Online ISSN 2456-6489

Research Article

Indian Journal of Agroforestry
Vol. 27, No. 2, April–June 2025

Variability, Association and Principal Component Analysis in Gmelina Arborea

K.T. Parthiban*, N. Krishnakumar, S. Revathi, V. Subbulakshmi and R. Ashick Rajah

[1]*Professor (Forestry), Forest College and Research Institute, Tamil Nadu Agricultural University, Mettupalayam – 641301, Tamil Nadu*
[2]*Forest Range Officer (T), Kanniyakumari Forest Division, Tamil Nadu Forest Department, Nagercoil – 629001, Tamil Nadu*
[3]*Senior Research Fellow, Forest College and Research Institute, Tamil Nadu Agricultural University, Mettupalayam – 641301, Tamil Nadu*
[4]*Scientist (Agroforestry), ICAR-Central Arid Zone Research Institute, RRS, Bikaner – 334 004, Rajasthan*
[5]*Doctoral Research Scholar, Forest College and Research Institute, Tamil Nadu Agricultural University, Mettupalayam – 641301, Tamil Nadu*

* Corresponding author. E-mail: ktparthi2001@gmail.com
https://doi.org/10.48165/ija.2025.27.02.10

ARTICLE INFO
Received: 02.08.2024
Accepted: 02.06.2025

Keywords:
Gmelina arborea
Variability
Heritability
Association studies
Principal Component Analysis

ABSTRACT

%%TABLE%%

ABSTRACT: *Gmelina arborea is commonly known as gamhar belongs to the family lamiaceae is one of the important multipurpose and fast growing tree species highly amenable for multifarious industrial utility. However, this species received little research attention and hence a systematic tree improvement programme has been started with collection of 32 superior progenies from its natural and introduced ranges distributed in three southern states of India. The progeny evaluation test indicated that all progenies exhibited significant variation for height, clean bole height, girth at breast height, basal girth, volume and clean bole volume. Among 32 progenies evaluated, the superiority of progeny viz., FCRI GA 08 and FCRI GA 09 is very well witnessed due to higher growth attributes. The genetic analysis indicated that, phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all the six traits. High heritability with high genetic advance was observed for tree height and Girth at breast height. Basal girth showed positive correlation and direct effect on clean bole volume. The genetic diversity analysis resolved 32 progenies into six clusters and cluster I was largest with 17 progenies. Highest cluster mean for tree height, basal girth and volume was exhibited by cluster V and cluster VI for clean bole height, girth at breast height and clean bole volume. Maximum divergence was contributed by girth at breast height and clean bole volume. Six principal components were grouped in PCA in which PC 1 and PC 2 contributed 86.72% of total variability. In a holistic perspective, the study identified superiority of two progenies viz FCRI GA 08 and FCRI GA 09 for immediate adoption and revealed the existence of wide range of genetic diversity thus extends greater scope for future breeding programme in Gmelina arborea.*

%%ENDTABLE%%

INTRODUCTION

Gmelina arborea is a fast growing deciduous tree locally known as gamhar, occurring naturally throughout greater part of India at altitudes up to 1,500 meters belongs to the family Verbanaceae. This species is propagated through seeds. *Gmelina* is known for its reasonably strong for its timber weight and is used in constructions, furniture, carriages pulpwood and musical instruments. It acts as a good substitute for high value white teak. Parthiban *et.al (2019)* reported *G. arborea* to be extremely site sensitive, yet it is capable of surviving as a stunted bushy tree in adverse conditions. The foliage of *Gmelina* was consumed by cattles and rabbits. Such a multi-utility tree species received little research attention. The agroforestry promotional activities in

India is concentrated in promoting species with multifarious industrial utility and also evolving superior genetic stocks for deployment in agroforestry promotion (Parthiban *et.al.,* 2019) The National Agroforestry Policy (2014) suggested to prioritise 20 species in each state which predominately included *Gmelina arborea.* However for want of improved superior genetic resources, incorporation of *G. arborea* in agroforestry promotion is dismally modest. Under such circumstances, the current study is planned to evolve superior genetic stocks through selection followed by systematic progeny test in order to assess the variability and identify improved genotypes. It is very essential to estimate the phenotypic and genotypic coefficients of variations for different characters of economic importance. It is an important index ofcharacters transmission from parents to offspring. Among the multivariate techniques, principal component analysis (PCA) and cluster analysis has been shown to be very useful in selecting genotypes for breeding program that meet the objective of a plant breeder (Mohammadi and Prasanna, 2003). However such systematic progeny evaluation coupled with determination of genetic estimates and diversity are not available in this species. Against this backdrop, the current study was carried out to estimate the genetic parameters, correlation, path analysis, divergence analysis and principal component analysis for the identified 32 *Gmelina arborea* progenies.

