larger, healthier crowns contributing significantly to growth potential. The study prioritized traits such as clean bole height, bole shape, and branching patterns when selecting *Artocarpus hirsutus* Lam.

The height of the selected trees ranged from 13 m (FCV AH-28) to 30 m (FCV AH-2), with an average tree height of 19.6 m and a standard deviation of 3.8. The tallest trees were recorded in Engandiyoor, with several trees exceeding 25 m, while Amarambalam and Maranchery had shorter trees on average. The GBH ranged from 1.15 m (FCV AH-28) to 2.21 m (FCV AH-21), with an average GBH of 1.43 m with a standard deviation of 0.22. Crown width varied from 2.5 m to 12.5 m with an average crown width of 8.85 m. the correlation between the quantitative characters of all the plus trees is given in Table 3. A significant correlation was observed in the height of the tree and girth at breast height at 0.05 level.

Several researchers have applied the baseline method in selecting plus trees of hardwood species and found it to be effective Plus trees of *Casuarina equisetifolia* L. from the eastern coastal plain of Odisha have been selected using the baseline method (Mohapatra, 2024). Binu and Santhoshkumar (2019) used the baseline method to select plus trees of *Melia dubia* from various regions of Kerala. The baseline selection method has also been employed in the selection of plus trees of *Tilia amurensis* (Lee *et al.*, 2023).

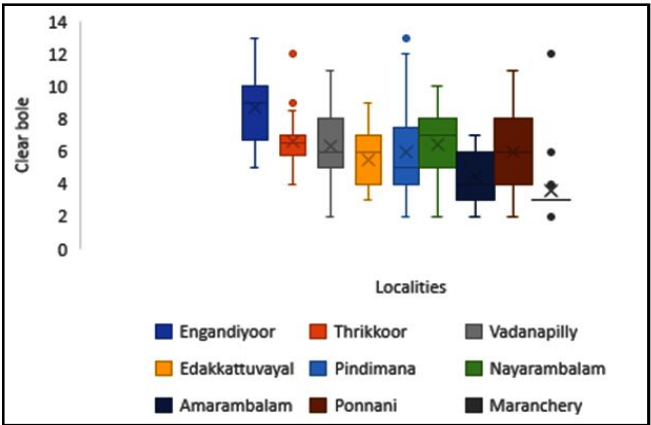


Fig. 4: Box and whisker plot illustrating the variations in the clear bole (m) of *Artocarpus hirsutus* Lam. trees.

The qualitative characteristics scores for the selected plus trees ranged from 50 for several trees, including FCV AH- 4, FCV AH-10, FCV AH-11, FCV AH-12, FCV AH-13, and FCV AH-17. Trees with slightly lower scores, such as FCV AH-15, FCV AH-16, FCV AH-18, FCV AH-22, and FCV AH-21, achieve a total score between 45 and 46.

The qualitative characteristics of the selected plus trees show a range of total scores, reflecting variations in important traits. Several trees, such as FCV AH-10 (50), FCV AH-11 (49), and FCV AH-3, FCV AH-8, and FCV AH-9 (48), achieved the highest total scores. Other trees, such as FCV AH-15 (42), FCV AH-18 (42), and FCV AH-30 (42), scored lower. Overall, the data indicates relatively minor differences in qualitative characteristics, with traits like apical dominance and cross-section showing the most influence on total score variation, which further supports the idea that these traits are genetically determined with minimal environmental influence.

An intensive survey in Haryana, Rajasthan, and Gujarat identified 21 plus trees of *Ailanthus excelsa* Roxb. based on phenotypic traits like stem straightness, self-pruning ability, clear bole height, and disease resistance etc. (Daneva *et al.*, 2018). Other successful selections made based on qualitative traits are in *Melia dubia* (Clark *et al.*, 2018), *Salix alba* (Paray 2017), *Melia dubia* (Binu and Santoshkumar, 2019), *Ailanthus triphysa* (Lalnunpuia *et al.*, 2021), *Azadirachta indica*

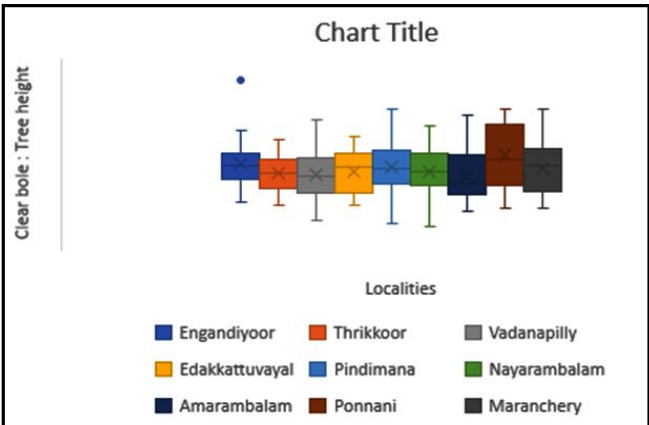


Fig. 5: Box and whisker plot illustrating the variations in the CB:TH (m) of *Artocarpus hirsutus* Lam. trees.

Table 6: Matrix showing inter and intra cluster distance of *Artocarpus hirsutus* Lam. based on quantitative characters.

