

GENETIC VARIABILITY, GROWTH PERFORMANCE AND MULTIVARIATE ANALYSIS OF *PONGAMIA PINNATA* CLONES AT EARLY GROWTH STAGE

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ABSTRACT

Pongamia pinnata is a multipurpose, nitrogen-fixing tree with considerable potential for bioenergy and agroforestry. Identification of genetically superior clones is essential for developing high-yielding genotypes to meet feedstock requirements for biofuel production. The present study was undertaken to assess genetic variability, growth relationships and multivariate diversity among thirty *P. pinnata* clones. The clones were evaluated in a randomized block design with three replications at 4 m × 2 m spacing. Plant height, basal diameter and volume index were recorded at different stages of growth, while genetic parameters, correlation, path analysis, principal component analysis (PCA), cluster analysis and Smith–Hazel selection index were employed using six-month growth data to identify promising clones. Significant clonal variation was observed, with mean plant height, basal diameter and volume index of 87.54 cm, 11.80 mm and 135.37 cm³, respectively. Volume index recorded the highest GCV (53.72%), PCV (61.57%) and genetic advance as per cent of mean (96.68%), along with high heritability of 76.11%, indicating substantial potential for selection. Strong positive association was observed between basal diameter and volume index at both genotypic (0.97) and phenotypic (0.96) levels, while basal diameter showed the highest direct effect on volume index (0.704). PCA revealed that the first principal component explained 90.1% of the total variation. Cluster analysis grouped the clones into four distinct clusters, while the Smith–Hazel selection index identified P08, P11 and P13 as top-performing clones based on six-month growth performance. These clones represent promising early selections that require further evaluation.

KEYWORDS: *Pongamia*; biofuels; genetic evaluation; variability; correlation; clonal evaluation

1. INTRODUCTION

Pongamia pinnata (L.) Pierre, commonly known as karanj, is a multipurpose, nitrogen-fixing tree belonging to the family Fabaceae and is widely distributed in India and other parts of South and Southeast Asia. The species has gained considerable attention because of its non-edible seed oil, adaptability to diverse environments and potential for biofuel production, besides its importance in agroforestry, soil improvement, carbon sequestration and land rehabilitation. Its ability to grow under relatively low-input conditions makes it a promising tree for sustainable biofuel and bioenergy production. In India, *P. pinnata* has been recognized as an important candidate species for biodiesel production, increasing the need for genetically superior planting material. Considerable variation in seed and oil production has been reported among pongamia trees, indicating the influence of genetic and environmental factors on productivity and the importance of selecting superior genetic material (Sunil et al., 2009; Ahlawat et al., 2014; Dalemans et al., 2022).

Genetic variability is the fundamental requirement for genetic improvement because the magnitude and nature of variation determine the effectiveness of selection. Studies on *P. pinnata* have demonstrated substantial variation in seed, seedling and morphological traits. Palanikumar et al. (2016) reported significant variability for seed and seedling characteristics among *P. pinnata* sources evaluated under Tamil Nadu conditions, while Garg and Kaushik (2021) observed considerable genetic variation, heritability and genetic gain for morphological traits among *P. pinnata* progenies. Patil and Naik (2016) reported substantial variability among candidate-plus trees of *P. pinnata* for pod, seed and progeny growth traits, with high heritability and genetic advance for several important traits, highlighting the potential for selection. Such findings indicate that systematic evaluation of genetically diverse material can help identify promising sources for further improvement. However, seed- or progeny-based evaluation may not provide the same level of uniformity as vegetatively propagated material. Clonal selection

therefore offers an effective approach for capturing and multiplying superior genotypes while maintaining their desirable characteristics.

The usefulness of clonal evaluation has been demonstrated in several important tree species. Studies in *Eucalyptus tereticornis* have reported significant differences among clones for growth characteristics, demonstrating the potential for identifying superior clones at relatively early stages (Kumar et al., 2010; Vennila et al., 2017; Kumar et al., 2020; Sahoo et al., 2021). Similarly, considerable genetic variation for growth and wood traits has been observed among *Casuarina* clones, supporting their use in genetic improvement and plantation forestry (Garg et al., 2023; Kirandeep et al., 2024). Studies in *Dalbergia sissoo*, *Salix* and *Populus* have further demonstrated the usefulness of clonal evaluation for characterizing growth variation, genetic divergence and identifying superior planting material (Kumar et al., 2011; Palial and Thakur, 2021; Jin et al., 2019). In *Neolamarckia cadamba*, evaluation of clones revealed substantial genetic variability for growth traits, while correlation and path analysis helped identify important characters associated with volume production (Selvan and Parthiban, 2020). These studies indicate that evaluation based on multiple growth attributes can provide a more reliable basis for tree improvement than selection based on a single character.

