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Genetic Variations among Open Pollinated Families of Selected Better Trees in Melia Dubia

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Abstract

Twenty open pollinated families in Melia dubia were selected and evaluated for growth attributes and genetic divergence. The experiment was conducted at Forest College and Research Institute, Tamil Nadu Agricultural University; Mettupalayam situated at 11° 19' N longitude, 76° 56' E latitude at 300 MSL during January - December 2010. The study indicated significant differences among the selected families for various growth attributes. Among 20 open pollinated families evaluated, three families viz., FCRIMD 11, FCRIMD 14 and FCRIMD 15 exhibited consistent superiority over growth periods for height, basal diameter and volume index. Genetic divergence studies resulted in grouping of the selected families into six clusters which indicated the existence of adequate genetic divergence. Among the clusters, cluster I was the largest with 10 open pollinated families. While the maximum intra cluster distance was recorded in cluster II. The intra and inter cluster distance revealed that maximum inter cluster distance was recorded between cluster I and VI which indicated the presence of wide genetic distance between Melia dubia open pollinated families. Among the various growth attributes, volume index contributed maximum towards genetic divergence followed by plant height. These two characters could act as a reliable indicator for future improvement programme in this economically important species. Genetic analysis of the families indicated adequate variability in the population. The PCV and GCV estimates exhibited superiority of volume index followed by basal diameter and plant height. Whereas, plant height and volume index exhibited moderate heritability. The genetic advance was high for volume index followed by plant height which indicated the reliability of these two parameters for inclusion in future improvement programme.

Keywords: *Melia dubia*, open pollinated families, genetic divergence, inter and intra cluster distance, variability, heritability.

Introduction

Melia dubia is a fast growing, indigenous and economically important multipurpose tree species that grows naturally in certain parts of the Western Ghats of South India. It is a moderate light demander in the young stage and grows vigorously in the moist deciduous forest. Natural propagation is mostly through seeds whose germinability is poor. It coppices well and produces root suckers when the roots are injured. It pollards well and clusters of new shoots are emerging out from dormant buds on stems and branches. The species has been classified as a moderately difficult to root species[1]. It is also reported to be found in the Eastern Himalayas, Sikkim, North Bengal, upper Assam, Khasi hills, Hills of Odisha and North Circars. It is also distributed in Sri Lanka, Malaysia, Java, China and Australia. Due to its wide distribution, the tree is capable of withstanding a wide range of climatic conditions. It is a multipurpose industrial wood species suitable for making packing cases, cigar boxes, ceiling planks, building and construction materials, agricultural implements, pencils, matchboxes, splints, kattamarans, musical instruments, tea boxes, and plyboard. It is also a good fuelwood. The species has been identified as one of the potential alternate pulpwood species[2]. Such a species with multivarious uses has gained only limited research attention especially with inference to tree improvement. It holds good potential for various industrial utilities and also amenable for agroforestry and farm forestry. Lack of sufficient studies in terms of family selection, evaluation and identification of potential genetic resources necessitated the current study to select and analysis potential open pollinated families by assessing the existing variability.

Material and Methods

Plant Material: The predominant *Melia dubia* growing areas of Tamil Nadu were surveyed and 20 plus trees were selected based on growth attributes *viz*. basal diameter, plant height and volume index. The geographic range *of* the selected open pollinated families is furnished (table 1).

From each open pollinated family, a total of 15 fruits were collected and depulped by removing the pericarp and mesocrap manually and the seeds were washed several times in running water. The depulped seeds were then dried under shade and used for raising seedlings. Germination started after 90 days and a total of 30 seedlings from each open pollinated family were pricked out and raised in 10 x 20 cm poly containers and maintained in the nursery for period of six months.

