

VARIABILITY AND GENETIC DIVERSITY STUDIES ON *NEOLAMARCKIA CADAMBA* GENETIC RESOURCES

Parthiban KT, Thirunirai-Selvan R*, Palanikumar B & Krishnakumar N

Forest College and Research Institute, Tamil Nadu Agricultural University, Mettupalayam, Tamilnadu 641301, India

*selvanforester@gmail.com

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Agroforestry in India is gaining significance due to increase in demand for wood and wood products and the felling restriction on natural forest resources. However, the agroforestry promotion is detracted due to the availability of high yielding, short rotation varieties amenable for agroforestry. For this purpose, systematic improvement program has been initiated for *Neolamarckia cadamba* (kadam) genetic resources which is identified as one of the potential fast growing tree species amenable for agroforestry system. Accordingly, 20 progenies of kadam genetic resources were evaluated, and the results on variability and diversity were furnished in this study. The progenies differed significantly which resulted in superiority progeny, FCRIK17, recommended for immediate adoption in the agroforestry system and to incorporate them in future breeding program. The variability studies indicated that volume recorded was maximum followed by height and girth at breast height (gbh). The volume also registered high heritability followed by height and gbh. The genetic diversity studies resolved 20 progenies of kadam into 5 clusters, and the cluster III registered higher intra-cluster distance. The inter-cluster distance was maximum between cluster I and IV. Among the growth attributes, volume contributed maximum towards genetic divergence. Hence, the higher the volume registered by progeny FCRIK17, followed by higher heritability, addresses the issue of availability of short rotation genetic resources for incorporation in agroforestry program.

Keywords: Heritability, genetic advance, growth attributes, cluster composition, agroforestry

INTRODUCTION

Neolamarckia cadamba (kadam), belonging to the family of Rubiaceae, is an evergreen tree, distributed naturally in India, Nepal through Thailand and Indo-china and eastward in Malaysia to Papua New Guinea. It is successfully introduced in Africa and Central America. Within the natural distribution, it is found below 1000 m altitude and normally in the areas receiving rainfall more than 1500 mm year⁻¹ but it can also withstand less rainfall of about 200 mm year⁻¹. It is light demanding, intolerant to frost and can withstand periodic flood.

Kadam is a multipurpose tree with utility of pulp and paper, splints and veneer production. The bark of the plant contains anti-inflammatory, digestive, carminative, constipating and antiemetic properties. The flowers are used as vegetable and raw material for attar production with sandalwood as the base. Leaves are slightly aromatic and the decoction of the leaves are used to cure ulcers, wounds and mettorrhea. The leaves are also used for fodder production due to its low mimosine content.

Kadam is a lightweight hardwood with a density of 290–560 kg m⁻³ at 15% moisture content. It has a fine to medium texture, straight grain, low luster and has no characteristic odour or taste (Joker 2000). On a very conservative estimate, the yield of 0.4 m³ wood can be easily obtained from a Kadam tree under rotation of 10 years by which time each tree will have a girth varying from 90 cm to 1 m (Ho et al. 2012).

Such a multifarious and fast growing species has received little research attention particularly on improvement of the species through systematic tree breeding program. Hence, the current study was designed to improve the species through systematic tree improvement program.

MATERIALS AND METHODS

The experimental materials for this study consisted of 20 genotypes of kadam selected from various locations in India (Table 1). The seed source evaluation experiments were carried out in the field of Forest College and Research