2. MATERIALS AND METHODS

2.1. Experimental materials

Thirty two progenies of *Gmelina arborea* were collected from different places in Tamil Nadu, Pondicherry, Kerala and Karnataka. The seedlings were raised and systematic progeny test was carried out during the period between 2016 and 2022. The parental pedigree of the identified progenies are furnished in Table 1. These progenies were evaluated through progeny test in a Row Column Design with a spacing of 2 m x 2 m with three replications for the assessment of analysis of variance as suggested by Panse and Sukhatme (1967). The progenies were

assessed periodically for various growth attributes such as tree height, clean bole height, girth at breast height, basal girth, volume and clean bole volume.

2.2. Statistical analysis

The data gathered from the evaluation were analyzed using AGRES software and tabulated. Estimates of mean, variance and standard error were worked out as per the procedure described by Panse and Sukhatme (1978).The significance test was carried out by referring to the standard 'F' table of Snedecor (1961). The observations recorded at 5 years after planting were subjected to variability (Burton and Devane, 1953), heritability (Lush, 1940) and association studies (Goulden, 1952). The Principal Components Analysis (PCA) was carried out to establish the numbers of clusters using Statistical Package for Social Studies (SPSS) version 16.0.1 software in order to identify the patterns of variation (PCA).

3. RESULTS

3.1. Growth performance

The progenies of *Gmelina arborea* were collected from different ecological sources in India and the growth performance was estimated. The progenies of *Gmelina arborea* differed significantly for various growth attributes like height, clean bole height, girth at breast height, basal girth, volume and clean bole volume and the results are furnished in table 2. Among the progenies evaluated, the highest mean height was exhibited by FCRI GA 18 (13.33 m) and lowest was exhibited by FCRI GA 27 (5.90 m). Five progenies *viz*., FCRI GA 18 (13.33 m), FCRI GA 09 (10.94 m), FCRI GA 31 (10.83 m), FCRI GA 29 (10.50 m) and FCRI GA

08 (10.13 m) showed significant and higher tree height. With respect to clean bole height, two progenies FCRI GA 25 (5.09 m) and FCRI GA 26 (4.89 m) registered superior clean bole height compared to the average clean bole height (4.16 m). The girth at breast height and basal girth showed non-significant observations. The girth at breast height ranged from 29.61 cm (FCRI GA

22) to 40.33 cm (FCRI GA 14) and the basal girth ranged between 39.89 cm (FCRI GA 22) and 54.78 cm (FCRI GA 14). Compared to the population mean volume (0.0551 m3), six progenies viz., FCRI GA 08 (0.0886 m3), FCRI GA 09 (0.0823 m3), FCRI GA 24 (0.0704 m3), FCRI GA 18 (0.0748 m3), FCRI GA 13 (0.0727 m3) and FCRI GA 14 (0.0744 m3) exhibited significantly higher volume. However, among these top six significant progenies, the superiority of two progenies *viz*., FCRIGA 08 and FCRIGA 09 was very well witnessed. Though the clean bole volume registered non- significant observations, the two progenies namely FCRI GA 08(0.0342 m3 and FCRI GA 09 (0.0308 m3) registered maximum values.