Table–1
Details of *Melia dubia* genetic resources and their location

Location	Name of the CPTs	District	State	Latitude	Longitude	Altitude
Thalamalai - I	FCRIMD 1	Erode	Tamil Nadu	11°36’N	77°00’E	3093
Nellithurai, MTP	FCRIMD 2	Coimbatore	Tamil Nadu	11°20’N	76°51’E	1550
Kallar - I	FCRIMD 3	The Nilgiris	Tamil Nadu	11°20’N	76°51’E	1890
Black thunder, MTP, I	FCRIMD 4	Coimbatore	Tamil Nadu	11°20’N	76°51’E	1895
Kallar - II	FCRIMD 5	The Nilgiris	Tamil Nadu	11°20’N	76°51’E	3079
Thalamalai Thoddapuram	FCRIMD 6	Erode	Tamil Nadu	11°36’N	77°00’E	3019
Thalamalai II	FCRIMD 7	Erode	Tamil Nadu	11°46’N	77°00’E	2707
Thalamalai, Kodipuram	FCRIMD 8	Erode	Tamil Nadu	11°37’N	77°00’E	2950
Thalamalai, Sikkallli	FCRIMD 9	Erode	Tamil Nadu	11°36’N	77°00’E	3019
Kallar Horticulture	FCRIMD 10	The Nilgiris	Tamil Nadu	11°20’N	76°51’E	1905
Black thunder, MTP, II	FCRIMD 11	Coimbatore	Tamil Nadu	11°20’N	76°51’E	1897
Thalamalai Muthiyanur	FCRIMD 12	Erode	Tamil Nadu	11°43’N	77°01’E	3329
Thalamalai, Gundapuram	FCRIMD 13	Erode	Tamil Nadu	11°44’N	77°01’E	2779
Thalamalai, Neithalapuram	FCRIMD 14	Erode	Tamil Nadu	11°44’N	77°01’E	2707
Thalamalai, Kodipuram	FCRIMD 15	Erode	Tamil Nadu	11°37’N	77°00’E	3016
Thalavadi I	FCRIMD 16	Erode	Tamil Nadu	11°37’N	76°53’E	3001
Thalavadi II	FCRIMD 17	Erode	Tamil Nadu	11°17’N	76°55’E	1780
Thalamalai Sivanakalli	FCRIMD 18	Erode	Tamil Nadu	11°36’N	77°00’E	3012
Thalamalai, Thoddapuram	FCRIMD 19	Erode	Tamil Nadu	11°37’N	76°59’E	2984
Bhavanisagar	FCRIMD 20	Erode	Tamil Nadu	11°38’N	76°59’E	2261

Experimental Design: Six month old seedlings of all families were planted in the field following a complete randomized block design (CRBD) with three replications. In each replication, nine plants were planted at an espacement of 3m x 3m. Due to non – availability of any variety, a check was not included in the trial. The mean of tested materials was used for estimating the superiority of the selected open pollinated families. The experiment was conducted at Forest College and Research Institute, Tamil Nadu Agricultural University, Mettupalayam situated at 11° 19’ N longitude, 76° 56’ E latitude at 300 MSL during January – December 2010. The experimental site receives an average rainfall of 800 mm/annum with the maximum and minimum temperatures of 33.8°C and 21.2°C respectively. The soil is predominantly red lateritic with a pH of 7.1. The data for statistics is based on plot mean. Observation *viz.*, plant height, basal diameter and volume index were recorded once in every 4 months in all the nine plants in a replication. Volume index was calculated using the following formula[3].

Volume index = (Collar diameter) ^{2} x Height

Data Analysis: Biometric data for plant height, basal diameter and volume index were subjected to analysis of variance[4] and genetic divergence of the open pollinated families were studied following Mahalanobis D^2 statistics[5]. Grouping of the superior open pollinated families into various clusters was made by Tocher’s method[6]. On completion of clustering, the *intra* and *inter* cluster relationships were studied and the mutual relationship between clusters and their distances were represented. The average *intra* cluster distance was measured using the formula.

$D^2 = D_1^2 / n$

Where D^2 was the sum of the distances between all possible combinations of the open pollinated families included in a cluster whereas the average *inter* cluster divergence was arrived at by taking into consideration all the component D^2 values possible among the numbers of the two clusters. The genetic distance ‘D’ between the clusters were obtained from the square root of the average D^2 values.

Estimation of genetic parameters *viz*., variability, PCV and GCV were computed[7]. Heritability and genetic advance were computed[8, 9].