For effective selection among clones, estimation of genotypic and phenotypic variability, heritability and genetic advance provides information on the potential response to selection. Correlation and path analysis help identify relationships among growth traits and determine the relative contribution of individual characters to productivity. Multivariate approaches such as principal component analysis and cluster analysis further facilitate characterization of genetic diversity and identification of distinct groups, while selection indices allow simultaneous consideration of several economically important traits. Recent studies in *Casuarina* and *Gmelina arborea* have demonstrated the value of integrating genetic parameters, multivariate analyses and selection criteria for identifying promising genotypes for tree improvement program (Nayak et al., 2025; Singh, 2026). Although considerable information is available on seed, oil and progeny variation in *P. pinnata*, comparatively limited information is available on the integrated evaluation of clones using growth variation, genetic parameters, trait relationships, multivariate diversity and composite selection.

Therefore, the present study was undertaken to assess genetic variability among *P. pinnata* clones, determine relationships among important growth attributes, characterize clonal diversity through multivariate approaches and identify superior clones using a composite selection index. The study aims to provide a scientific basis for identifying promising *P. pinnata* clones for further evaluation and genetic improvement.

2. METHODS

2.1 Experimental material

The study was conducted at the Forest College and Research Institute, Tamil Nadu Agricultural University, Mettupalayam (11°19' N, 76°56' E; 300 m above mean sea level) during 2023–2025. Initially, sixty-two genetic resources were identified based on morphological characteristics and pod yield from different pongamia-growing regions of Tamil Nadu through field surveys, following the subjective grading approach for selection of candidate plus trees (Zobel and Talbert, 1984). The selected trees were further screened for yield and oil content, and thirty high-ranked superior genetic resources were identified, vegetatively multiplied through cleft grafting and designated as clones.

2.2 Clonal evaluation

The clonal test was established in a randomized block design with three replications at 4 m × 2 m spacing. Observations were recorded at different growth stages and growth data at six months after planting (MAP) were analysed. Plant height was measured from above the graft union to the shoot tip and expressed in cm, while basal diameter was measured immediately above the graft union and expressed in mm. Volume index was calculated as the product of basal diameter squared and plant height after expressing basal diameter in centimetres (Hatchell, 1985; Manavalan, 1990).

2.3 Genetic and statistical analyses

Analysis of variance was performed to determine the significance of differences among clones. Genotypic and phenotypic variances were estimated as per the method described by Johnson et al. (1955). Genotypic and phenotypic coefficients of variation (GCV and PCV) were calculated following Burton (1952). Heritability was estimated as the ratio of genotypic to phenotypic variance (Lush, 1940), while genetic advance and genetic advance as percentage of mean were estimated following Johnson et al. (1955). Path co-efficient analysis was carried out as suggested by Dewey and Lu (1959) to study the genotypic correlation coefficients in to direct and indirect effects.

Genetic divergence among clones was assessed using Mahalanobis' D² statistics (Mahalanobis, 1936). For the present analysis, standardized clone means for basal diameter, plant height and volume index were used to calculate Euclidean distances, and hierarchical clustering was performed using Ward's minimum-variance method to group the thirty clones. Principal component analysis (PCA) was performed on standardized trait values to identify the major components contributing to total variation. A Smith–Hazel selection index (Smith, 1936) was used to combine information from the growth traits and identify superior clones based on their overall performance. The statistical analyses and graphical representations were performed using R software version 4.4.1.

3. RESULTS

Significant clonal variation was observed for growth traits at six months after planting, with mean plant height, basal diameter and volume index of 87.54 cm, 11.80 mm and 135.37 cm³, respectively. For plant height, TNPP 08 recorded the maximum value (122.50 cm), followed by TNPP 11 (116.17 cm) and TNPP 13 (111.83 cm). Basal diameter was highest in TNPP 25 (16.42 mm), followed by TNPP 13 (16.04 mm) and TNPP 11 (15.77 mm). Volume index ranged widely, with TNPP 11 recording the highest value (293.53 cm³), followed by TNPP 13 (288.92 cm³) and TNPP 08 (285.29 cm³). The clones TNPP 08, TNPP 11, TNPP 13, TNPP 25 and TNPP 35 recorded higher values for basal diameter and volume index. Among these, TNPP 08, TNPP 11 and TNPP 13 showed particularly high and consistent performance across all three growth attributes (Fig 1 & 2; Table 1).