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Table 1

S.No.	Location	State	Latitude	Longitude	Altitude (m)	Assigned Number
1.	Coimbatore	Tamil Nadu	11°01'00" N	76°56'43" E	437	FCRI GA 01
2.	Karamadai	Tamil Nadu	11°14'11" N	76°57'24" E	379	FCRI GA 02
3.	FC & RI	Tamil Nadu	11°19'23" N	76°56'06" E	313	FCRI GA 03
4.	Mettupalayam I	Tamil Nadu	11°19'08" N	76°56'56" E	314	FCRI GA 04
5.	Mettupalayam II	Tamil Nadu	11°19'25" N	76°54'54" E	331	FCRI GA 05
6.	Sirumugai	Tamil Nadu	11°19'21" N	77°00'10" E	283	FCRI GA 06
7.	Gobichettipalayam	Tamil Nadu	11°27'47" N	77°27'20" E	221	FCRI GA 07
8.	Kurumanthur I	Tamil Nadu	11°27'28" N	77°20'57" E	228	FCRI GA 08
9.	Kurumanthur II	Tamil Nadu	11°27'28" N	77°20'57" E	228	FCRI GA 09
10.	Sathyamangalam	Tamil Nadu	11°35'04" N	77°11'29" E	354	FCRI GA 10
11.	Perundurai	Tamil Nadu	11°22'02" N	77°47'11" E	193	FCRI GA 11
12.	SPB, Erode	Tamil Nadu	11°13'28" N	78°16'46" E	233	FCRI GA 12
13.	Namakkal	Tamil Nadu	11°16'51" N	77°33'49" E	301	FCRI GA 13
14.	Karur	Tamil Nadu	11°02'47" N	77°59'34" E	156	FCRI GA 14
15.	Manaparai	Tamil Nadu	10°41'18" N	78°23'10" E	283	FCRI GA 15
16.	Thuraiyur	Tamil Nadu	11°08'42" N	78°37'49" E	333	FCRI GA 16
17.	Trichy	Tamil Nadu	10°50'45" N	78°36'54" E	176	FCRI GA 17
18.	Dindigul	Tamil Nadu	10°21'51" N	77°57'09" E	263	FCRI GA 18
19.	Neduvasal	Tamil Nadu	10°21'28" N	79°07'53" E	45	FCRI GA 19
20.	Pattukottai	Tamil Nadu	10°29'23" N	79°17'46" E	30	FCRI GA 20
21.	Attur, Salem	Tamil Nadu	11°36'14" N	78°35'38" E	221	FCRI GA 21
22.	Kanchipuram	Tamil Nadu	12°50'57" N	79°39'57" E	87	FCRI GA 22
23.	Hosur	Tamil Nadu	12°42'26" N	77°51'40" E	830	FCRI GA 23
24.	Krishnagiri	Tamil Nadu	12°23'35" N	78°13'10" E	461	FCRI GA 24
25.	Dharmapuri	Tamil Nadu	12°08'41" N	78°09'44" E	451	FCRI GA 25
26.	Cuddalore	Tamil Nadu	11°39'14" N	79°43'30" E	21	FCRI GA 26
27.	Pondicherry	Tamil Nadu	12°00'01" N	79°42'35" E	26	FCRI GA 27
28.	Adimali	Kerala	10°02'03" N	77°02'59" E	977	FCRI GA 28
29.	Kallar	Kerala	10°01'56" N	76°58'55" E	993	FCRI GA 29
30.	Thrissur	Kerala	10°32'58" N	76°16'30 " E	41	FCRI GA 30
31.	Palakad	Kerala	10°44'51" N	76°37'50" E	86	FCRI GA 31
32.	Bangalore	Karnataka	13°00'42" N	77°34'16" E	942	FCRI GA 32

DOI: https://doi.org/10.48165/ija.2025.27.02.10

Table 2: Biometric attributes of *Gmelina arborea* genetic resources

S.No.	Progeny	Tree Height (m)	Clean bole height (m)	Girth at Breast Height (cm)	Basal Girth (cm)	Volume (m3)	Clean Bole Volume (m3)
1.	FCRI GA 01	6.06	4.74	34.44	47.44	0.0407	0.0315
2.	FCRI GA 02	6.24	3.84	35.67	49.22	0.0447	0.0272
3.	FCRI GA 03	6.98	4.50	36.00	48.33	0.0512	0.0330
4.	FCRI GA 04	6.94	4.33	38.44	55.33	0.0574	0.0360
5.	FCRI GA 05	7.04	4.37	37.56	51.22	0.0557	0.0342
6.	FCRI GA 06	6.89	4.54	34.78	50.22	0.0466	0.0305
7.	FCRI GA 07	8.28	4.22	29.72	42.78	0.0411	0.0209
8.	FCRI GA 08	10.13*	4.21	37.44	47.00	0.0886**	0.0342
9.	FCRI GA 09	10.94**	4.10	36.33	49.39	0.0823**	0.0308
10.	FCRI GA 10	8.56	4.11	31.44	44.78	0.0472	0.0226
11.	FCRI GA 11	7.00	4.20	33.33	47.11	0.0452	0.0272
12.	FCRI GA 12	7.56	4.72	32.22	43.44	0.0455	0.0278
13.	FCRI GA 13	8.19	3.83	40.00	53.78	0.0727**	0.0341
14.	FCRI GA 14	8.21	3.94	40.33	54.78	0.0744**	0.0358
15.	FCRI GA 15	8.17	4.06	34.11	47.78	0.0531	0.0264
16.	FCRI GA 16	7.00	4.00	35.33	48.11	0.0487	0.0278
17.	FCRI GA 17	8.50	3.50	29.94	42.78	0.0450	0.0176
18.	FCRI GA 18	13.33**	3.50	31.61	41.56	0.0748**	0.0195
19.	FCRI GA 19	8.17	3.50	30.00	41.78	0.0414	0.0176
20.	FCRI GA 20	8.28	4.11	30.94	42.22	0.0442	0.0218

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Table 2: Biometric attributes of *Gmelina arborea* genetic resources (continued)