Results and Discussion

Significant differences were found among the families of *Melia dubia* for growth characteristics *viz.*, plant height, basal diameter and volume index during the three growth stages. Superiority of three families *viz*., FCRIMD 11 (127.33 cm, 339.27 cm and 7.00 m for height at 4, 8 and 12 MAP), (2.46 cm, 6.04 cm and 0.11 m for basal diameter at 4, 8 and 12 MAP) and (770.14cm^3, 12382.72cm^3 and 0.09 m^3 for volume index at 4, 8 and 12 MAP) FCRIMD 14 (129.67cm, 336.80 cm and 7.02 m for height at 4, 8 and 12 MAP), (2.44 cm, 5.88 cm and 0.11 m for basal diameter at 4, 8 and 12 MAP) and (774.60 cm^3, 11651.56 cm^3 and 0.08 m^3 for volume index at 4, 8 and 12 MAP), FCRIMD 15 (135.13 cm, 370.39 cm and 7.20 m for height at 4, 8 and 12 MAP), (2.81cm, 6.68 cm and 0.12 m for basal diameter at 4, 8 and 12 MAP) and (1112.52 cm^3, 16569.92 cm^3 and 0.10 m^3 for volume index at 4, 8 and 12 MAP) (table 2) was evidenced consistently in all the three growth periods investigated.

Table–2
***Melia dubia* progeny variation for plant height, basal diameter and volume index at three growth periods**

	Plant height			**Basal diameter**			**Volume index**		
Name of the Progeny	**4MAP (cm)**	**8MAP (cm)**	**12MAP (m)**	**4MAP (cm)**	**8MAP (cm)**	**12MAP (m)**	**4MAP (cm^3)**	**8MAP (cm^3)**	**12 MAP (m^3)**
FCRIMD 1	97.88	279.13	6.25	1.80	4.50	0.10	327.09	5906.89	0.06
FCRIMD 2	84.57	269.67	6.50	1.49	4.31	0.11	209.51	5029.44	0.07
FCRIMD 3	101.29	295.87	6.24	1.84	4.85	0.10	346.99	7038.33	0.06
FCRIMD 4	73.79	270.07	6.29	1.45	5.01	0.10	172.37	6837.22	0.07
FCRIMD 5	92.17	276.07	6.67	1.62	4.33	0.10	251.95	5204.11	0.07
FCRIMD 6	89.67	274.53	6.63	1.89	4.63	0.11	337.76	5904.40	0.07
FCRIMD 7	90.09	277.13	6.23	1.91	4.95	0.10	329.94	6919.08	0.06
FCRIMD 8	90.71	288.60	6.00	1.90	6.02*	0.11	351.63	10591.94	0.07
FCRIMD 9	97.16	268.00	6.22	1.72	4.90	0.10	296.72	6601.79	0.07
FCRIMD 10	71.13	250.87	6.26	1.20	4.45	0.10	110.59	5096.00	0.06
FCRIMD 11	127.33*	339.27*	7.00*	2.46*	6.04*	0.11	770.14*	12382.72*	0.09*
FCRIMD 12	101.33	341.07*	6.63	2.00	4.85	0.11	430.81	8086.35	0.08
FCRIMD 13	101.87	283.33	6.28	1.89	4.66	0.10	388.17	6357.58	0.07
FCRIMD 14	129.67*	336.80*	7.02*	2.44*	5.88*	0.11	774.60*	11651.56*	0.08
FCRIMD 15	135.13*	370.39*	7.20*	2.81*	6.68*	0.12*	1112.52*	16569.92*	0.10*
FCRIMD 16	105.60	337.27*	6.19	2.55*	5.84*	0.11	683.52	11530.37*	0.08
FCRIMD 17	104.67	300.93	6.44	1.88	5.10	0.11	381.67	7862.68	0.07
FCRIMD 18	104.27	340.47*	6.49	2.62*	5.90*	0.11	715.10*	11923.51*	0.08
FCRIMD 19	107.80	288.07	6.59	1.60	4.46	0.10	285.27	5827.48	0.07
FCRIMD 20	105.67	290.27	6.71	1.87	4.55	0.10	390.61	6138.80	0.07
Mean	**100.59**	**298.89**	**6.49**	**1.95**	**5.10**	**0.11**	**433.35**	**8173.01**	**0.07**
SEd	12.34	18.60	0.22	0.24	0.37	0.01	138.74	1426.48	0.01
CD (p=0.05)	24.98	37.66	0.45	0.49	0.74	0.01	280.87	2887.79	0.02

