

Studies on Growth Performance and Variance Components in *Madhuca Indica* Genotypes

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Abstract— During 2012, in the month of August, the study was undertaken at School of Forestry and Environment, SHUATS, Allahabad, Uttar Pradesh, India, to ascertain the growth performance and variance components of *Madhuca indica* genotypes. The experiments were conducted in open field environmental conditions using a Randomized Block Design with three replications. Twenty genotypes collected from candidate plus trees in different parts of Allahabad, Uttar Pradesh, and its adjoining areas were assessed for eleven traits namely seedling height, collar diameter, internodal length, number of leaves per seedling, leaf area, fresh and dry shoot weight, fresh and dry root weight, shoot/root ratio and total biomass of seedling. Based on the growth performance of these genotypes at six months after sowing of seeds in poly-bags, the following genotypes: G12, G20, G19, G9, and G13, in that order, were found to be superior to other genotypes. Since all the traits showed moderately high heritability and genetic gain, it appears that selection based on these traits would be effective for further improvement of the tree as such the tree being highly valued for having multipurpose uses and one among the tree borne oil seed plants.

Keyword: *Madhuca indica*, growth performance, variance components, genetic gain

I. INTRODUCTION

The ever increasing demand for edible oils in India has necessitated the immediate need for indigenous production of edible oil seeds to ensure self sufficiency and thus reduce importation and its attendant ill effects on the economy. Presently, production of edible oils is achieved through non-traditional oil crops such as Mahua (*Madhuca indica* J.F.Gmel) and other oil seed crops. Accordingly the plant is given prime priority and has assumed greater significance in the recent past. This is because it is seen as a potential source of edible oils with seed oil content varying from 33 to 43% by weight of the kernel (Kureel et al., 2009).

Mahua belongs to the family "Sapotaceae" and is one of those multipurpose forest tree species that provide food, fodder and fuel. It is widely distributed in the South Asian countries (Banerji and Mitra, 1996). Mahua is a deciduous, medium sized tree, attaining a height of 12-18 m, usually with a short bole and a girth of 2-4 m. The tree is mostly found in dry tropical and sub-tropical climate, performs well in the areas with rainfall between 800 and 1800 mm. The tree grows on a wide variety of soils but prefers sandy and alluvial soils (Troup, 1921). Mahua flowers are used as vegetable, for making cake, liquor and flower juice which is used in the treatment of neurotic disorder (Kureel et al., 2009). The derived liquor desired from the fermentation of flowers is considered to be a tonic and nutritive.

The Genus *Madhuca* includes more than 800 tree species many of which are used for the production of latex. There are about 84 species of Mahua, out of which *Madhuca latifolia*, *Madhuca longifolia*, *Madhuca butyracea* (Local name: phulwara), *Madhuca neriifolia/malabarica*, *Madhuca bourdillonii* are commonly found in India. Few species have also been found in Malaysia, Pakistan, Sri-Lanka, Australia and New Guinea. Recently, four new species i.e. *M. chai-ananii*, *M. Chiangmaiensis*, *M. Klackenbergii* and *M. Smitinandii* have also been isolated from Thailand (Gupta, Choudhary and Sharma, 2012). Biodiesel producers are looking for alternative feed-stocks which are non- agricultural and non-food crops, and *Madhuca indica* has the ability to substitute the requirement of low cost feed-stock with the potential for high oil seed production and diesel comparable characteristics and the added benefit of an ability to grow on marginal land. However, studies and information on utilization of the available variability for genetic improvement in this aspect are scanty. Hence, it is important to identify superior genotypes having adequate variability in order to utilize them in tree improvement programme. With this background a study was initiated in School of Forestry and Environment, SHIATS, Allahabad, Uttar Pradesh to assess the growth performance and variance components of *Madhuca indica* genotypes.