Table 1 Details of *Neolamarckia cadamba* genetic resources and locations

Location	Genotype	State	Latitude	Longitude	Altitude (m)
Tripura	FCRIK1	Tripura	23°49'	91°17'	78
Khowai	FCRIK2	Tripura	24°04'	91°36'	46
Tripura	FCRIK3	Tripura	23°55'	91°50'	89
Mettupalayam	FCRIK4	Tamil Nadu	11°17'	76°56'	330
Assam	FCRIK5	Assam	26°33'	90°26'	69
Assam	FCRIK6	Assam	26°33'	90°26'	69
Coimbatore	FCRIK7	Tamil Nadu	11°17'	76°56'	330
Coimbatore	FCRIK8	Tamil Nadu	11°17'	76°56'	330
Coimbatore	FCRIK9	Tamil Nadu	11°17'	76°56'	330
Coimbatore	FCRIK10	Tamil Nadu	11°17'	76°56'	330
Dapoli	FCRIK11	Maharashtra	17°45'	73°11'	175
Maharashtra	FCRIK12	Maharashtra	21°08'	79°05'	313
Tirupathi	FCRIK13	Andhra Pradesh	13°37'	79°25'	155
Andhra Pradesh	FCRIK14	Andhra Pradesh	13°37'	79°25'	155
Hyderabad	FCRIK15	Andhra Pradesh	17°22'	78°29'	502
Andhra Pradesh	FCRIK16	Andhra Pradesh	17°22'	78°29'	502
Karnal	FCRIK17	Haryana	29°41'	76°59'	251
Haryana	FCRIK18	Haryana	29°41'	76°59'	251
Thrissur	FCRIK19	Kerala	10°31'	79°13'	54
Bangalore	FCRIK20	Karnataka	12°58'	77°35'	910

FCRIK1-20 = *Neolamarckia cadamba* progenies

Institute, Tamil Nadu Agricultural University, Mettupalayam (11° 19' N, 76° 56' E), 300 msl, 800 mm, pH 7.1) during 2010–2016. Twenty superior progenies were planted in a randomised block design (rbd) with four replications and the spacing adopted was 3 m × 3 m. Rainfall, temperature and humidity details during the growing periods of the years under study are given in Table 2.

The observations *viz.*, girth at breast height (gbh), height and volume were recorded on all genotypes at 12 months after planting (12 MAP), 24 months after planting (24 MAP), 36 months after planting (36 MAP), 48 months after planting (48 MAP) and 60 months after planting (60 MAP). The following growth attributes *viz.*, height, gbh and volume were recorded and subjected to genetic analysis.

Variability, heritability and association study

Variability studies were estimated as per the method described by Johnson et al. (1955).

Genotypic variance (GV)

$$\text{Genotypic variance} = \frac{\sigma^2g - \sigma^2e}{r}$$

where σ^2g = genotypic mean square, σ^2e = error variance, r = number of replications

Phenotypic variance (PV)

$$\text{Phenotypic variance} = \sigma^2g - \sigma^2e$$

where σ^2g = genotypic variance, σ^2e = error variance. Phenotypic (PCV) and genotypic (GCV) coefficients of variances were computed following Burton (1952).

Phenotypic co-efficient of variability

Phenotypic co-efficient of variability (PVC) was arrived by using the formula as given below

$$\text{PCV \%} = \frac{\text{Phenotypic variance}^{1/2}}{\text{General mean}} \times 100$$

Table 2 Meteorological data during the growing periods

Year	Temperature (°C)		Relative humidity (%)	Rainfall (mm)
	Max.	Min.		
2010	33.76	21.24	53.09	1161.7
2011	33.53	19.37	54.54	991.00
2012	34.14	20.38	49.82	643.00
2013	34.12	21.04	50.57	781.60
2014	34.13	20.98	48.96	1132.00
2015	33.48	21.07	52.10	1139.00

Genotypic co-efficient of variability

Genotypic co-efficient of variability (GCV) was arrived by using the formula as given below

$$\text{GCV \%} = \frac{\text{Genotypic variance}^{1/2}}{\text{General mean}} \times 100$$

Heritability (h^2)

Broad sense heritability (h^2) was calculated according to Lush (1940)

$$h^2 = \frac{\sigma^2_g}{\sigma^2_p}$$

Heritability percentage = $h^2 \times 100$

Genetic advance

Genetic advance will be worked out after Johnson et al. (1955).

$$\text{Genetic advance} = \frac{\text{Genotypic Variance}}{\text{Phenotypic variance}^{1/2}} \times K$$

where K = 2.06, a selection differential at 5% selection intensity.