S.No.	Progeny	Tree Height (m)	Clean bole height (m)	Girth at Breast Height (cm)	Basal Girth (cm)	Volume (m3)	Clean Bole Volume (m3)
21.	FCRI GA 21	8.11	4.11	33.39	44.00	0.0507	0.0255
22.	FCRI GA 22	7.50	3.83	29.61	39.89	0.0379	0.0192
23.	FCRI GA 23	7.94	4.06	32.78	47.00	0.0487	0.0247
24.	FCRI GA 24	8.22	3.67	38.56	53.11	0.0704*	0.0304
25.	FCRI GA 25	8.01	5.09**	38.50	51.33	0.0660	0.0421
26.	FCRI GA 26	6.46	4.89*	39.26	48.81	0.0555	0.0420
27.	FCRI GA 27	5.90	4.62	36.22	49.28	0.0443	0.0344
28.	FCRI GA 28	7.32	4.12	33.17	45.19	0.0456	0.0262
29.	FCRI GA 29	10.50*	4.17	33.89	46.89	0.0688*	0.0267
30.	FCRI GA 30	9.56	4.20	30.22	44.00	0.0501	0.0223
31.	FCRI GA 31	10.83**	4.07	32.83	47.56	0.0653	0.0245
32.	FCRI GA 32	9.89	3.83	31.89	44.39	0.0593	0.0232
Mean		8.21	4.16	34.37	47.20	0.0551	0.0281
SE.d		0.87	0.35	3.27	4.50	0.0060	0.0148
Maximum		13.33	5.09	40.33	55.33	0.0886	0.0421
Minimum		5.90	3.50	29.61	39.89	0.0379	0.0176
CD (p=0.05)		1.73	0.70	NS	NS	0.0120	NS
CD (p=0.01)		2.30	0.93	NS	NS	0.0160	NS
CV (%)		12.91	10.26	NS	NS	26.2100	NS

Table 3

S. No.	Characters	GCV (%)	PCV (%)	Heritability (%)	Genetic Advance (%) of Mean
1.	Tree Height	18.39	22.47	67.00	31.00
2.	Clean bole height	7.27	12.57	33.39	8.65
3.	Girth at Breast Height	6.53	13.35	23.95	6.59
4.	Basal Girth	5.10	12.75	16.00	4.20
5.	Volume	14.87	36.14	16.93	12.61
6.	Clean Bole Volume	17.53	31.53	30.90	20.08

3.2. Variability and Heritability Estimation

The variability and heritability estimates indicated the presence of wider variation among the growth attributes investigated. In general, the PCV values are higher than their corresponding GCV values for all growth attributes. In the current study, high phenotypic coefficient of variation was observed in volume (36.14%), clean bole volume (31.5%) and tree height (22.47%) whereas girth at breast height (13.35%), basal girth (12.75%) and clean bole height (12.57%) showed moderate PCV. In case of GCV, moderate genotypic coefficient of variation was exhibited by tree height (18.39%), clean bole volume (17.53%) and volume (14.87%). Clean bole height, girth at breast height and basal girth recorded low GCV of 7.27%, 6.53% and 5.10% respectively. High heritability was recorded in tree height (67.00%) and moderate heritability for clean bole height (33.39%) and clean bole volume (30.90%) whereas girth at breast height (23.95%), basal girth (16.00%) and volume (16.93%) exhibited low heritability range. High genetic advance as per cent of mean was observed in tree height (31.00%) and clean bole volume (20.08%). Volume (12.61%) registered moderate genetic advance as per cent of mean. All other traits viz., clean bole height (8.65%), girth at breast height (6.59%) and basal girth (4.20%) exhibited low genetic advance as per cent of mean (Table 3).

3.3. Association studies

The phenotypic and genotypic correlation coefficient of morpho-metric traits on clean bole volume is furnished in table 4. The genotypic correlation coefficients were found to be higher than the phenotypic correlation coefficients. Girth at breast height (0.930** and 0.910**) and basal girth (0.774** and 0.834**) showed positive and significant correlation at genotypic and phenotypic levels on clean bole volume. Clean bole height (0.804**) exhibited significant and positive correlation on clean bole volume at genotypic level and volume (0.623**) showed positive and significant correlation at phenotypic level. Tree height had negative correlation on clean volume but significant as observed at genotypic level (-0.702**). Tree height showed negative significance through clean bole height (- 0.693**), girth at breast height (-0.593**), basal girth (-0.773**) whereas through volume (0.707**) showed positive significant correlation on clean bole volume. Positive significance at phenotypic level from volume through tree height (0.646**), girth at breast height (0.732**) and basal girth (0.655**) on clean bole volume was also witnessed.

Path analysis

The estimates of direct and indirect effect of growth attributes on clean bole volume are furnished in table 5.

