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Research Article

GENETIC DIVERSITY OF *MELIA DUBIA* USING ISSR MARKERS FOR NATURAL POPULATIONS AND PLANTATIONS

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Abstract- *Melia dubia* Cav. (Family: Meliaceae) is a deciduous tree species native to India. It is an important plantation species with short rotation and multipurpose uses, highly valued as a pulpwood and plywood. Genetic variation was assessed in eleven natural populations and seven plantations across eight districts of Karnataka comprising 232 samples through 15 ISSR markers. At species level, genetic diversity estimates *viz*., Percentage polymorphism (94.6), percentage of polymorphic loci (PPL) (98.8), observed number of alleles (Na=1.98), effective number of alleles (Ne= 1.59), Nei's gene diversity (H) (0.34±0.15) and Shannon's information index (I) (0.51±0.19) were found to be high. In individual populations H ranged from 0.10±0.19 to 0.32±0.18 and I ranged from 0.15±0.26 to 0.47±0.25. Among different natural populations, Bhadravati exhibited the highest level of variability while in plantations Hunsur had maximum variability. Analysis of Molecular Variance showed that much of the genetic variation resided within the populations (68%) than among populations. The dendrogram obtained by using Unweighted Pair-Group method with Arithmetic average did not reflect geographical sub clustering of genetic diversity except for few populations. Based on the genetic variability found, superior seed sources can be identified and tree improvement strategies could be developed for conservation and further improvement of the species.
Keywords- *Melia dubia*, ISSR markers, Genetic Diversity, Superior seed sources

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Introduction

Melia dubia Cav. synonym *Melia composita*, (Family – Meliaceae), is a large deciduous, fast growing tree species native to India. Outside India, it is found in Sri Lanka, Malaysia, Java, China and Australia [1]. In Karnataka state, it is predominantly found in Southern parts [2] and commonly known as Malabar neem. The tree reaches 20 to 25 m height with a straight bole of about 9 to 12 m and nearly 1.5 m in girth at breast height. It grows well on variety of soils, however in deep fertile sandy loam soils it shows optimum growth. The timber is used for packing cases, ceiling planks, building purposes, agricultural implements, match boxes and Kattamarans [3]. The tree with the minimum size of 40cm girth is saleable at the minimum rate of Rs 2000 per ton for match, veneer and pulp industry [1]. It is an ideal species for plywood and pulpwood industry apart from being extensively used in afforestation [1].Considering its fast growing ability and multipurpose uses, it is also accepted as an ideal agroforestry species. Large scale plantations of *M. dubia* have been raised by various state forest departments and private entrepreneurs in Southern India [4]. Fruits (drupes) of *M. dubia* are used for propagation. The trees growing in southern part of India produces fruits with hard endocarp, due to which, the germination is inherently low and varies from 14 -34.5% [5-7]. During the field survey, it was observed that trees in general were found to be scattered. Most of these isolated trees had profuse fruiting which formed the source for raising plantations. The species is reported to be predominantly self-fertilized [8]. We believe that the progenies raised from such seeds may harbour low diversity. Despite its large scale cultivation and its importance, there is no information available on the extent of genetic diversity existing in this species. Documentation of genetic variation in different populations of *M. dubia* would facilitate in carrying out programmes aimed at its improvement, conservation, sustainable management and utilisation. For this, suitable molecular markers are required which can reliably assess existing genetic variation. In the early 1990's, the 'Inter-Simple sequence repeat (ISSR)' markers belonging to a class of multilocus, dominant genetic markers were independently developed by several research groups [9-12]. The generation of ISSR markers makes use of microsatellite sequences that are highly variable, ubiquitously distributed across the genome, higher reproducibility and costs less in terms of time and money compared to AFLPs. All these properties make ISSR an ideal genetic marker for various genetic studies, most notably on genetic variation/diversity [13, 14], DNA fingerprinting [15] and phylogenetics [16].

Considering its self-pollinating nature, fragmented natural populations and low germination, the present study was aimed to assess the genetic diversity of *M. dubia* existing in natural populations as well as in plantations in Karnataka.