Determination of genetic divergence

The D^2 statistics are adopted for the estimation of genetic divergence (Mahalanobis 1928). Using D^2 statistical results, the clustering of progenies was done.

RESULTS

Growth performance

The progenies differed significantly for all growth attributes investigated of all growth periods. Twenty progenies differed significantly at 48 MAP

and 60 MAP for tree height. In 60 MAP, FCRIK17 (8.43 m) registered higher tree height followed by FCRIK19 (8.21 m), FCRIK1 (7.95 m), FCRIK5 (7.85 m) and FCRIK14 (7.64 m) compared to general mean (6.46 m) at 5% significance level (Table 3).

The gbh differed significantly at 60 MAP and two progenies viz., FCRIK17 (45.43 cm) and FCRIK19 (44.93 cm) have shown higher gbh (Table 3). Among the 20 progenies, two progenies viz., FCRIK17 (0.145 m³) and FCRIK19 (0.138 m³) recorded significantly higher volume growth compared to general mean (0.081 m³) at 5% level of significance (Table 3).

Variability and heritability parameters

The tree height exercised moderate phenotypic and low genotypic coefficient of variations of 24.11 and 14.27 percent respectively. The phenotypic and genotypic coefficient of variations for gbh was low viz., 19.74 and 14.04% respectively. The volume recorded maximum PCV (56.23) and GCV (40.53) compared to other parameters.

Tree height, gbh and volume recorded a moderate heritability of 0.35, 0.50 and 0.51% respectively. Tree height registered low genetic advance, as percent of mean, was 17.40 and moderate genetic advance, as percent of mean, was 20.57, recorded for GBH. The genetic advance as percent of mean recorded by volume was 60.18 which was maximum among all traits. (Table 4).

Determination of genetic diversity

Genetic divergence

The mean values were transformed into standardised uncorrelated mean values. The D^2 values were computed for all positive pairs. 20 accessions of Kadam were placed under five