Fig 1. Reproductive structures of *P. pinnata*



Fig 2. Performance of *P. pinnata* clones at 6 MAP

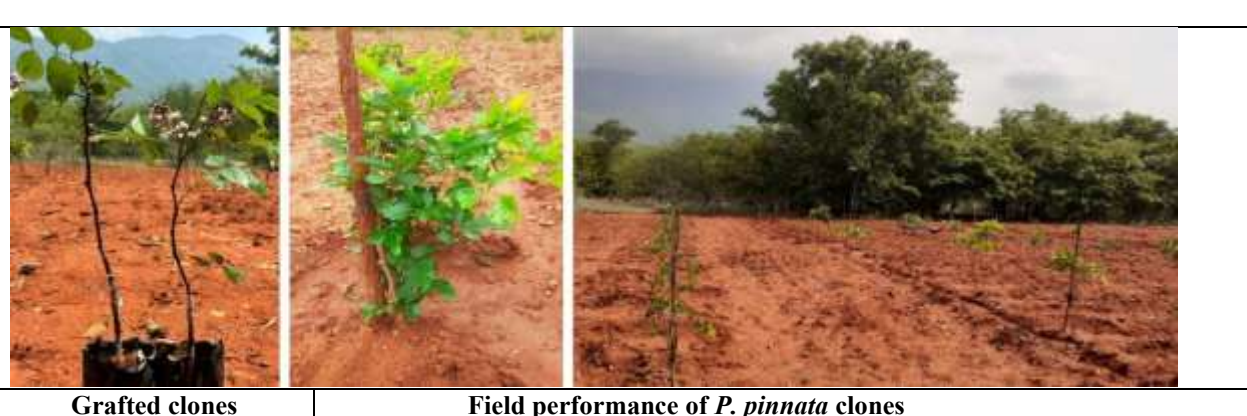


Table 1. Clonal variation for growth in *P. pinnata* clones at 6 months after planting

Sl. No.	Name of the Clone	Plant height (cm)	Basal diameter (mm)	Volume Index
1	TNPP 01	87.50	13.26	154.40
2	TNPP 05	95.67*	12.92	161.65
3	TNPP 07	101.25*	13.64	188.89
4	TNPP 08	122.50*	15.20*	285.29*
5	TNPP 11	116.17*	15.77*	293.53*
6	TNPP 12	112.64*	12.52	179.72
7	TNPP 13	111.83*	16.04*	288.92*
8	TNPP 15	98.67*	13.32	178.84
9	TNPP 18	110.33*	12.31	170.31
10	TNPP 20	67.83	9.66	65.23
11	TNPP 21	93.33*	13.46	169.03
12	TNPP 24	80.17	11.40	104.12
13	TNPP 25	98.50*	16.42*	268.61*
14	TNPP 26	74.75	11.51	100.08
15	TNPP 27	97.00*	8.51	70.77
16	TNPP 30	82.17	11.69	113.02

17	TNPP 31	73.00	9.87	75.88
18	TNPP 35	97.67*	15.10*	224.98*
19	TNPP 37	62.17	10.10	64.03
20	TNPP 39	67.20	9.21	57.33
21	TNPP 40	84.83	10.21	88.54
22	TNPP 43	90.00	11.75	124.99
23	TNPP 46	69.00	10.86	81.72
24	TNPP 47	95.00*	12.49	156.23
25	TNPP 48	67.33	8.61	50.23
26	TNPP 52	72.00	10.13	73.86
27	TNPP 54	62.31	10.35	67.60
28	TNPP 55	75.00	10.59	84.83
29	TNPP 56	63.67	8.29	43.80
30	TNPP 61	96.77*	8.78	74.65
Mean		87.54	11.8	135.37
	SEd	2.11	1.29	33.26
	CD (0.05)	4.24	2.59	66.76