Materials and methods

Extensive survey was carried out in eight districts of Karnataka (which fall under four different agroclimatic zones), 11 natural populations and seven plantations were identified and a total of 232 trees were selected to assess the genetic variability. In the present study, natural populations refers to those trees growing in forest areas, isolated trees along roadside and farmer's fields, which would not have been planted but grown naturally. In plantations, trees were selected randomly at a minimum distance of 50 m. The samples were collected from Bangaluru (IWST), Nelamangala (NEL), Hunsur (HNSR), Periyapatna (PRPT), Kushalnagar (DBRE), Gundlupet (GNDPT), H D Kote (HDK), Ramnagar (RAM), Shimoga (SMG), Bhadravati (BDR), Kollegal (KOL) and Hiriyur (HIR) areas, distance ranging from 11°51'22.5" N to 14°3'15.37" N [Table-1].

Sample collection: Fully matured healthy leaves were collected, labelled, cleaned, dried in silica gel and later stored in freezer at -20ºC.

DNA isolation: DNA was extracted from all the 232 samples and quantity and quality of extracted DNA was checked using Biospectrophotometer (Eppendorf, Germany) and agarose gel electrophoresis [17].

DNA amplification and primer selection: The amplification was performed in a total volume of 25 µL containing 30 ng/µL of template DNA, 0.2 mM of each of dNTPs, 1.5 mM of $MgCl_2$, 2U of Taq polymerase, 10X PCR buffer and Milli-Q water [17]. The amplifications were conducted in thermal cycler (Eppendorf Mastercycler Gradient, Germany) under following conditions. The initial cycle of denaturation at 94°C for 3 minutes, followed by 39 cycles of 94ºC for 30 seconds, 45-61°C (depending on the primer used) for 30 seconds, 72ºC for 1 minute and final extension cycle of 72ºC for 10 minutes. Amplified products were mixed with 4 µL of 1X loading dye (bromophenol blue) and run for two and half hours at 50 V in 2% agarose gel immersed in 1X TAE buffer [2M Tris base: 242.28 g, Glacial acetic acid 57.1 ml and 0.5 M Na_2EDTA, 100 ml (pH 8.0)]. After running, the gel was visualized and photographed under Gel documentation system (Herolab, Germany). From the 100 primers screened (UBC 801 to 900), finally 15 primers showing clear bands and high polymorphism were selected [Table-2]. The annealing temperatures of the selected primers were also standardized.

Scoring and analysis of data: Robust and unambiguous bands were evaluated excluding the low intensity and coalescing bands on the basis of size comparison with 100 bp plus DNA ladder (Thermo scientific). The ISSR fragments were encoded using binary method of Wendell and Weeden (1989) for presence (1) or absence (0) of bands. Diversity for following parameters; Percentage of Polymorphic Loci (PPL), observed number of alleles, effective number of alleles, Nei's gene diversity (H) and Shannon diversity index (I) [18, 19] were estimated using POPGENE v1.32 [20]. The parameters *viz*. PPL, H and I were calculated at population level (intrapopulation) and species level (interpopulation). The analysis of molecular variance (AMOVA) was carried out using GenAlEx software [21]. Dendrogram was drawn based on Nei's genetic distances using Unweighted Pair Group Method with Arithmetic Mean (UPGMA)