II. MATERIALS AND METHODS

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The experiments were conducted, during 2012, in the month of August, in the Forest Nursery of SHIATS, located at 25° 28'N latitude and 81° 55'E longitude. The area is situated at an altitude of 98 m average mean sea level and enjoys sub-tropical type of climate. The experiments were conducted in open field environment using a Randomized Block Design with three replications. From natural populations, plantations and roadside avenues in different locations of Allahabad, Uttar Pradesh and its adjoining areas, fresh and fully ripened open pollinated seeds of twenty genotypes/candidate plus trees (CPTs) of *Madhuca indica* were collected and used in this investigation (Table 1). Biometric traits such as height, Diameter at Breast Height (DBH), seed length, seed width, straightness of trees, non-forked cylindrical bole and free from insect-pests were considered for selection of superior genotypes/candidate plus trees (Pitcher and Dorn, 1967). Candidate plus tree and four comparison trees (comparison made by characters of trees such as height, DBH, form, age, and crown expansion almost of same size and shape free from diseases and insect pests representing each stand were selected and the above observations were recorded for both candidate and comparison trees. Out of these, the best was selected as plus tree/phenotypically superior genotype and marked with yellow paint after removing the bark. Uniform healthy seeds were graded to constitute the seed lot of each plus tree for experimental purposes for sowing in experimental site in open field environment for the evaluation of growth performance and variance components of the families of plus trees/genotypes (Table 1).

Healthy, fresh and fully matured seeds from each plus tree/genotype free from injury, disease and insect pests were collected and labeled separately. Observations on seeds length, seed diameter and weight of seeds (separately) were recorded manually. Hundred (100) seed weight was also recorded. Three replications of 40 seeds each in open field environment were used for the test. One hundred and twenty (120) seeds of each plus tree/genotype in open field environment were simultaneously sown in polythene bags (one seed per bag) of size 10 x 20 cm with 1:1:1 (fine textured sand: clayey soil: FYM) ratio at a distance of 10 cm from seed to seed and 30 cm from row to row at a depth of 1.0 cm during last week of July.

A uniform pre-treatment was given to the seeds by soaking in warm water, allowed to cool and kept soaked for 24 hours. Watering was done daily and polythene bags of size 10 x 20 cm were placed on raised beds to avoid water logging. Regular weeding was done as per

requirements. Observations on seedling height, collar diameter, inter-nodal length, number of leaves per seedling, leaf area was determined by leaf area meter for average number of leaves for average number of 10 seedlings per replication per treatment, shoot fresh and dry weight was determined by taking fresh weight and oven dry weight for averaged number of 10 shoots per replication per treatment on physical balance, similarly root fresh and dry weight was determined by taking fresh weight and oven dry weight for averaged number of 10 roots per replication per treatment on physical balance, shoot-root ratio and total biomass of seedling, were taken after one growing season. Twenty (20) seedlings per replication i.e. 60 seedlings per plus tree/genotype were taken for the purpose of the observations. Data were subjected to analysis of variance in order to test for significant differences among the different genotypes/seed sources (Panse and Sukhatme, 1967). Coefficient of variation and genetic gain were estimated using Burton and Devane (1953) method while heritability was calculated following Lush (1940) method.

Table 1: Passport details and Morphological observations of 20 Genotypes/Candidate Plus Tree (G1-G20) of *Madhuca indica*.