	Cluster1	Cluster2	Cluster3	Cluster4	Cluster5
C-1	0				
C-2	7.19586	0			
C-3	5.69589	10.0692	0		
C-4	7.50179	14.0357	5.5614	0	
C-5	6.1068	10.3601	5.7209	6.0082	0
C: Cluster					

(Neethu 2023) and *Swietenia macrophylla* (Moor *et al.*, 2021).

Cluster analysis

The selected plus trees were grouped into five clusters using hierarchical cluster analysis (Fig. 6). Cluster IV contained the most CPTs (13), while clusters VI contained only one CPT, potentially representing either superior or inferior quality. The clustering indicated that trees from the same geographic region were distributed across different clusters, suggesting that geographic diversity did not align with genetic diversity. Selection should prioritize genetic diversity, with distant clusters offering potential for hybridization to enhance progeny quality.

In this study, hierarchical cluster analysis was carried out on the morphological characteristics of different tree accessions.

The mean values for these traits across clusters and the inter-cluster distances were analysed to determine the genetic diversity present among the groups. From the inter-cluster distance matrix, it can be seen that the highest genetic distance exists between Cluster 2 and Cluster 4 (14.04), which suggests that these two groups are the most genetically diverse. This large genetic distance makes them ideal candidates for hybridization if the goal is to maximize genetic variation in future generations. On the other hand, the smallest inter-cluster

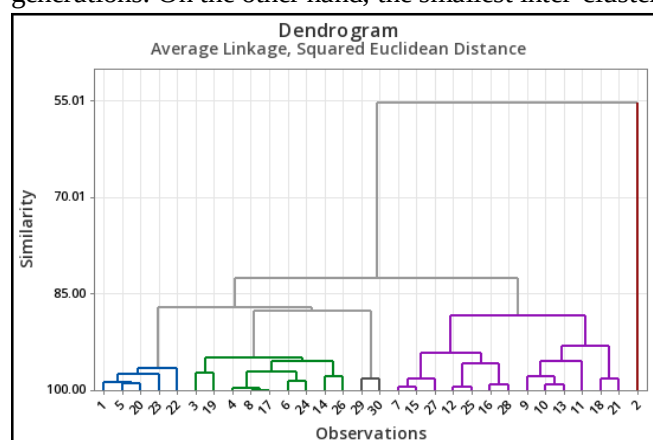
distance is between Cluster 3 and Cluster 4 (5.56), indicating more similarity between these groups. Therefore, hybridization between these two clusters may not offer as much variation.

This study aligns with previous investigations on tree species like *Melia dubia* (Binu and Santhoshkumar 2019), *Ailanthus triphylla* (Lalnunpuia *et al.*, 2021), *Swietenia macrophylla* (Moor *et al.*, 2022). These findings can contribute to the effective management and breeding programs for *Artocarpus hirsutus* Lam., ensuring optimal resource utilization and future improvement. Chauhan

Discussion

The results of this study reveal significant variations in the general characteristics of *Artocarpus hirsutus* Lam. across different geographic locations, underscoring the influence of both genetic and environmental factors on tree growth. The analysis of tree height, GBH, clean bole height, and crown width within and between locations provides valuable insights into the phenotypic diversity of the species. Height variations were significant, with Engandiyoor, Thrikkooor, and Vadanapilly showing the tallest trees on average, while Maranchery had the shortest. The larger range in height values in Engandiyoor suggests a wider genetic diversity in this region. Nayarambalam exhibited the largest average GBH, indicating older or more robust trees, while Amarambalam and Ponnani had smaller GBH values, potentially due to younger trees or less favourable conditions. Clear bole height followed a similar pattern, with Engandiyoor having the longest clean boles and Maranchery the shortest, reflecting differences in light competition or tree management practices. Crown width also varied significantly, with Thrikkooor having the largest average width, suggesting favorable growth conditions, while Amarambalam and Maranchery displayed smaller crown widths, possibly due to competition for resources. The CB:TH ratio in Engandiyoor indicated trees with longer, branch-free trunks, enhancing timber potential, while Nayarambalam had more spread-out trees with a lower CB:TH ratio. These variations indicate that differences in tree size and local environmental conditions are likely shaped by both genetic and micro-environmental factors.

The selection of 30 candidate plus trees based on growth characteristics showed significant genetic diversity across regions. These trees exhibited considerable variation in height, GBH, crown width, and clear bole height, essential traits for tree improvement programs. Qualitative traits such as verticality, straightness, and self-pruning ability showed minimal

**Fig. 6:** Dendrogram on morphological characters of plus trees of *Artocarpus hirsutus* Lam.

variation, suggesting these are largely genetically controlled. The hierarchical cluster analysis grouped the selected CPTs into distinct clusters, highlighting genetic diversity across regions, with significant inter-cluster distances suggesting hybridization potential to enhance progeny quality.

Conclusion

The variations in growth characteristics and the substantial genetic diversity observed among *Artocarpus hirsutus* Lam. trees across different locations underscore the importance of genetic and environmental factors in tree development. These findings provide valuable insights for the selection of plus trees and the implementation of tree improvement programs. By prioritizing genetic diversity and selecting trees with superior phenotypic traits, this study can contribute to the sustainable management and enhancement of *Artocarpus hirsutus* Lam populations, ensuring optimal resource utilization and future forest improvement efforts.

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