Results

The annealing temperatures for most of the primers selected for the study were 2 to 3ºC higher than the melting temperature. The fifteen primers selected, generated 166 reproducible bands of which 157 (94.6%) were polymorphic and the sizes ranged from 167 to 2054 bp. The number of bands varied from 4 (UBC 845) to 18 (UBC 810). Out of the 15 primers, eight of them showed 100 percent polymorphism, whereas lowest percent polymorphism (84.6) was observed with primer UBC 811 [Table-2]. At species level diversity estimates in terms of PPL (98.8%), H (0.34) and I (0.51) were found to be high [Table-3]. Diversity in terms of PPL, gene diversity and Shannon information index respectively were higher in plantations (63.51, 0.24 and 0.36) as compared to natural populations (50.77, 0.21 and 0.30) [Table-4]. Among the natural populations, BDR (NP) exhibited the highest level of variability while population SMG (NP) possessed the lowest value of variability. In case of plantations, HNSR (P) [Fig-1] had maximum variability whereas KNK (P) had minimum variability [Table-4]. Among individual populations, the PPL ranged from 24.70 (SMG NP) to 83.73 (HNSR P). Nei's gene diversity (H) varied from 0.10±0.19 (SMG NP) to 0.32±0.18 (HNSR P). Shannon's information index (I) ranged from 0.15±0.26 (SMG NP) to 0.47±0.25 (HNSR P) [Table-4]. The values for observed number of alleles and effective number of alleles followed the same trend. AMOVA revealed that 68% variation resided within the populations while 32% among populations [Table-5]. The matrix of Nei's (1978) unbiased measures of genetic distance is presented in [Table-6]. The smallest genetic distance was measured between NALL (P) and PHIR. (P) (0.06) while largest distance was found between SMG (NP) and KNK (P) (0.37). The UPGMA dendrogram constructed based on Nei's genetic distance (Nei, 1978) [Fig-2] showed two major clusters and clustering of the most of the populations was not based on geographic distance. In sub clusters a few exceptions were found where clustering was based on geographic distance *viz*. KNK (P) and RAM (NP) were closer; GNDPT (NP) and HDK (NP) were clustered together. HNSR (NP), HNSR (P) and PRPT (P) clustered together and were geographically closer.

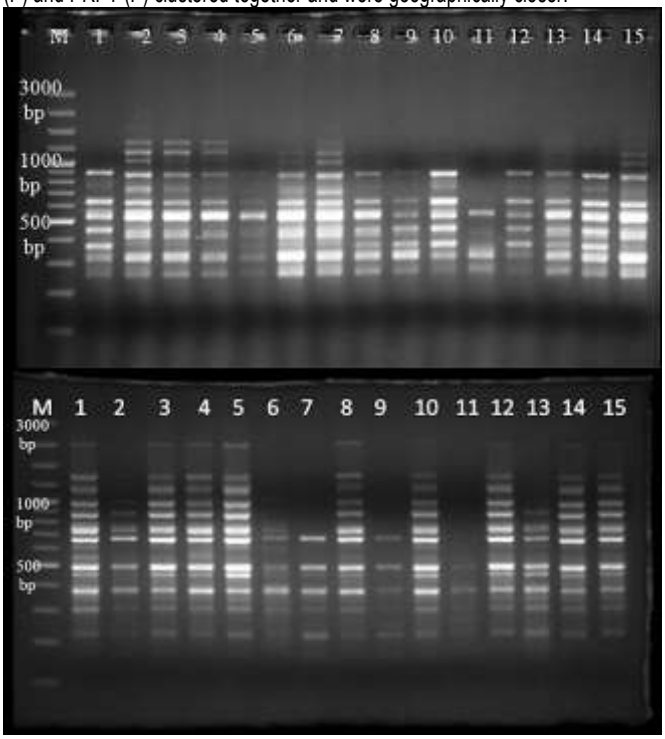

Fig-1 Gel electrophoresis pattern of amplified loci among 15 *M. dubia* genotypes of Hunsur plantation using primer UBC 810 (a) and UBC 880 (b)

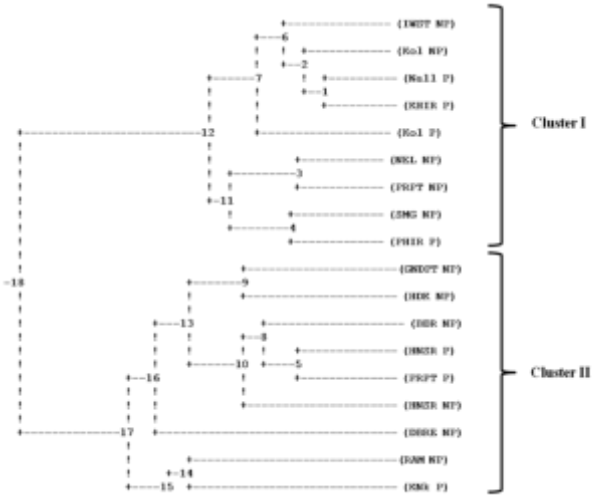

Fig-2 UPGMA dendrogram for 18 *M. dubia* populations based on Nei's (1972) genetic distance method