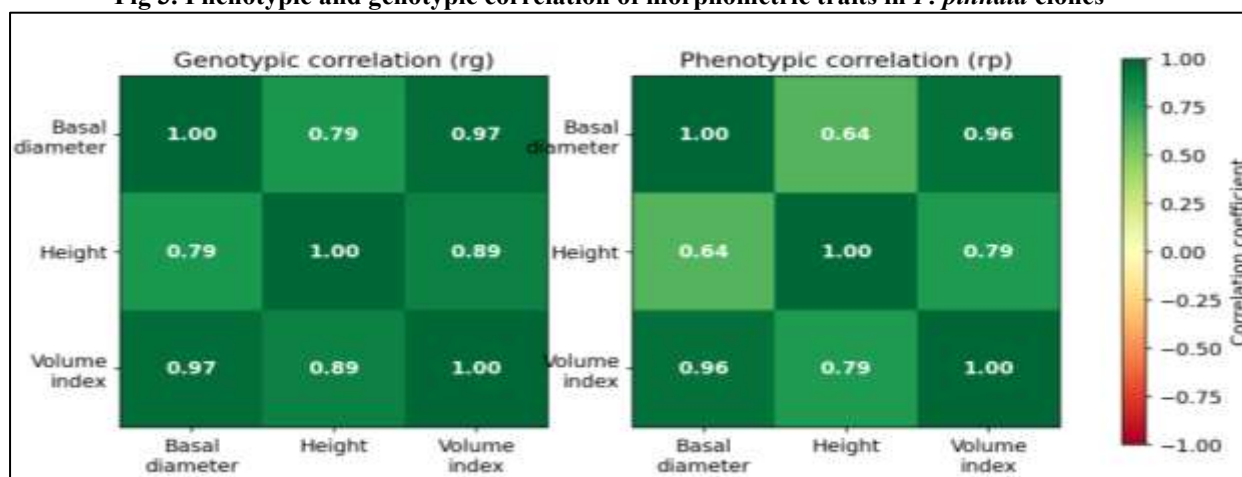
* Significance at 5 % level

The genetic estimates revealed considerable variability among the morphometric traits, with volume index recording the highest GCV (53.72%) and PCV (61.57%). Heritability was highest for plant height (97.85%), followed by volume index (76.11%) and basal diameter (65.36%). Genetic advance as per cent of mean was highest for volume index (96.68%), while plant height recorded 40.74% and basal diameter recorded 30.70% (Table 2). Genotypic correlations were generally stronger than the corresponding phenotypic correlations among the morphometric traits. Basal diameter showed a strong positive correlation with volume index at both genotypic (0.97) and phenotypic (0.96) levels. Plant height was positively correlated with volume index (0.89 genotypically and 0.79 phenotypically), while its association with basal diameter was comparatively lower (0.79 and 0.64, respectively). Overall, all three morphometric traits exhibited positive associations at both levels (Fig 3).

Table 2. Genetic estimates of morphometric traits

Trait	GCV (%)	PCV (%)	Heritability h ² (%)	GA as % of Mean (GAM)
Basal diameter (mm)	18.41	22.77	65.36	30.70
Height (cm)	19.96	20.18	97.85	40.74
Volume index (cm ³)	53.72	61.57	76.11	96.68

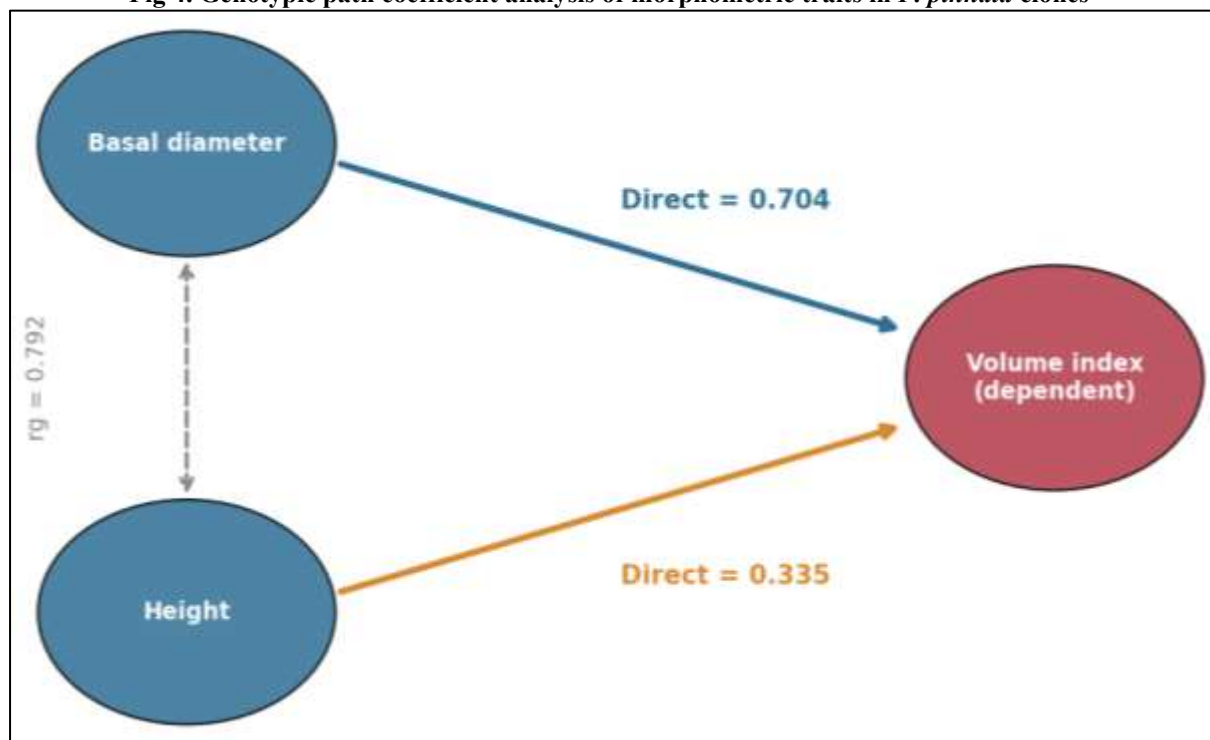
Fig 3. Phenotypic and genotypic correlation of morphometric traits in *P. pinnata* clones