The residual effect was observed as 0.1320. Among the growth attributes investigated, volume (0.6499), clean bole height (0.6356) and basal girth (0.3040) showed

high positive direct effect whereas tree height (-0.5433) showed negative direct effect on clean bole volume. High positive and indirect effect was exhibited by tree height through volume (0.4594) and negative through clean bole height (-0.4405) and basal girth (-0.2351) on clean bole volume. Girth at breast height recorded high positive indirect effect on clean bole volume through tree height (0.3221), clean bole height (0.3416) and moderate indirect effect on basal girth (0.2732). Volume alone exhibited negative indirect effect through tree height (-0.3841), clean bole height (-0.2771), girth at breast height (-0.0134) and basal girth (-0.0605) on clean bole volume

3.4. Diversity analysis

The genetic divergence studies resolved 32 progenies into 6 clusters wherein the cluster I was largest with 17 progenies followed by cluster IV with 6 progenies; cluster VI with 3 progenies and cluster II, III & V

represented two progeny each (Table 6). The inter and intra cluster D2 and D values among the six clusters are presented in Table 7. The maximum intra cluster distance was observed in cluster IV (28.548) followed by cluster VI (24.260) and cluster I (8.879). The maximum inter cluster distance was observed between cluster V and cluster VI (35.414) followed by cluster IV and cluster VI (33.524) and cluster I and cluster IV

Table 4: Phenotypic and Genotypic correlation coefficient of morphometric traits

Traits	Tree Height	Clean bole height	Girth at Breast Height	Basal Girth	Volume	Clean Bole Volume
Tree Height	1.000	-0.693**	-0.593**	-0.773**	0.707**	-0.702**
Clean bole height	-0.231	1.000	0.537**	0.419**	-0.436**	0.804**
Girth at Breast Height	-0.003	0.250	1.000	0.899**	0.138	0.930**
Basal Girth	-0.010	0.232	0.924**	1.000	-0.199	0.774**
Volume	0.646**	0.037	0.732**	0.655**	1.000	-0.085
Clean Bole Volume	-0.085	0.611	0.910**	0.834**	0.623**	1.000
** Significant at 1% level * Significant at 5% level						
Genotypic correlation coefficient - Above the diagonal						
Phenotypic correlation coefficient - Below the diagonal						

Table 5: Path coefficient analysis of morphometric traits on clean bole volume

Traits	Tree Height	Clean bole height	Girth at Breast Height	Basal Girth	Volume
Tree Height	-0.5433	-0.4405	0.0574	-0.2351	0.4594
Clean bole height	0.3766	0.6356	-0.0520	0.1275	-0.2833
Girth at Breast Height	0.3221	0.3416	-0.0968	0.2732	0.0899
Basal Girth	0.4202	0.2666	-0.0870	0.3040	-0.1294
Volume	-0.3841	-0.2771	-0.0134	-0.0605	0.6499
* Residual Effect= 0.1320 (Diagonal values are direct effect)					

(21.384). The minimum distance was observed between cluster II and cluster III (3.065) followed cluster I and cluster III (6.659) and cluster I and cluster II (6.861). The cluster mean values for morpho-metric traits are presented in Table 8. The highest cluster mean for tree height was observed in cluster V (10.888) followed by cluster IV (9.261) and cluster II (8.195) and lowest was observed in cluster III (7.412). For clean bole height, the highest mean was recorded in cluster VI (4.574) and lowest mean in

cluster IV (3.939). Cluster VI (37.640) and cluster III (31.388) exhibited maximum and minimum cluster mean for girth at breast height. For basal girth and volume, cluster V (48.472, 0.074) exhibited highest cluster mean and lowest was observed in cluster III (42.538, 0.042). The maximum and minimum cluster mean for clean bole volume was recorded in cluster VI (0.037) and cluster III (0.023). The percentage contribution of morphometric traits towards genetic divergence are depicted in Table 9. Among the six traits studied, maximum divergence was contributed

Table 9. Percentage contribution of morphometric traits to genetic divergence

by girth at breast height (26.01%) followed by clean bole volume (24.60%), basal girth (19.36 %) and minimum divergence by volume (6.65%).

3.5. Principal component analysis

The Principal Component Analysis, is one of the multivariate analysis that provides easier understanding of impacts and connections among different traits and also help to identify the best genotypes for selection in breeding programme. To find the extent of variability in the progenies, PCA was estimated for all six growth traits. The Number of Principal Components calculated from correlation matrix was six. Six principal components were grouped, in which two components PC1 and PC2 exhibited more than one Eigen values and contributed 86.72 per cent of total variability among the progenies (Table 10). In biplot diagram (Fig.3.), the traits and progenies were scattered around the origin. Based on the biplot, tree height below the origin and having variation. All other remaining traits were above the origin and exhibited positive variation. The progenies FCRI GA 17, FCRI GA 18, FCRI GA 19,

FCRI GA 22, FCRI GA 25 and FCRI GA 26 recorded more variation for all the traits observed.