Discussion

A total of 232 *M. dubia* trees from eleven natural populations and seven plantations were analysed in this study. Fifteen selected dominant ISSR primers had produced different number of bands depending on the primer sequence and the extent of variation. Most of the primers showing high polymorphism contained di- nucleotide repeats *viz*. GA, CT, CA, GT, AC, AG and TC indicating abundance of these repeats in *M. dubia* genome. Similarly, abundance of di-nucleotide repeats has been reported in other species like *Curculigo latifolia, Populus cathayana, Medicago* species [22-24], whereas, abundance of tri-nucleotide repeats in *Azadirachta indica* [25] and tri and tetra repeat in *Tectona grandis* [26] have been reported. The size of the amplified DNA fragments ranged from 167 to 2054 bp [Table-2]. Similar trend was observed in *C. latifolia, Haloxylon ammodendron* and *Hippophae rhamnoides* [22, 27, 28]. However, in *A. indica*, also of Meliacceae family, band size ranged between 125 to 5500 bp [29].

Table-1 *Details of 18 Melia dubia populations identified across Karnataka*

SN	Location	Code	District	Trees selected	Latitude (North)	Longitude (East)	Agroclimatic zone
1	IWST campus, Bangalore	IWST NP	Bangalore Urban	9	13°00'41.3"	77°34'17.6"	Eastern Dry zone
2	Nelamangala	NEL NP	Bangalore Rural	10	13°00'39.9"	77°34'14.9"	Eastern Dry zone
3	Hulyal, Hunsur	HNSR NP	Mysore	7	12°23'0.96"	76°21'38.4"	Southern transition zone
4	Baslapura, Periyapatna	PRPT NP	Mysore	8	12°22'36.0"	76°08'44.6"	Southern transition zone
5	Dubare Elephant Camp, Kushalnagar	DBRE NP	Kodagu	3	12°22'07.7"	75°54'15.2"	Southern transition zone
6	Maddur, Gundlupet	GNDPT NP	Chamrajnagar	8	11°51'22.5"	76°40'24.7"	Southern dry zone
7	Heggadadevana Kote (H D Kote)	HDK NP	Mysore	7	12°07'20.7"	76°16'50.4"	Southern dry zone
8	Ramanagara	RAM NP	Ramanagara	6	12°41'39.64"	77°14'48.27"	Eastern dry zone
9	Shettihalli Wildlife range, Shimoga	SMG NP	Shimoga	11	13°55'36"	75°25'46.2"	Southern dry zone
10	Channagiri Range, Bhadravati	BDR NP	Shimoga	9	13°50'28.7"	75°51'26.2"	Southern transition zone
11	Gundal dam, Wild life Range, Kollegal	KOL NP	Chamrajnagar	10	12º04'30.6"	77º12'20.1"	Southern dry zone
12	Arepalya, Kollegal	KOL P	Chamrajnagar	20	12°04'30.6"	77°12'20.1"	Southern dry zone
13	Chennabasappa's Farm Hulyal, Hunsur	HNSR P	Mysore	21	12°23'0.96"	76°21'38.4"	Southern transition zone
14	Galli Bore Estate, Kamplapura, Periyapatna	PRPT P	Mysore	20	12°23'31.9"	76°10'08.8"	Southern transition zone
15	Kanakapura	KNK P	Ramanagara	20	12°33'30.6"	77°25'30.17"	Eastern dry zone
16	Yeshwantpur Nursery, Nallal, Hoskote	NALL P	Bangalore Rural	25	13°06'8.20"	77°50'44.04"	Eastern dry zone
17	Pooja Farm, Hariyabbe, Hiriyur	PHIR P	Chitradurga	19	14°3'15.37"	76°49'25.99"	Central dry zone
18	Kumar's Farm, Ishweregerre, Hiriyur	KHIR P	Chitradurga	19	14°1'22.04"	76°44'20.42"	Central dry zone

Note: NP – Natural populations, P-Plantations

Table-2 *Fifteen ISSR marker codes, sequence, Tm, Ta, percent polymorphism (%) and range of amplification*