Notation	CPT No.	CPT (Location Name)	Latitude	Longitude	Height (m)	DBH (m)	Seed length (cm)	Seed diameter (cm)
G ₁	1/010	Hanumanganj	25° 42' N	82° 04' E	14.5	2.8	3.5	1.7
G ₂	5/010	Choorpur (Mankawar)	25° 18' N	81° 46' E	14.8	3.2	3.4	1.5
G ₃	6/010	Phulpur (Munshikapur)	26° 06' N	82° 06' E	16.2	2.5	3.4	1.6
G ₄	7/010	Jhansi (Sarianayat)	25° 25' N	81° 54' E	13.7	3.5	3.7	1.4
G ₅	8/010	Naini (Kharkawati)	25° 21' N	81° 51' E	17.1	2.9	3.5	1.7
G ₆	9/010	Naini (Chakka)	25° 27' N	81° 51' E	13.5	2.8	3.2	1.5
G ₇	10/010	SAhson (Badrahiikapur)	25° 29' N	81° 58' E	12.3	3.9	3.8	1.6
G ₈	13/010	Dandi (Mihabatganj)	25° 24' N	81° 50' E	17.5	2.3	3.1	1.5
G ₉	14/010	Jhalwa (Peepal)	25° 25' N	82° 46' E	14.2	3.6	3.4	1.8
G ₁₀	18/010	Mathewa (Agri-field)	25° 24' N	81° 51' E	15.6	3.2	3.9	1.7
G ₁₁	19/010	Gousi (Aravikalla)	25° 26' N	82° 05' E	12.3	4.1	3.2	1.6
G ₁₂	21/010	Phulpur (Malaka)	25° 33' N	81° 02' E	18.3	2.7	3.3	1.7
G ₁₃	24/010	Sarila	25° 46' N	79° 45' E	13.9	3.7	3.0	1.6
G ₁₄	27/010	Jalalpur (Khurd)	25° 36' N	81° 27' E	14.8	3.2	3.4	1.8
G ₁₅	28/010	Dandi (Muradpur)	25° 22' N	81° 51' E	17.3	3.6	3.2	1.8
G ₁₆	29/010	Naini (Tilakwar)	25° 19' N	81° 52' E	12.7	3.5	3.3	1.4
G ₁₇	31/010	Gaubania (Govti)	25° 14' N	81° 41' E	16.8	2.9	3.1	1.5
G ₁₈	32/010	Nawabganj	26° 56' N	82° 12' E	16.5	4.2	3.9	1.9
G ₁₉	33/010	Naini (Madhupur)	25° 43' N	82° 16' E	15.9	3.4	3.3	1.5
G ₂₀	34/010	Karhedahm (Theu)	25° 26' N	81° 50' E	18.2	3.7	3.6	1.8

III. RESULTS AND DISCUSSION

Morphological traits of the 20 genotypes are shown in Table 2. Analysis of variance revealed significant differences among the treatments. Genotype (G20) recorded maximum values for maximum of four traits which include collar diameter (6.73 mm), leaf area (43.20 cm²), fresh shoot weight (8.77 g) and dry shoot weight (2.14 g). Genotype (G12) recorded the highest values for three characters (fresh root weight (15.23 g), dry root weight (3.93 g) and total seedling biomass (23.00 g). Maximum value for seedling height (24.02 cm) and shoot/root ratio (0.80) was recorded for Genotype (G1). The highest values for internodal length (3.25 mm) and number of leaves per seedling (9.73) were observed from genotypes (G7) and (G15), respectively. Among the 20 genotypes, two genotypes (G20 and G12) had superior performance than the rest of the genotypes with respect to their highest recorded values for maximum four and three traits respectively as described above.

Variations refer to the observable differences in individual for a particular trait. These differences may partly be due to genetic factors and partly due to environmental effect. The observed value of a trait is the phenotypic value of that individual. The related magnitude of these components determines the genetic properties of any particular species (Jain, 1982). The extent of variations observed in seedling height (CV = 18.51 %), internodal length (CV = 18.89 %), fresh root weight (CV = 18.59), dry root weight (CV = 17.84 %), shoot/root weight (CV =15.54 %), and total seedling biomass (CV = 16.57 %) were found to be moderately high compared to other morphological traits (Table 2).

Table 2. Mean performance of morphological and biomass characters of 20 different *Madhuca indica* genotypes.