Table 3 Growth attributes at various growth periods

Genotype	Height (m)					Girth at breast height (cm)					Volume (m ³)				
	12 MAP	24 MAP	36 MAP	48 MAP	60 MAP	12 MAP	24 MAP	36 MAP	48 MAP	60 MAP	12 MAP	24 MAP	36 MAP	48 MAP	60 MAP
FCRIK1	3.71	5.13	5.45	6.44	7.95*	8.98	28.63	34.18*	38.80	44.03	0.002	0.037	0.056	0.081	0.128*
FCRIK2	3.66	4.63	4.74	5.64	6.35	9.15	25.50	30.45	32.18	37.63	0.003	0.026	0.039	0.058	0.084
FCRIK3	4.33	5.65	5.75	6.18	6.83	10.16	25.13	27.98	32.68	35.75	0.004	0.034	0.043	0.057	0.075
FCRIK4	4.18	6.18	6.35	6.60	6.79	10.01	25.88	29.25	31.73	34.35	0.003	0.035	0.044	0.053	0.066
FCRIK5	4.23	6.13	6.23	6.35	7.85*	8.04	26.00	29.68	37.96	43.73	0.002	0.034	0.045	0.079	0.128*
FCRIK6	4.35	4.93	5.31	5.53	5.61	10.83	21.50	24.05	27.00	29.88	0.004*	0.019	0.026	0.034	0.041
FCRIK7	4.44	5.85	5.94	6.11	6.25	10.70	26.85	31.23	35.70	39.15	0.004*	0.034	0.048	0.062	0.079
FCRIK8	3.75	4.64	4.74	4.98	5.28	9.23	21.88	24.55	26.50	29.75	0.003	0.020	0.026	0.030	0.040
FCRIK9	3.78	4.70	4.93	5.09	5.23	9.65	21.95	26.00	29.08	31.25	0.003	0.019	0.029	0.037	0.044
FCRIK10	3.74	4.04	4.24	4.45	4.66	8.82	20.30	24.58	27.60	29.58	0.002	0.014	0.021	0.028	0.035
FCRIK11	4.00	4.51	5.19	5.51	5.83	9.66	20.03	24.55	28.23	31.03	0.003	0.016	0.027	0.037	0.048
FCRIK12	4.21	5.77	5.94	6.09	6.19	10.51	24.25	27.53	33.00	37.08	0.004*	0.030	0.037	0.054	0.074
FCRIK13	4.21	5.08	5.30	5.75	5.91	10.30	24.10	26.83	29.75	32.60	0.004*	0.026	0.032	0.043	0.054
FCRIK14	4.05	5.08	5.54	6.00	7.64*	11.34	26.90	30.35	33.80	43.13	0.004*	0.031	0.044	0.057	0.123
FCRIK15	3.89	4.88	5.15	5.21	5.23	9.13	20.90	24.43	27.78	32.40	0.003	0.018	0.025	0.031	0.048
FCRIK16	4.04	5.49	5.74	5.99	6.28	10.76	26.58	30.60	37.25	42.43	0.004*	0.035	0.049	0.071	0.100
FCRIK17	4.16	6.01	6.14	7.55*	8.43*	10.97	27.70	30.78	36.33	45.43*	0.004*	0.040	0.050	0.084*	0.145*
FCRIK18	4.05	5.64	5.78	6.63	7.33	8.45	26.18	31.15	36.88	42.65	0.002	0.033	0.047	0.078	0.115
FCRIK19	4.00	5.56	5.69	7.40*	8.21*	9.78	24.30	27.50	32.03	44.93*	0.003	0.029	0.036	0.063	0.138*
FCRIK20	2.64	3.89	4.00	5.00	5.46	8.51	19.40	23.03	27.40	31.80	0.002	0.014	0.021	0.033	0.049
Mean	3.97	5.19	5.41	5.92	6.46	9.75	24.20	27.93	32.08	36.93	0.003	0.027	0.037	0.054	0.081
SEd	0.30	0.47	0.52	0.51	0.50	0.82	2.78	2.81	3.47	3.62	0.001	0.008	0.010	0.015	0.022
CD (0.05)	0.60	0.94	1.05	1.02	1.00	1.65	5.57	5.63	6.95	7.26	0.001	0.016	0.020	0.030	0.043
CD (0.01)	0.80	1.25	1.40	1.36	1.33	2.20	7.41	7.49	9.25	9.66	0.002	0.022	0.027	0.040	0.058

FCRIK1-20 = *Neolamarkia cadamba* progenies, MAP = months after planting, SED = standard error of differences, CD = critical differences

Table 4 Genetic parameters for growth traits among *Neolamarckia cadamba*

Character	GCV	PCV	Heritability	GA (%) of Mean
Height	14.27	24.11	0.3502	17.40
Girth at Breast Height	14.04	19.74	0.5057	20.57
Volume	40.53	56.23	0.5195	60.18

GCV = genotypic co-efficient of variability, PCV = phenotypic co-efficient of variability, GA = genetic advance

clusters on the basis of Mahalanobis D² clustering techniques.

Cluster components

The clustering pattern revealed that the 20 progenies were resolved into five different clusters. Cluster I constituted of 2 progenies, FCRIK8 and FCRIK10, cluster II consisted of 2 progenies, FCRIK15 and FCRIK20, cluster III consisted of 6 progenies, FCRIK1, FCRIK2, FCRIK3, FCRIK4, FCRIK5 and FCRIK19, cluster IV consisted of 6 progenies, FCRIK6, FCRIK7, FCRIK9, FCRIK11, FCRIK12 and FCRIK13, and cluster V consisted of 4 progenies, FCRIK14, FCRIK16, FCRIK17 and FCRIK18 (Table 5).