SN	Marker code	Sequence (5'-3')	Tm (°C)	Optimum Ta (°C)	Total no. of bands	No. of polymorphic bands	Percent polymorphism (%)	Range of amplification (bp)
1	UBC-809	AGAGAGAGAGAGAGAGG	46.6	50.0	6	6	100	316-386
2	UBC-810	GAGAGAGAGAGAGAGAT	42.9	45.0	19	18	94.7	222-1419
3	UBC-811	GAGAGAGAGAGAGAGAC	43.3	45.0	13	11	84.6	182-1388
4	UBC-813	CTCTCTCTCTCTCTCTT	45	50.4	8	8	100	190-1265
5	UBC-823	TCTCTCTCTCTCTCTCC	47.5	50.0	8	7	87.5	222-1792
6	UBC-840	GAGAGAGAGAGAGAGAYT	45.8	47.0	17	16	94.1	182-1388
7	UBC-845	CTCTCTCTCTCTCTCTRG	43.4	47.0	4	4	100	466-1144
8	UBC-847	CACACACACACACACARC	54.2	53.0	9	9	100	262-1357
9	UBC-855	ACACACACACACACACYT	60.2	61.0	10	9	90	167-1361
10	UBC-857	ACACACACACACACACYG	57.1	58.0	7	7	100	271-1894
11	UBC-864	ATGATGATGATGATGATG	51.2	52.0	12	12	100	295-1484
12	UBC-880	GGAGAGGAGAGGAGA	49	44.7	16	15	93.7	185-2054
13	UBC-888	BDBCACACACACACACA	52.3	55.4	18	16	88.8	199-1652
14	UBC-890	VHVTGTGTGTGTGTGTG	51.8	52.0	8	8	100	218-673
15	UBC-891	VHVGTGTGTGTGTGTGT	51.8	55.0	11	11	100	214-1668

Note: Tm- melting temperature, Ta- annealing temperature

Table-3 *Different diversity parameters analysed in 18 populations (n=232) in M. dubia*

Parameters	Overall diversity estimates
PPL	98.80%
Observed number of alleles	1.98±0.10
Effective number of alleles	1.59±0.32
H	0.34±0.15
I	0.51±0.19

Table-4 *Different diversity parameters, PPL, observed number of alleles, effective number of alleles, H and I analysed for 18 populations of M. dubia using ISSR primers*

SN	Population	PPL	Observed number of alleles±SD	Effective number of alleles±SD	H±SD	I±SD
1	IWST(NP)	58.43	1.58±0.49	1.46±0.42	0.25±0.22	0.36±0.32
2	NEL(NP)	56.63	1.57±0.50	1.44±0.43	0.24±0.22	0.34±0.32
3	HNSR(NP)	66.27	1.66±0.47	1.51±0.43	0.28±0.22	0.40±0.31
4	PRPT(NP)	51.20	1.51±0.50	1.39±0.41	0.21±0.22	0.31±0.31
5	DBRE(NP)	49.40	1.49±0.50	1.34±0.39	0.20±0.21	0.29±0.30
6	GNDPT(NP)	52.41	1.52±0.50	1.34±0.39	0.19±0.21	0.29±0.30
7	HDK (NP)	36.75	1.37±0.48	1.27±0.40	0.15±0.21	0.22±0.30
8	RAM(NP)	30.12	1.30±0.46	1.23±0.38	0.13±0.20	0.18±0.29
9	SMG(NP)	24.70	1.25±0.43	1.18±0.35	0.10±0.19	0.15±0.26
10	BDR(NP)	69.88	1.70±0.46	1.52±0.40	0.29±0.21	0.42±0.29
11	KOL(NP)	62.65	1.63±0.49	1.48±0.41	0.26±0.22	0.38±0.31
	Mean	50.77	1.51	1.38	0.21	0.30
12	KOL(P)	60.24	1.60±0.49	1.41±0.39	0.23±0.21	0.34±0.30
13	HNSR(P)	83.73	1.84±0.37	1.56±0.36	0.32±0.18	0.47±0.25
14	PRPT(P)	78.92	1.79±0.41	1.52±0.36	0.30±0.19	0.44±0.26
15	KNK(P)	41.57	1.42±0.49	1.28±0.38	0.16±0.20	0.24±0.29
16	NALL(P)	71.69	1.72±0.45	1.48±0.36	0.28±0.19	0.41±0.28
17	PHIR(P)	53.01	1.53±0.50	1.34±0.38	0.20±0.21	0.29±0.29
18	KHIR(P)	55.42	1.55±0.50	1.37±0.38	0.21±0.21	0.31±0.30
	Mean	63.51	1.64	1.42	0.24	0.36