Plethora of workers reported the existence of significant differences and superiority of few seed sources, open pollinated families and provenances in tree species like *Lagerstroemia* spp[10] in different age gradations which lend support to the current findings in open pollinated families of *Melia dubia*.

Assessment of genetic variability is a key to progress in tree improvement programme[11] and is a useful tool in determining the strategies for tree improvement and breeding of any species.

The extent and pattern of genetic diversity in forest trees are influenced by their native system and the movement of genes between dispersed populations of the same species. Measuring genetic diversity in trees has typically been done either by provenance testing[12]. or electrophoresis analysis of the enzymes[13] and also by DNA based molecular techniques[14,15]. In the current study, genetic diversity in the selected families of *Melia dubia* had been assessed through Mahalanobis D^2 techniques using the growth attributes recorded in the field experiment.

Cluster composition: D^2 statistics is an important tool in plant breeding for estimating genetic divergence. The application of D^2 clustering technique in *Melia dubia* genetic resources resolved the twenty genotypes into six clusters. Among the six clusters, the clusters I and II were the biggest with 10 and 5 members respectively. The Cluster III contains 3 members and remaining cluster constitutes one progeny each. In *Tectona grandis* using D^2 clustering technique 80 batches of teak had been grouped into eight clusters, of which group A formed the largest cluster containing 46 batches[16]. In the present investigation it was observed that the open pollinated families 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 dependant upon the geographic locations. Inclusion of geographically divergent provenances of teak in the same cluster may be attributed to the fact that the factors other than geographic distribution might be responsible for their genetic similarity[17] (table 3).

The *intra* and *inter* cluster analysis indicated that the clusters IV, V and VI showed that there is no *intra* cluster generalized distance since they contained only one family. This may be due to introduction and demonstration during past years as evidenced in *Bombax ceiba*[18]. The maximum *intra* cluster distance was shown by the cluster II (1.803).

Table–3
Clustering pattern in *Melia dubia* for morphometric attributes

Cluster No.	Number of open pollinated families	Members
I	10	FCRIMD 1, FCRIMD 2, FCRIMD 3, FCRIMD 4, FCRIMD 5, FCRIMD 6, FCRIMD 7, FCRIMD 8, FCRIMD 9, FCRIMD 10
II	5	FCRIMD11, FCRIMD12, FCRIMD13, FCRIMD14, FCRIMD19
III	2	FCRIMD17, FCRIMD18
IV	1	FCRIMD16
V	1	FCRIMD20
VI	1	FCRIMD 15

Table–4
Intra (diagonal) and intra cluster D^2 and D (parantheses) values of *Melia dubia* for morphometric attributes

Cluster	1	2	3	4	5	6
I	1.389 (1.929)	2.020 (4.081)	1.321 (1.746)	2.156 (4.649)	2.018 (4.073)	4.173 (17.414)
II		1.803 (3.252)	1.598 (2.553)	2.879 (8.288)	1.712 (2.930)	3.231 (10.441)
III			0.830 (0.689)	1.896 (3.594)	2.026 (4.104)	3.345 (11.189)
IV				0.000 (0.000)	3.063 (9.381)	3.913 (15.315)
V					0.000 (0.000)	3.795 (14.406)
VI						0.000 (0.000)

From the *inter* cluster distance, it is inferred that the cluster I and III (1.321) were the closest while the maximum *inter* cluster distance was recorded between cluster I and VI (4.173) which indicated the presence of wider genetic distance between *Melia dubia* open pollinated families (table 4). Such *inter* and *intra* cluster distance among *Pinus gerardiana* reported which lend support to the current findings[19].