Path coefficient analysis revealed that basal diameter exerted a higher direct effect (0.704) on volume index than plant height (0.335). The genotypic association between basal diameter and plant height was positive and relatively strong ($r_g = 0.792$). The results indicated that basal diameter had a greater direct contribution towards

volume index than plant height. The residual effect of the genotypic path analysis was low (0.1373), indicating that basal diameter and plant height together accounted for a major proportion of the variation in volume index. Overall, both traits showed positive direct effects on volume index (Fig 4).

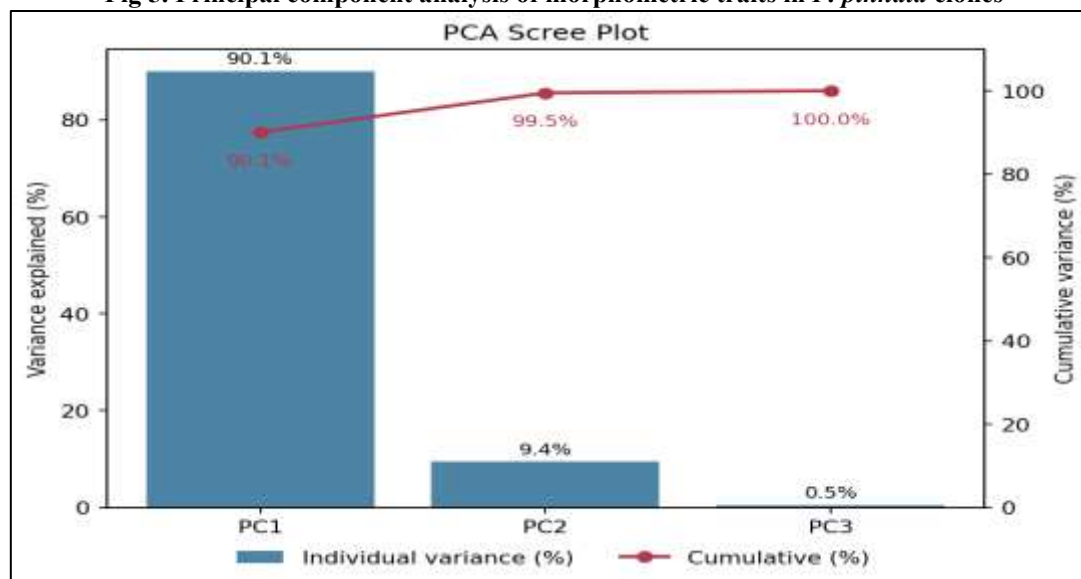
Fig 4. Genotypic path coefficient analysis of morphometric traits in *P. pinnata* clones



* Residual effect: 0.1373

Principal component analysis showed that PC1 explained 90.1% of the total variation and was strongly associated with basal diameter, plant height and volume index, with loadings of -0.578 , -0.550 and -0.603 , respectively. PC2 accounted for 9.43% of the variation, with a relatively stronger contribution from plant height (-0.800), followed by basal diameter (0.573). PC3 contributed only 0.50%, being mainly associated with volume index (0.777) and basal diameter (-0.582). Thus, PC1 primarily represented overall growth variation, while PC2 and PC3 accounted for smaller, trait-specific components of variation (Fig 5).