Note: PPL- Percentage of Polymorphic loci, H- Nei's gene diversity, I- Shannon's information index, SD-standard deviation

Table-5 *AMOVA for 18 populations, 11 natural populations and seven plantations of M. dubia with 15 ISSR markers*

Source	Df	SS	MS	Est. Var.	%	P-value
Among 18 Population	17	1987.600	116.918	7.907	32%	0.001
Within Population	214	3540.103	16.543	16.543	68%	
Total	231	5527.703		24.450	100%	
Among 11 natural population	10	712.609	71.261	6.907	29%	0.001
Within natural population	76	1289.827	16.971	16.971	71%	
Total	86	2002.437		23.879	100%	
Among seven plantations	6	1177.794	196.299	8.702	35%	0.001
Within plantations	138	2250.275	16.306	16.306	65%	
Total	144	3428.069		25.008	100%	

Note: Significance test (999 permutations), Df-degrees of freedom, SS-sum of square, MS-mean sum of square, Est. Var.-estimated variance, %-percentage of Variation

Table-6 *Nei's (1972) unbiased measure of genetic distance for 18 populations of M. dubia*

	IWST (NP)	KOL (NP)	NEL (NP)	GNDPT (NP)	HDK (NP)	RAM (NP)	SMG (NP)	BDR (NP)	PRPT (NP)	HNSR (NP)	NALL (P)	PHIR (P)	KHIR (P)	KOL (P)	HNSR (P)	PRPT (P)	KNK (P)	DBRE (NP)
IWST (NP)	****																	
KOL (NP)	0.06	****																
NEL (NP)	0.11	0.11	****															
GNDPT (NP)	0.22	0.23	0.17	****														
HDK (NP)	0.19	0.20	0.14	0.08	****													
RAM (NP)	0.29	0.29	0.22	0.12	0.17	****												
SMG (NP)	0.17	0.14	0.13	0.24	0.16	0.35	****											
BDR (NP)	0.20	0.18	0.15	0.08	0.11	0.16	0.20	****										
PRPT (NP)	0.13	0.12	0.06	0.21	0.16	0.31	0.13	0.17	****									
HNSR (NP)	0.19	0.20	0.15	0.14	0.17	0.18	0.24	0.12	0.14	****								
NALL (P)	0.06	0.06	0.10	0.25	0.19	0.27	0.14	0.20	0.09	0.18	****							
PHIR (P)	0.08	0.07	0.12	0.29	0.21	0.33	0.14	0.23	0.11	0.21	0.05	****						
KHIR (P)	0.12	0.12	0.08	0.20	0.14	0.29	0.08	0.18	0.09	0.18	0.12	0.09	****					
KOL (P)	0.09	0.07	0.12	0.18	0.15	0.26	0.12	0.16	0.11	0.17	0.08	0.06	0.08	****				
HNSR (P)	0.23	0.21	0.20	0.14	0.21	0.15	0.32	0.09	0.24	0.12	0.24	0.26	0.25	0.20	****			
PRPT (P)	0.18	0.17	0.15	0.08	0.12	0.10	0.22	0.08	0.18	0.11	0.19	0.21	0.17	0.14	0.06	****		
KNK (P)	0.28	0.25	0.23	0.14	0.21	0.14	0.37	0.15	0.29	0.21	0.28	0.34	0.31	0.23	0.15	0.09	****	
DBRE (NP)	0.25	0.23	0.20	0.19	0.26	0.22	0.32	0.16	0.23	0.15	0.25	0.31	0.27	0.27	0.16	0.14	0.16	****