Genotypes	Seedling height (cm)	Collar diameter (mm)	Internodal length (cm)	No. of leaves per seedling	Leaf area (cm ²)	Fresh weight of shoot/seedling ^g (g)	Dry weight of shoot/seedling ^g (g)	Fresh weight of root/seedling ^g (g)	Dry weight of root/seedling ^g (g)	Shoot/Root ratio	Total biomass of seedling (g)
G ₁	13.33	4.27	1.93	7.33	31.30	5.37	1.46	7.60	1.92	0.80	12.97
G ₂	14.63	6.31	1.85	8.40	27.90	6.77	1.73	10.80	2.90	0.60	17.57
G ₃	13.00	5.05	2.15	6.33	22.40	7.57	2.00	14.37	3.76	0.54	21.93
G ₄	13.90	5.27	1.50	9.34	32.50	5.82	1.48	9.76	2.66	0.55	15.38
G ₅	17.85	4.95	2.50	8.87	28.50	7.90	2.04	14.60	3.85	0.53	22.50
G ₆	22.15	5.53	2.47	9.13	26.80	5.68	1.38	9.80	2.65	0.52	15.48
G ₇	18.18	5.90	3.25	6.00	20.70	6.27	1.52	13.28	3.59	0.42	19.55
G ₈	24.02	5.60	2.83	8.73	33.40	7.28	1.77	12.60	3.38	0.52	19.88
G ₉	17.07	3.48	1.95	9.00	28.40	8.04	1.98	11.97	3.18	0.62	20.01
G ₁₀	18.50	6.03	2.10	9.03	40.00	7.23	1.70	12.42	3.22	0.53	19.66

G ₁₁	18.83	6.17	2.29	9.20	27.00	5.41	1.39	10.77	3.01	0.46	16.18	
G ₁₂	19.75	5.33	2.57	8.00	26.50	7.77	1.91	15.23	3.92	0.49	23.00	
G ₁₃	22.88	6.27	2.34	9.63	31.60	7.44	1.77	13.00	3.48	0.51	20.44	
G ₁₄	13.14	4.93	1.48	9.10	25.30	3.43	1.32	8.53	2.33	0.57	13.97	
G ₁₅	21.11	6.00	2.12	9.73	25.20	7.00	1.55	11.83	3.12	0.50	18.83	
G ₁₆	18.31	4.73	2.44	8.80	38.30	5.74	1.39	11.44	3.13	0.45	17.18	
G ₁₇	14.27	4.48	1.93	7.73	24.50	5.95	1.44	8.67	2.24	0.64	14.62	
G ₁₈	19.00	5.13	2.23	8.47	36.70	7.16	1.74	12.73	3.39	0.51	19.90	
G ₁₉	20.10	6.33	2.27	9.27	40.00	7.60	1.81	14.90	3.77	0.48	22.50	
G ₂₀	18.73	6.73	1.94	9.53	43.20	8.77	2.14	13.60	3.56	0.60	22.37	
Mean	17.94	5.54	2.21	8.58	30.51	6.81	1.68	11.90	3.15	0.54	18.70	
Range	Minimum	13.00	4.27	1.48	6.00	20.70	5.37	1.32	7.60	1.92	12.97	
	Maximum	24.02	6.73	3.25	9.73	43.20	8.77	2.14	15.23	3.92	23.00	
Coefficient of variation		18.51	11.81	18.89	12.03	15.05	15.05	15.05	18.59	17.84	15.54	16.57
(CV %)												
S.E.D. (%)		1.59	0.53	0.20	0.62	0.40	0.70	0.19	1.30	0.34	0.05	1.92
C.D. at 5%		3.23	1.08	0.40	1.25	0.82	1.42	0.39	2.64	0.69	0.10	3.90

The trees have long gestation period, hence the study of their growth at juvenile age is imperative to determine the relative performance of the different genotypes (Chaturvedi and Pandey, 2005). If there exists a good correlation between the measured traits of genotypes at young ages in the course of tree development, prediction of growth at an advanced age may be possible. Two genotypes (G20 and G12) showed significantly difference, exhibiting highest values for more than one traits i.e. collar diameter (6.73 mm), leaf area (43.20 cm²), fresh shoot weight (8.77 g) and dry shoot weight (2.14 g) and (fresh root weight (15.23 g), dry root weight (3.93 g) and total seedling biomass (23.00 g) respectively at the age of six months and thus exhibiting the superiority of these genotype selections/locations over others. Similar findings in a two year old *Gmelina arborea* genotypes were reported by Burley and Wood (1976). On the basis of the total seedling biomass, G12, G20, G19, G9 and G13 genotypes were found to be superior to the other genotypes. However, to witness the elite genotype in the ongoing seedling trial, testing has to be carried out for a longer duration. Genotypes are also expected to do well in the controlled conditions as positive correlation between nursery and open field performance in a number of tree species (Gupta et al., 1991).