Intra- and inter-cluster average distance

The average inter- and intra-cluster D² and D values among the five clusters are presented in Table 6. Intra- and inter-cluster ranged from 0.01 to 2.32 and 0.45 to 9.75 respectively. Intra-cluster distance was maximum in cluster III (2.32) with six accessions and minimum in cluster I with one accession. Highest inter-cluster was between cluster I and V (9.75), followed by cluster I and III (7.30) suggesting that there is a wide genetic diversity between these groups. The minimum inter-cluster distance was between cluster I and II (0.45).

Cluster mean performance

The cluster mean for the traits was estimated and furnished in Table 7. Cluster mean expressed significant variation among the clusters for all traits. The members in cluster V showed the highest performance of 7.38 for tree height followed by cluster III (7.26) while, the minimum was observed for cluster I (4.84). The maximum cluster mean of 43.41 was observed for gbh in cluster IV whereas the least cluster mean for gbh (29.76) was exhibited by cluster I. In case of

volume, the cluster mean was highest for cluster V (0.118) and the lowest for cluster I (0.037). In general, cluster V and cluster I had highest and lowest mean values for most of the traits respectively.

Contribution of characters towards genetic divergence

The number of times each character ranking first was counted and percentage contribution towards divergence were calculated and presented in Table 8. Volume contributed maximum percentage towards divergence (57.90%) followed by height (25.26%). Contribution towards divergence was least in gbh (16.84%).

DISCUSSION

Growth performance

The progeny test showed significant differences among 20 progenies of Kadam for growth attribute *viz.*, height, gbh and volume at 12, 24, 36, 48 and 60 MAP. Significant variation was found in all growth characteristics *viz.*, tree height, gbh and volume among 20 progenies. Considering all the 20 progenies, the superiority of FCRIK17 progeny was consistent. A plethora of workers reported the existence of significant differences and superiority of few seed sources, progenies and provenances in various trees such as *Azadirachta indica* (Syed et al. 2013), *Populus deltoides* (Jha 2012), *Gmelina arborea* (Kumar 2007) *Eucalyptus tereticornis* (Ginwal et al. 2004) and *Dalbergia sissoo* (Tewari et al. 1996) which lend support to the result of current study.

Similarly, Teak provenance exhibited variation in growth characteristics (Rawat et al. 1998, Rao et al. 2001). Significant variation in height, girth and number of internodes were also reported in teak progeny evaluation (Lakshmikantham et al. 1974). The provenance from konni of kerala exhibited best score for growth characters (Rao

Table 5 Composition of clusters for growth traits among *Neolamarckia cadamba*

Cluster No	Members
I	FCRIK8, FCRIK10
II	FCRIK15, FCRIK 20
III	FCRIK1, FCRIK2, FCRIK3, FCRIK4, FCRIK5, FCRIK19
IV	FCRIK6, FCRIK7, FCRIK9, FCRIK11, FCRIK12, FCRIK13
V	FCRIK14, FCRIK16, FCRIK17, FCRIK18

FCRIK = *Neolamarckia cadamba* progenies

Table 6 Estimates of inter- and intra-cluster distances for growth traits in *Neolamarckia cadamba* (Kadam)

	I	II	III	IV	V
I	0.0073 (0.0857)	0.4540 (0.6738)	7.3016 (2.7021)	1.8089 (1.3449)	9.7522 (3.1229)
II		0.0660 (0.2569)	4.7866 (2.1878)	0.8271 (0.9095)	6.6076 (2.5705)
III			2.3243 (1.5246)	3.9401 (1.9850)	1.9213 (1.3861)
IV				1.4277 (1.1949)	5.4373 (2.3318)
V					1.3789 (1.1743)

Table 7 Cluster mean value for growth traits among *Neolamarckia cadamba*

Cluster	Height (m)	Girth at breast height (cm)	Volume (m ³)
I	4.84	29.76	0.037
II	5.34	32.10	0.048
III	7.26	40.07	0.103
IV	5.85	33.50	0.057
V	7.38	43.41	0.118

Table 8 Contribution of different growth traits to total divergence among *Neolamarckia cadamba*

Character	No. of first rank	% Contribution
Height	48	25.26
Girth at Breast Height	32	16.84
Volume	110	57.90
Total	190	100

et al. 2001). The provenances of Parambikulam, Nilambur, Malayattur consistently recorded better biomass production and better relative growth (Jayasankar et al. 1999). All these studies registered a few genetic resources which lend support to the superiority of FCRIK17 progeny, witnessed in the current investigation. Genetic selection of rapid juvenile growth rate was also advocated as a means of improving competitive ability of forest trees (Gall & Taft 1973, Steiner 1986) which extend the scope of selection of a

progeny in the current study, based on superiority during the period under evaluation.