4. DISCUSSION

4.1. Growth performance

The *Gmelina arborea* progeny evaluation test indicated significant variation among the progenies due to growth attributes. Among the 32 progenies evaluated, six progenies *viz*., FCRI GA 08 (0.0886 m3), FCRI GA 09

Table 6: Clustering pattern of *Gmelina arborea* genetic resources

Cluster No.	Number of progenies	Members
I	17	FCRI GA 01, FCRI GA 02, FCRI GA 03, FCRI GA 04, FCRI GA 05, FCRI GA 06, FCRI GA 07, FCRI GA 10, FCRI GA 11, FCRI GA 12, FCRI GA 13, FCRI GA 14, FCRI GA 15, FCRI GA 16, FCRI GA 17, FCRI GA 29, FCRI GA 30
II	2	FCRI GA 20, FCRI GA 21
III	2	FCRI GA 22, FCRI GA 28
IV	6	FCRI GA 18, FCRI GA 19, FCRI GA 23, FCRI GA 24, FCRI GA 25, FCRI GA 32
V	2	FCRI GA 09, FCRI GA 31
VI	3	FCRI GA 26, FCRI GA 27, FCRI GA 08

Table 7: Inter (diagonal) and intra cluster D2 and D (parentheses) values of *Gmelina arborea* for morphometric attributes

Cluster	I	II	III	IV	V	VI
I	8.879 (2.980)	6.861 (2.619)	6.659 (2.580)	21.384 (4.624)	18.063 (4.250)	19.325 (4.396)
II	-	1.085 (1.042)	3.065 (1.751)	15.510 (3.938)	10.039 (3.168)	16.974 (4.120)
III	-	-	2.053 (1.433)	16.856 (4.106)	15.523 (3.940)	15.084 (3.884)
IV	-	-	-	28.548 (5.343)	16.463 (4.057)	33.524 (5.790)
V	-	-	-	-	4.049 (2.012)	35.414 (5.951)
VI	-	-	-	-	-	24.260 (4.925)

(0.0823 m3), FCRI GA 24 (0.0704

m3), FCRI GA 18 (0.0748 m3), FCRI GA 13 (0.0727

m3) and FCRI GA 14 (0.0744 m3) exhibited significantly higher performance in terms of growth attributes. Among these six progenies two progenies viz., FCRI GA 08 (0.0886 m3), FCRI GA 09 (0.0823

m3), recorded increased volume and reigned supreme and extend scope for its early deployment. The variation among the progenies / clones / genotypes / seed sources are commonly used as estimates of total genetic variation and used to calculate the degree of genetic control for a particular trait (Foster and Shah, 1988). The analysis of variance for 32 different progenies showed that all the growth attributes intended for study exhibited significant variability. A plethora of workers indicated variations in growth attributes due to progenies viz., Casuarina (Parthiban *et al.*, 2018), Thornless bamboos (Krishnakumar *et al.*, 2017) *Melia azedarach* (Meena *et al.*, 2014), *Albizia lebbeck* (Takur *et al.*, 2014) and *Eucalyptus tereticornis* (Kumar *et al.*, 2010). Generally, variation is a prerequisite for genetic improvement of any species and desired improvement is achieved only through exploitation of genetic variation. Hence the variations recorded for growth attributes like tree height, clean bole volume, girth at breast height, basal girth, volume and clean bole volume in the present study extend scope for selection of progenies with increased values for growth attributes. Among the 32 progenies evaluated two progenies *viz.*, FCRI GA 08 and FCRI GA 09 registered significantly higher values which could be deployed for immediate adoption in Agroforestry promotional programme. The evaluation of juvenile plantation is an early starter to raise agroforestry plantations to satisfy the demands of both domestic and industrial utility as evidenced in *Toona ciliata* (Parthiban *et al.*, 2019).

4.2. Variability and heritability estimates

1.1. Variability is the key for progressing tree improvement program. Selection of any trees is based on phenotypic

superiority. However the phenotypic superiority needs

to be tested for its genetic superiority. For this purpose, the genetic estimates are very useful tool in pre-

Table 8: Cluster mean values for morphometric attributes

Cluster / character	Tree Height	Clean bole height	Girth at Breast Height	Basal Girth	Volume	Clean Bole Volume
I	7.745	4.194	34.555	48.117	0.052	0.028
II	8.195	4.112	32.167	43.112	0.047	0.024
III	7.412	3.978	31.388	42.538	0.042	0.023
IV	9.261	3.939	33.888	46.528	0.060	0.026
V	10.888	4.085	34.585	48.472	0.074	0.028
VI	7.497	4.574	37.640	48.363	0.063	0.037

Table 9

Traits	% Contribution
Tree Height	8.67
Clean bole height	14.72
Girth at Breast Height	26.01
Basal Girth	19.36
Volume	6.65
Clean Bole Volume	24.60
Total	100.00

dicting amount of gains expected in a short period (Foster and Shaw., 1988). The genetic estimates in the current study revealed that the PCV values are higher than their corresponding GCV values and suggest that these characters are influenced by the environment. Among the growth attributes, volume followed by clean bole volume and tree height exhibited higher PCV values with a moderate GCV values. Similar higher PCV values than their corresponding GCV was also reported in Kadam (Parthiban *et al*., 2019) which lend support to the current investigation. The influence of environment was attributable to the higher PCV than their corresponding GCV for all the growth attributes studied was also reported in various species viz., Sandalwood

Table 10. Eigen values, % variance and cumulative variability of *Gmelina arborea*

(Krishnakumar *et al*., 2017) and *Salix alba* (Paray *et al*., 2017). Hence the higher PCV exhibited in the current investigation for various growth attributes might be due to the influence of environment.