Contribution of traits towards genetic divergence: Volume index contributed the maximum towards genetic divergence (65.26 %) followed by height (25.79 %) and the least by basal diameter (8.95%) (Table 5). Similar results in six Eucalyptus species and twelve *inter* specific hybrids[20] in *D. sissoo*[21] in *Pinus roxburghii*[22] and in Eucalyptus[23] 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 earlier works in other species and the present finding, the contribution of volume index for genetic divergence indicated that this derived factor could be used as an index in *Melia dubia* tree improvement programme.

Table–5
Percentage contribution of morphometric traits to genetic divergence at -12 MAP

Character	No. of first rank	% contribution
Basal diameter	17	8.95
Plant height	49	25.79
Volume index	124	65.26
Total	190	100

Variability parameters: To understand the causes of variation, apportioning of total phenotypic variation essential. The genetic variation which is heritable can be exploited for further improvement programme. In the current study, volume index registered high PCV (17.13) and GCV (11.25). Plant height recorded moderate PCV (5.96) and GCV (4.24) followed by basal diameter (table 6). Higher GCV for volume index in teak[24]. The number of branches in *Eucalyptus tereticornis* and low GCV for height in the same species were earlier reported[20]. The exhibition of low to moderate PCV and GCV for plant height and basal diameter in the present study is in conformity with the above assertions. The genotypic and phenotypic coefficient of variation for height, basal diameter and volume index recorded in the current study provided evidences for existence of adequate genotypic variations[25] and thus extend the scope for exploitation of genetic variability for further improvement in this multiple utility species.

Table–6
Genetic estimates for growth attributes at 12 MAP

Traits	GCV	PCV	Heritability	GA (%) of mean
Basal diameter	3.90	7.12	0.30	4.40
Plant height	4.24	5.96	0.51	6.21
Volume index	11.25	17.13	0.43	15.21

In the current study, the genotypic coefficient of variation was found to be of low magnitude than the phenotypic coefficient of variation for all the traits studied. This indicates that these traits are influenced by the local environmental factors as evidenced in neem[26] and also in progenies of *Dalbergia sissoo* [27].

Heritability: Heritability expresses the degree to which a character is influenced by heredity as compared to the environment[25]. Estimation of broad sense heritability for various characters showed low to moderate heritability for height (0.51), volume index (0.43) and basal diameter (0.30) (table 6). The results are in agreement with the studies carried out[28] in

Eucalyptus globulus who reported low heritability for DBH during field evaluation of 8 sub - races. Similarly low to moderate heritability was also recorded in *Eucalyptus globulus* and in *Eucalyptus nitens*[29] for different genetic parameters and low to moderate heritability for height and tree volume in *Eucalyptus grandis*[30]. The authors also reported that the heritability varied with changing environment and age.

Though heritability in broad sense may give useful indication about the related value of selection, heritability along with associated genetic gain should be considered together for valid, reliable and useful conclusion. In the current study, the trend of genetic advance as per cent of mean was maximum in volume index (15.21) followed by plant height (6.21) and basal diameter (4.40) (table. 6) indicating a wide scope for genetic improvement in the species. The findings of current study are in line[31] in *Heracleum candicans*. In a holistic view, the existence of adequate variability for different growth attributes coupled with low to moderate heritability indicates the possibility for identification of the best family suitable for commercial utilization.

Conclusion

A total of twenty candidate plus trees have been selected in three dominant *Melia dubia* growing areas of Tamil Nadu by subjective grading system. It is revealed that the three progenies *viz.*, FCRIMD 11, FCRIMD 14 and FCRIMD 15 proved superior in terms of important biometric attributes investigated. Considering this experiment in to account three progenies *viz.*, FCRIMD 11, FCRIMD 14 and FCRIMD 15 are brought under sharp focus for immediate utilization and deployment for future improvement programme. The variability study *indicated* that volume index, registered highest phenotypic coefficients of variances (PCV) and genotypic coefficients of variances (GCV). The application of D^2 clustering technique in *Melia dubia* genetic resource resolved the twenty progenies into six clusters. The *intra* and *inter* cluster distance indicated the presence of wider genetic distance between *Melia dubia* progenies. Among the growth attributes volume index contributed maximum to genetic divergence.

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