Variability parameters

The success of the tree improvement program depends on the variability present in the material and hence studies were conducted to characterise the variability existed among kadam genetic resources. In the present study, volume recorded highest phenotypic coefficient of variation and

moderate genotypic coefficient of variation. Characters like tree height and gbh exhibited low to moderate genotypic and phenotypic coefficient of variation. Current findings are similar to studies in *Melia dubia* which showed low GCV and PCV for plant height, basal diameter and volume index (Kumar et al. 2013). Similarly, low GCV and PCV for height and collar diameter were also reported in *Bambusa pallida* (Singh & Beniwal 1993).

In general, for all the traits, phenotypic coefficients of variations were higher than their respective genotypic ones. Such results are expected when the environmental variances are larger because phenotypic variances consist of genotypic and environmental variation. In other words, expression of the traits has been affected by the influence of the environmental factors as evidenced in Neem (Dhillon et al. 2003), *Dalbergia sissoo* (Dogra et al. 2005) and in progenies of *Eucalyptus grandis* (Subramanian et al. 1995).

Heritability and genetic advance

Heritability has an important place in tree improvement programme as it provides an index of the relative strength of heredity versus environment. It is also useful for ranking importance of each trait in the cross breeding programme. Heritability expresses the degree to which a character is influenced by heredity as compared to the environment.

Estimation of broad sense heritability for various characters showed moderate heritability for tree height (0.35), gbh (0.50) and volume (0.51). The results are on par with the studies carried out by Raymond (2002) on *Eucalyptus globulus* and *Eucalyptus nutens* which recorded low to moderate heritability for different genetic parameters. Low to moderate heritability was recorded for height and tree volume in *E. grandis* (Osorio et al. 2001) and for clean stem height and collar diameter in *Eucalyptus tereticornis* (Ginwal et al. 2004).

Volume registered high heritability as compared to gbh and height. Similar results were found in the studies of Hodge and White (1992) which registered moderate to high heritability for height, diameter and volume was found in *Eucalyptus grandis* and *Pinus elliotti* (Lambeth et al. 1994). Since height, gbh and volume showed moderate to high heritability percentage, the selection for these traits would be effective and

improvement would be made through mass selection.

High heritability indicates the effectiveness of selection based on good phenotypic performance but does not necessarily mean a high genetic gain for particular traits. Heritability estimates, in the broad sense, will be reliable if accompanied by high genetic advance (Burton & Devane 1953). In the present study, the trend of genetic advance as percent of mean was maximum in volume followed by gbh and height, indicating a wide scope of genetic improvement possibility in the species. The findings of the current study are in line with those of Ramachandra (1996) in *Acacia catechu*. Other research workers have also reported similar results in *Terminalia arjuna* (Srivastava et al. 1993), *Grewia optiva* (Sharma & Sharma 1995) and also in *Eucalyptus grandis* (Subramanian et al. 1995) which lend support to the results of the current investigation.

In teak, low heritability estimates for height and GBH (Rao et al. 2001) and high heritability estimates for height (Anmol kumar et al. 1997) and moderate heritability estimate for growth attributes (Callister and Collins 2007) which indicated wider variation and extend support to the findings of this study.

Determination of genetic diversity

The nature and degree of genetic divergence in the seed sources is useful for classifying them into groups on the basis of their diversity, particularly when overlapping for one or more characters is frequent. The genetic divergence analysis also helps in identifying the desirable genotypes for improvement programme, presuming that genetic diversity would provide greater livelihood of promising genetic rearrangement. In the current study, genetic diversity existed among the 20 selected progenies of Kadam, assessed through D² analysis, which resolved the 20 progenies into five clusters.