The analysis of variance proved that the values of all the traits were highly significant. Among the traits investigated, leaf area recorded higher genotypic (20.78 %) and phenotypic (20.84 %) coefficient of variation (Table 3). The other traits registered moderate values of Genotypic Coefficient of Variation and Phenotypic Coefficient of Variation. Among all the observed traits, the Genotypic Coefficient of Variation (GCV) was found to be slightly lower than the Phenotypic Coefficient of

Variation (PCV), indicated the lesser effect of environmental variation (Reddy et al., 2011)

Table 3. Genetic parameters estimation for different characters in 20 genotypes of *Madhuca indica*

Characters	Seedling Height (cm)	Collar Diameter (mm)	Internodal Length (cm)	Leaves/Seedling	Leaf Area (cm ²)	Shoot Fresh Weight (g)	Shoot Dry Weight (g)	Root Fresh Weight (g)	Root Dry Weight (g)	Shoot/Root Ratio	Total Biomass of Seedling (g)
Genetic parameters											
Genotypic variance (σ^2_g)	9.75	0.29	0.15	0.88	40.19	0.81	0.04	4.04	0.26	0.01	7.75
Phenotypic variance (σ^2_p)	13.57	0.71	0.21	1.44	40.44	1.54	0.10	6.59	0.43	0.01	13.30
Genotypic Coefficient of Variation	17.41	9.67	17.80	10.91	20.78	13.19	12.64	16.90	16.10	14.19	14.88
Phenotypic Coefficient of Variation	20.53	15.22	20.70	14.00	20.84	18.22	18.93	21.59	20.49	17.80	19.50
Broad Sense heritability (h^2) (%)	0.72	0.40	0.73	0.61	0.99	0.52	0.45	0.61	0.59	0.64	0.58
Genetic advance	5.45	0.70	0.69	1.50	13.02	1.34	0.29	3.24	0.81	0.13	4.38
Genetic advance as percent of mean (%)	30.40	12.67	31.25	17.51	42.68	19.67	17.39	27.25	25.55	23.29	23.41

Proper utilization of the observed variation in a species would be a prerequisite to know the extent of variation and its cause, whether it is due to genetic (heritable) or the environmental factors (non-heritable). The proportion of total variation which is heritable is termed as heritability in broad sense (Kumar, 2007). Knowledge of heritability magnitude gives us an idea about scope of effecting genetic improvement through selection. High genetic gain is usually more useful than the heritability value alone in predicting the resultant effect from selecting the best genotype/seed source. Therefore, a heritability estimate alone does not necessarily mean an increased genetic advance (Lush, 1937).

Among the traits studied, leaf area (0.99 %) followed by inter-nodal length (0.73 %) had maximum heritability (Table 3). The highest value for genetic gain was recorded for leaf area (42.68 %) followed by internodal length (31.25 %) and seedling height (30.40 %) while as all other traits registered moderate values. Heritability and genetic gain of all the investigated traits were found to range from high to moderate. Maximum heritability and genetic gain were recorded for leaf area. Similar findings were reported by Johnson et al. (1955) and Bhareti et al. (2011)

IV. CONCLUSION

On the basis of the total seedling biomass, G12, G20, G19, G9 and G13 genotypes were found to be superior in that order to the other genotypes. Among the traits investigated, the leaf area recorded higher genotypic and

phenotypic coefficients of variation. The GCV of the traits evaluated were lower than the PCV and thus indicating the lesser effect of environmental variation. Maximum heritability and genetic gain were recorded for leaf area. Since all the traits showed moderately high heritability and genetic gain, it appears that selection based on these traits would be effective. However, long term growth assessment of *Madhuca indica* genotypes for confirmation is recommended.

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