Heritability is an important indicator for a breeder for selection and it may provide more reliable conclusion along with genetic gain. High heritability along with the high genetic gain is known to be good selection indicator and is controlled by additive genes. In the current study, tree height, clean bole height and clean bole volume recorded high heritability values and tree height and volume exhibited high genetic advance as mean values which indicated that these traits are under strong genetic control and could be reliable indicators in *Gmelina* tree improvement program. It is also observed that heritability estimates accompanized by high genetic advance are more reliable (Burton and Devana, 1953) which lend support to the findings of current study. Such a high heritability coupled with high genetic advance for various growth parameters have been witnessed in the same species *Gmelina arborea* (Kumar, 2007) which also support the results of current findings. In the present study, high heritability accompanied by high genetic advance for the growth attributes might be due to additive gene effect and play a vital role in *Gmelina* improvement program.

Selection will be effective when the traits exhibit high heritability. Heritability estimates in broad sense will be reliable if accompanied by genetic gain. In the present investigation, high to low estimates of heritability along with genetic gain were observed for six traits under study. This indicates the higher proportion of additive gene effects for expression of these traits. Hence individual clone selection would be effective for improvement of these characters. High heritability with high genetic advance is observed for tree height which indicates that the trait is controlled by additive genes and selection may be effective. The present results are in accordance with Behara *et al.* (2017) in Eucalyptus. Reports of Lokmal (1994) presented low heritability for tree height and girth at breast height in *Gmelina*.

Association studies

CORRELATION

In the present investigation, the genotypic correlation coefficients between growth traits on clean bole volume were observed to be higher than the phenotypic correlation coefficients. In genotypic correlation, girth at breast height, clean bole height, basal girth expressed significant and positive correlation whereas tree height showed significant and negative correlation on clean bole volume whereas in phenotypic correlation girth at breast height, basal girth and volume showed significant positive correlation on clean bole volume. Girth at breast height and basal girth plays significant role on clean bole volume and these two traits will be effective in selection of traits. Tree height and diameter at breast height were positively correlated in *E. camaldulensis* (Otegbeye and Samarawira 1992). Similarly, highly significant and positive correlation was also observed between volume with basal diameter in *Santalum album* (Manojkumar and Sukanya Subramanian, 1998). These results suggested that there exists strong inherent association between pairs of various characteristics and confirms the results of present study and earlier reports. Hence positive and highly significant correlation existed between girth at breast height and clear bole height would act as a clear selection indicator in *Gmelina arborea* tree improvement programme.

Path analysis

The path analysis gives an insight into a complex relationship between different characters in a biological system. The overall correlation observed between two variables is a function of series of direct and indirect relationship. In the current investigation, wide ranges of results were found for many characters with direct

Table 10

Traits	Principal components	Eigen values	% of variance	Cumulative %
Tree Height	PC1	3.362	56.038	56.038
Clean bole height	PC2	1.841	30.685	86.722
Girth at Breast Height	PC3	0.661	11.015	97.737
Basal Girth	PC4	0.114	1.906	99.643
Volume	PC5	0.016	0.273	99.916
Clean Bole Volume	PC6	0.005	0.005	100.000

negative effects and indirect positive effects. Among the characters, clean bole height, basal girth and volume showing high positive direct effect on clean bole volume whereas tree height showed negative and high direct effect on clean bole volume. This suggests that these traits will be used as selection criteria for *Gmelina* breeding programme. High and positive indirect effect of clean bole height, girth at breast height, basal girth through tree height on clean bole volume was recorded in this study. Remaining traits showed high to negligible indirect effects on clean bole volume. Similar results were indicated by Ashok kumar and Paramathma (2005) in Casuarina, Kumaran *et al.*, (2010) in *Simarouba glauca* and Parthiban, (2001) in Teak. The results of current study indicated that the biometric attributes like clean bole height, diameter and volume are reliable factors in *Gmelina arborea* improvement programme as evidenced in Kadam (Parthiban *et al.*, 2019)