Cluster composition

Application of Mahalanobis statistics and Tocher's technique allowed grouping of the 20 Kadam progenies into five distinct clusters, indicating adequate genetic variability among the clusters under study. Among the five clusters, cluster III & IV included the maximum of six genotypes each and cluster V included four genotypes. In *Pinus wallichiana*, 88 tree progenies were grouped into

10 distinct clusters on the basis of Mahalanobis D^2 statistic. A maximum number of genotypes (21) were grouped in cluster IV, followed by cluster III (18) and cluster X (14). Clusters V and VII consisted of 10 genotypes each followed by clusters I and VIII which included 8 and 4 genotypes, respectively. Cluster III, VI and IX were distinct and unique from others as each included only one genotype (Aslam et al. 2011). Similarly, 80 batches of teak had been grouped into eight clusters, of which group A formed the largest cluster containing 46 batches (Bagchi 2000).

In the present investigation, some clusters included genotypes from all the locations, while others included only a particularly unique and distinct genotype. It could be seen that the genotypes from different locations were grouped together to form a single major cluster, as evident in cluster III, and therefore the pattern of divergence was not dependent on geographic locations. These findings were in agreement with the results of Aslam et al. (2011) in *Pinus wallichiana* and suggested that all the genotypes from a given area may not necessarily form a single cluster. Thus, the pattern of divergence is not dependent on geographical nearness of the genotypes and such a pattern could be attributed to differences in the genetic make-up of the otherwise co-occurring genotypes (Chauhan & Sehgal 2001).

In the present study, the highest intra-cluster distance was observed for cluster III (2.32) and the minimum for cluster I (0.01). Cluster I had minimum intra-cluster value indicating that genotype within the cluster was similar, while cluster III showed maximum intra-cluster D^2 value followed by cluster IV (1.42), revealing the existence of diverse genotypes. The intra-cluster distance was much lower than inter-cluster one, suggesting heterogeneous and homogenous nature between and within clusters, respectively, and wide genetic diversity among the genotypes of different clusters than those of the same cluster. The data on inter-cluster distances and as per the performance of genotypes were used to select genetically diverse and silviculturally superior genotypes.

The genotypes, exceptionally good with respect to one or more characters, were desirable. A perusal of intra- and inter-cluster distances revealed that highest inter-cluster distance of 9.75 was between cluster I and V, followed by

cluster I and III (7.30). Genotypes drawn from genetically diverse clusters could be particular significant in the production of high heterotic effect during hybridisation (Aslam et al. 2011). Such inter- and intra-cluster distance among *Pinus gerardiana* was also reported by Anil Kant et al. (2006) supporting the results of current conclusion.

Contribution of traits towards genetic divergence

In the present investigation, among the growth attributes, volume contributed maximum (57.90%) towards genetic divergence followed by height and gbh. Paramathma (1992) reported similar results in six *Eucalyptus species* and twelve inter specific hybrids. Bagchi (2000) in *T. grandis* and Vennila (2009) in *Eucalyptus* also reported contribution of volume index along with other morphometric traits towards genetic divergence among the genotypes tested, which might be due to the existence of broader genetic base. Based on the current findings, the contribution of volume for genetic divergence indicated that the factor could be used as an index for Kadam tree improvement programme.

CONCLUSIONS

Kadam is one of the potential fast growing tree species amenable for various agroforestry systems but received little research attention towards improvement of the species. The current study is an intervention to resolve the issue through systematic progeny test program. The progenies differed significantly and exhibited the superiority progeny, FCRIK17, which is focused for immediate adoption. The studies on genetic estimates indicated that volume is the profound character for consideration towards kadam improvement program. Genetic diversity analysis indicated the existence of wide variation among the progenies, and extended scope towards further improving the species, both for biomass and wood quality.

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