Populations of *M. dubia* possessed high level of polymorphism (157 polymorphic bands detected by fifteen primers). At species level, *M. dubia* had high genetic diversity measures *viz*. PPL was 98.8%, however, using RAPD markers moderate level of diversity was observed in other members of Meliaceae family like *Melia azedarach* (51.5%) [30] and *A. indica* (68.4%) [29]. Nei's gene diversity was 0.34 and Shannon's information index was 0.51 where as in *Swietenia macrophylla* high H (0.45) was reported [31]. In other cross-pollinated species, high level of H (0.36) and I (0.54) were reported in *T. grandis* [26]. However lower level of H (0.29 and 0.28) and I (0.44 and 0.43) were reported in other tropical species such *as G. arborea* and *P. pinnata* [32, 33]. Among 11 natural populations, highest diversity was observed in BDR whereas lowest diversity in SMG population [Table-4]. Though both the populations are geographically nearer, it is of importance to mention that in case of Bhadravati the trees were well dispersed in the natural forest compared to Shimoga, where they were found along the forest road side. In plantations, HNSR (P) had showed high diversity and lowest was found in KNK (P). When compared to natural populations plantations showed higher genetic diversity. This phenomenon occurs when plantations are raised from germplasm collected from diverse populations in its native range. Similarly, genetic diversity was found higher in plantations compared to natural populations in *Neolamarckia cadamba* and *G. arborea* [34, 32]. AMOVA based on UPGMA method revealed 68% of the total variation resided within the natural populations of *M. dubia* whereas 32% variation among populations. Similarly, high variation was observed within (65%), than among (35%) populations in plantations. However, within population variation was more in natural populations compared to plantations. In *M. dubia* it has been reported that one of the major mode of seed dispersal is through herbivores as they feed on the fruits [2]. This might have resulted in high diversity within natural populations. Species whose seeds are dispersed by animal ingestion or by wind maintain high levels of within-population genetic variability [28, 35]. High variation within populations has been reported in other Meliaceae *members, S. macrophylla, M. azedarach* [31, 30] and in other tree species like; *Populus tremuloides, Abies nephrolepis, T. grandis* and *Prosopis cineraria* [20, 36, 26, and 37]. The data for *M. dubia* agrees with general observation that tree species, maintain most of their variation within the populations [38]. Cluster analysis revealed that the natural populations were not grouped according to the geographical distance except for GNDPT (NP) (11º51'22.5") and HDK (NP) (12º07'20.7"). In plantations, PRPT (12°23'31.9") and HNSR (12º23'0.96") which are located geographically closer also grouped together. Similarly no correlation between genetic distance and geographical distance have been reported in natural populations of number of species *viz*., *C. latifolia, Enterolobium contortisiliquum, Theobroma speciosum* and *H. rhamnoides* [22, 39, 40, 28]. However, correlation between genetic distance and geographical distance has been reported in other species like *G. arborea, Tectona grandis*, P. *pinnata* and *Acacia senegal* [32, 26, 33, 41]. Plantations of HNSR and PRPT clustered with natural population of HNSR and KNK plantation clustered with natural population of RAM. This could be because the seed source for raising plantation might have been from above natural populations. Such pattern was not observed in other plantations. This may be attributed to variation in source of origin of planting material [34]. The present study is the first attempt to analyze genetic variation in natural populations and plantations of *M. dubia*. It revealed over all high genetic diversity at species level. When compared to natural populations, the diversity estimates were higher in plantations, which may be due to fragmentation of populations and occurrence of isolated trees. It has been reported that *M. dubia* is predominantly self-pollinating species, however, large intra populations variation was observed which was similar to the other tree species that are outbreeding. In natural populations, BDR (NP) showed highest diversity followed by HNSR (NP) and KOL (NP) whereas in plantations HNSR (P) was found to be most diverse followed by PRPT (P) and NALL (P). Being a self-pollinating species, it is suggested to use germplasm from more than one population while raising plantations so that broad genetic base is maintained.

Conclusion

Genetic diversity assessed from eleven natural populations and seven plantations across eight districts of Karnataka revealed over all high genetic diversity at species level. Analysis of Molecular Variance showed that much of the genetic variation resided within the populations (68%) than among populations. Cluster analysis did not reflect geographical sub clustering except for few populations.

Application of research: This study would be helpful in selection of superior seed sources for raising plantations and forming a base for initiating tree improvement programs for this species.

Research Category: Genetic diversity

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