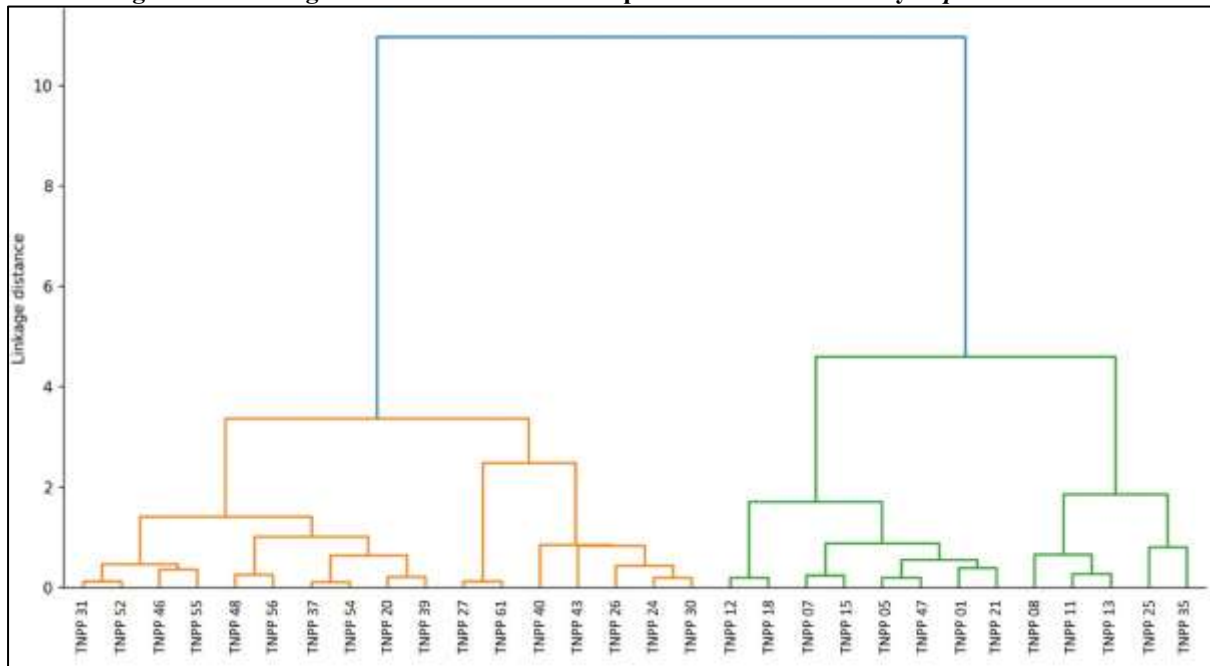
Fig 5. Principal component analysis of morphometric traits in *P. pinnata* clones



The cluster diagram constructed from the morphometric traits grouped the thirty *P. pinnata* clones into four distinct clusters, indicating considerable variability among the clones. Cluster II comprised five clones and showed comparatively higher morphometric values, whereas Cluster III consisted of eight clones with relatively lower values. The dendrogram clearly depicted the separation and relatedness among the clones based on the combined variation in basal diameter, plant height and volume index (Table 3; Fig 6).

Table 3. Clustering pattern of *P. pinnata* clones

Cluster	No. of clones	Members
Cluster 1	10	TNPP 20, TNPP 31, TNPP 37, TNPP 39, TNPP 46, TNPP 48, TNPP 52, TNPP 54, TNPP 55, TNPP 56
Cluster 2	7	TNPP 24, TNPP 26, TNPP 27, TNPP 30, TNPP 40, TNPP 43, TNPP 61
Cluster 3	8	TNPP 01, TNPP 05, TNPP 07, TNPP 12, TNPP 15, TNPP 18, TNPP 21, TNPP 47
Cluster 4	5	TNPP 08, TNPP 11, TNPP 13, TNPP 25, TNPP 35

Fig 6. Cluster diagram constructed from morphometric traits of thirty *P. pinnata* clones

Cluster-wise means revealed distinct variation among the morphometric traits, with Cluster IV recording the highest mean basal diameter (15.71 mm), plant height (109.33 cm) and volume index (272.27 cm³), indicating its superior early growth performance (Table 4). Cluster I recorded the lowest mean values for all the traits, whereas Clusters II and III showed intermediate performance. The grouping of clones with relatively higher growth values in Cluster IV further supports the presence of substantial multivariate variation among the evaluated clones.