4.3. Diversity analysis

The genetic diversity analysis studies among 32 progenies were grouped into six different clusters. Most forest trees are long lived, out breeding and generally highly heterozygous, which have developed a number of natural mechanisms to maintain heterozygosity and *intra* specific variations. These genetic mechanisms combined with the often variable environment, in which forest trees occur, have contributed to the fact that, with a few exceptions,forest trees seem to be among the most genetically variable of all organisms studied to date (Libby, 1987). In the current study, genetic diversity existed among the 32 selected genotypes of *Gmelina arborea* had been assessed through D2 analysis which resolved 32 progenies into six clusters. Out of 32 progenies, 17 progenies were grouped in cluster I. The progenies were collected from different districts of Tamil Nadu were grouped in cluster I which indicates that grouping will not be influenced by location from where it was collected. The clustering pattern of the obtained results coincides with Deve and Parthiban (2014) in *Dalbergia sisoo* and Selvan and Parthiban (2018) in *Neolamarckia cadamba.* Cluster IV, cluster VI and cluster I exhibited maximum intra cluster distance. Hence, based on desirable traits, selection within these clusters may be exercised for *Gmelina* improvement. The maximum inter cluster distance was observed between cluster V and cluster VI and cluster IV and cluster VI. In the present investigation it could be seen that the progenies from different locations got clubbed together to form a single major cluster as evident in cluster I and therefore the pattern of divergence was not depended on the geographic locations. The above findings also confirmed the earlier report of Vennila, 2009 in

EucalyptusLeucaena leucocephala (Chavan and Keerthika 2013) and *Melia dubia* (Saravanan, 2012). The inclusion of geographically divergent provenances in the same cluster may be attributed to the fact that the factors other than geographic distribution might be responsible for their genetic similarity and hence the divergent progenies used in the current project and grouped under one cluster might be due to the factor other than the geographical distribution as evidenced in *Santalum album* (Manojkumar, 1994) and *Prunus armeniaca* (Singh and Chaudhary, 1992). Based on the cluster mean performance, cluster V recorded maximum for tree height, basal girth and volume and cluster VI for clean bole height, girth at breast height and clean bole volume. Hence, the genotypes in these clusters may be selected for trait improvement. Girth at breast height contributed more divergence than other traits in the studied progenies (Fig.1). The obtained results were in accordance with the results of Pande *et al.*, (2013) in *Leucaena leucocephala*

1.1. PRINCIPAL COMPONENT ANALYSIS

The Principal Component Analysis is the important multivariate analysis and it provides easier understanding of impacts and connections among different traits. The principal component analysis is based on the height of Eigen values principal components or needed summary communality in percentage and the number of principal components rotated depends on the number of principal components chosen for the future analysis. The extent of variability in the studied progenies, PCA was estimated for all six morphometric traits. Six

principal components were grouped, in which two components PC1 and PC2 exhibited more than one Eigen values and contributed 86.72 per cent of total variability among the progenies (Fig.2.). Similar results were reported 81.73 % variability by four components in *Melia azedarach* by Thakur and Thakur (2015). Similar to the present study, PCA had also been used as an effective tool to confirm the impacts and connections among different traits in *Bambusa balcooa* (Krishnakumar *et al*., 2019) Eucalyptus (Paramathma., 1992) and *Casuarina equisetifolia* (Pinyopusarerk *et al*., 1996) which fall in line with the findings of the current investigation. Based on the biplot, tree height was found to be below the origin and having more variation. Remaining traits were above the origin and exhibited positive variation for the progenies. The progenies FCRI GA 17, FCRI GA 18, FCRI GA 19, FCRI GA 22, FCRI GA 25 and FCRI GA

26 recorded more variation for all the traits. So, these progenies are distantly related (heterogenous) and could be successfully employed in *Gmelina* hybridization and improvement programme

5. CONCLUSION

Gmelina arborea is the fast growing multipurpose tree species amenable for varied industrial utility. However, the research related to this species has received little research attention. Hence systematic tree improvement programme has been initiated in this species through collection of 32 progenies distributed across its natural and introduced ranges in India. The progenies differed significantly due to growth attributes which resulted in identification of two superior progenies viz., FCRI GA 08 and FCRI GA 09 and extend scope for its early deployment in industrial agroforestry development programme. The genetic analysis indicated variability among growth attributes and identified volume, tree height and clean bole volume as potential indicator for selection in this species. The association studies identified tree height, clean bole height and clear bole volume as potential factors dictating the growth relationship. The genetic diversity analysis registered wider genetic divergence among progenies. In case of PCA, among the progenies, all the six principal components were grouped, in which two components PC1 and PC2 exhibited more than one Eigen values and contributed

86.72 per cent of total variability and extended greater scope for further improvement in this species.

ACKNOWLEDGEMENT

The authors are grateful to members of Consortium of Industrial Agroforestry for funding the research projects wherein the current study formed a part of the objectives of the programme.

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How to Cite this Article: Parthiban K., Krishnakumar N., Revathi S., Subbulakshmi V., Ashick Rajah R.. (2025). Variability, Association and Principal Component Analysis in Gmelina Arborea. *Indian Journal of Agroforestry*, ***27***(2), 79-90. https://doi.org/10.48165/ija.2025.27.02.10