Table 4. Cluster mean values for morphometric attributes

Cluster / character	Basal diameter	Plant height	Volume index
I	9.77	67.95	66.45
II	10.55	86.53	96.60
III	12.99	99.30	169.88
IV	15.71	109.33	272.27

The clustering pattern revealed substantial divergence among the groups, with Cluster I and Cluster IV being the most divergent, while Cluster III and Cluster IV showed comparatively lower genetic divergence. Within-cluster variability was comparatively lower in Cluster I, whereas Cluster IV exhibited greater internal variability. Overall, the clustering indicated considerable genetic diversity among the thirty clones based on the morphometric traits (Table 5).

Table 5. Inter- and intra-cluster D^2 and D values among thirty *P. pinnata* clones

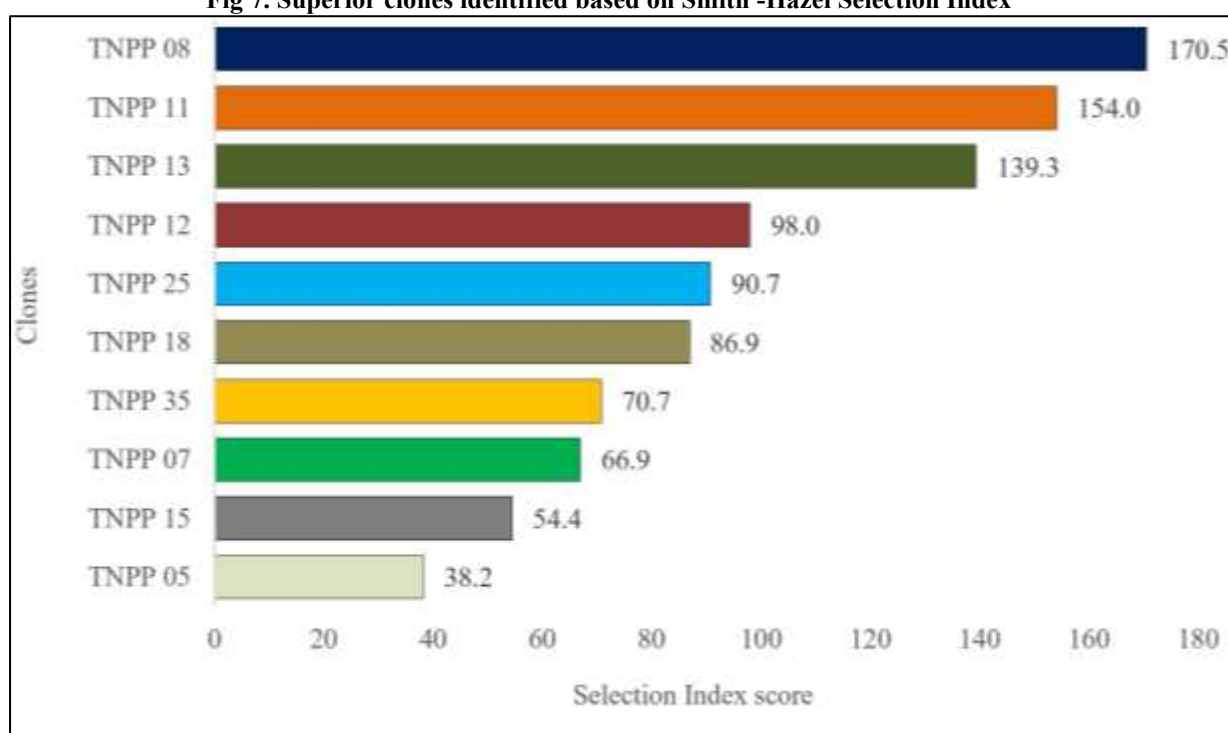
Cluster	I	II	III	IV
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I	8.24 (2.87)	70.05 (8.37)	168.43 (12.98)	278.65 (16.69)
II		24.73 (4.97)	46.37 (6.81)	108.38 (10.41)
III			22.82 (4.78)	44.03 (6.64)
IV				37.61 (6.13)

Note: Values outside parentheses represent D² (Mahalanobis squared distance), whereas values in parentheses represent D (Mahalanobis distance).

Among the thirty *P. pinnata* clones, the Smith–Hazel selection index identified the top 10 superior clones, with P08 recording the highest selection index score (170.5), followed by P11 (154.0) and P13 (139.3). The selection index scores of the top 10 clones ranged from 38.2 (P05) to 170.5 (P08), with P12, P25 and P18 occupying the subsequent ranks (Fig 7).

Fig 7. Superior clones identified based on Smith -Hazel Selection Index



4. DISCUSSION

The present study revealed substantial clonal variation in *Pongamia pinnata* for plant height, basal diameter and volume index at six months after planting, indicating considerable scope for early selection of superior clones. Similar variation in seedling and growth traits has been reported in *P. pinnata* genetic resources and progenies in India, where significant differences and considerable genetic variation were observed among seed sources and progenies (Palanikumar et al., 2016; Garg and Kaushik, 2021). The highest GCV (53.72%), PCV (61.57%) and genetic advance as per cent of mean (96.68%) recorded for volume index, together with high heritability of 76.11%, indicate substantial exploitable genetic variation for this composite growth trait. Comparable results have been reported in *Neolamarckia cadamba* clones, where volume exhibited high genetic variability and genetic gain (Selvan and Parthiban, 2020), and in *Santalum album* progenies, where considerable variation was observed for growth attributes (Krishnakumar et al., 2017). Clonal evaluation studies in *Eucalyptus tereticornis* have also demonstrated significant differences among clones for height, diameter and other growth attributes, with high heritability and genetic advance for important growth traits (Kumar et al., 2010; Kumar et al., 2020; Sahoo et al., 2021). Similarly, substantial genetic variation and heritable variation for growth and biomass-related traits have been reported in *Casuarina* clones (Garg et al., 2023; Garg et al., 2024). The stronger genotypic than phenotypic associations observed among the present growth traits suggest that the relationships were substantially influenced by genetic factors. In particular, the strong genotypic correlation of basal diameter with volume index (0.97) and its higher direct effect on volume index (0.704) indicate that basal diameter may serve as an important early selection criterion for overall growth. Similar positive relationships among diameter, height and volume and the usefulness of correlation and path analysis for identifying selection criteria, have been reported in *P. pinnata*, *N. cadamba* and *Toona ciliata* (Garg and Kaushik, 2021; Selvan and Parthiban, 2020; Parthiban et al., 2018). These findings are further supported by studies in *Casuarina* clones, where significant variation in growth traits, genetic

parameters, correlations and path coefficients demonstrated the potential of clonal material for genetic improvement (Garg et al., 2023; Garg et al., 2024).

The multivariate analyses further confirmed the existence of structured variation among the clones and supported the use of multiple traits for selection. PCA showed that PC1 accounted for 90.1% of the total variation and was associated with basal diameter, plant height and volume index, indicating that the major component of variation represented overall growth performance. Similar use of PCA and multivariate approaches has been reported for characterizing variation among *Salix* clones and other tree genetic resources (Palial and Thakur, 2021). The clustering analysis separated the thirty clones into four groups, with Cluster IV showing the highest mean values for the three morphometric traits, whereas Cluster I recorded the lowest values. The considerable inter-cluster divergence observed among the groups indicates the presence of distinct groups that can be useful for further selection and breeding. Comparable divergence among tree clones has been reported in *Dalbergia sissoo* and *Eucalyptus tereticornis*, where D² analysis successfully differentiated clones into distinct groups and helped identify superior and divergent clones (Kumar et al., 2011; Sahoo et al., 2021). Importantly, the Smith–Hazel selection index integrated the performance of the different growth attributes and identified P08, P11 and P13 as top-performing clone. The occurrence of these superior clones together in Cluster IV provided further agreement between individual performance, multivariate grouping and multi-trait selection. Such an approach is particularly useful in tree improvement because selection based on a combination of correlated traits can provide a more reliable basis for identifying promising clones than selection for a single trait. In *Populus ussuriensis*, multi-trait selection index analysis similarly enabled the identification of superior clones with improved diameter and volume performance (Jin et al., 2019). Recent studies in *Casuarina* have also demonstrated substantial clonal variation and the value of genetic parameters, association analysis and selection criteria for identifying promising clones under Indian conditions (Nayak et al., 2025; Kirandeep et al., 2024). Thus, the combined evidence from genetic variability, correlation, path analysis, PCA, cluster analysis and Smith–Hazel selection provides a comprehensive basis for identifying promising *P. pinnata* clones for subsequent evaluation.

5. CONCLUSION

The study revealed substantial genetic variability among the thirty *Pongamia pinnata* clones for growth traits, with volume index showing high genetic variability, heritability and genetic advance. Strong positive associations and the higher direct effect of basal diameter on volume index highlighted its importance as an early selection criterion. PCA and cluster analysis further demonstrated considerable diversity among the clones. Based on six-month growth performance, the Smith–Hazel selection index identified P08, P11 and P13 as promising early selections that require further evaluation.

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Conflict of interests

The authors declare no conflict of interest.

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