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Research Article

Genetic Dissection of Variability Using Morphological Traits in Drumstick (*Moringa oleifera* Lam.) Genotypes

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ABSTRACT

Twenty one moringa genotypes that were collected from different geographical regions of India were evaluated for variability, heritability and genetic advance for growth, yield and earliness characters and significant variations were recorded for the investigated traits. Widest range of variation was observed in pod length, number of pods per plant, single pod weight and pod yield per plant. Maximum genotypic and phenotypic coefficient of variation was observed for number of primary branches, pod length, number of pods per cluster, single pod weight and pod yield per plant. Higher value of heritability associated with high genetic advance as percent mean was observed for pod yield per plant, single pod weight, pod length, plant height, leaf length, pod girth, number of pod per cluster and number of branches per inflorescence. High heritability and genetic advance indicating additive gene action suggested that simple selection could be effective for the improvement of these traits.

Keywords: *Moringa, Variability, Heritability, Genetic advance.*

INTRODUCTION

Drumstick [*Moringa oleifera* Lam. (Syn. *M. pterygosperma Gaertn.*)] is one of the best known and most widely distributed and naturalized species of a monogeneric family Moringaceae with true diploid chromosome 2n=28. The genus *Moringa* has about 13 species of which two species viz., *M. oleifera* Lam. (syn. *M. pterygosperma* Gaertn.) and *M. concanensis* Nimmo occur in India and the former being the vegetable type (Panday et al., 2011). Drumstick is an important food commodity which has had enormous attention as the 'natural nutrition of the tropics'. It is an exceptionally nutritious vegetable tree with multiple uses and beneficial properties and has therefore been called a "miracle tree" (Fuglie, 1999) or "one of the world's most useful trees" (Lea, 2010).

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The miracle tree is a perennial softwood crop native to the sub-Himalayan ranges of India, Pakistan, Bangladesh and Afghanistan (Fahey, 2005). It is widely grown in the tropics of Asia, Latin America, the Caribbean, Florida and the Pacific Islands to West, East, and South Africa. India is the prime producer of Moringa (Drumstick) with an annual production of 2.20 to 2.40 million tonnes of tender fruits from an area of 38,000ha leading to the productivity of around 63 tonnes per ha.5 Among the different states, Andhra Pradesh leads in both area and production (15,665ha) followed by Karnataka (10,280ha) and Tamil Nadu (13250ha). In other states, it occupies an area of 4,613ha.

Moringa oleifera is a fast-growing, drought-resistant tree with many medicinal properties. Common names include moringa, drumstick tree (from the long, slender, triangular seed-pods), horseradish tree (from the taste of the roots, which resembles horseradish), and ben oil tree or benzolive tree. Flower favors cross pollination due to delayed stigma receptivity. The successful pollination requires large number of insect population, among which *Xylocopa* is most important. The zygomorphic gullet type flowers show a forenoon (6.00 h – 12.00 h) pattern of anthesis after which pollen anthesis takes place (7.00 h – 13.00 h) (Bhattacharya and Mandal, 2004). It is widely cultivated for its young seed pods and leaves, used as vegetables, for traditional herbal medicine and also used for water purification.

Moringa has many medicinal properties. Almost all parts *viz.*, root, bark, gum, leaf, fruit (pod), flower, seed and seed oil have been used for treatment of various inflammation and infectious diseases along with cardiovascular, gastrointestinal, haematological and hepatorenal, disorders (Singh et al., 2011). Flowers are used as stimulant, tonic and diuretic. They are useful in increasing the flow of bile. The seeds of *Moringa* are considered to be antipyretic, acrid, bitter (Oliveira et al., 1999) and reported to show antimicrobial activity. The seeds of *Moringa* are used as water purifier. The oil extracted from the seed known as "*Ben*" is used as lubricant in watches, for edible purpose and in cosmetics. The kernel of the seed is rich in crude protein, fatty oil and fiber. Leaves contain 4.0per cent moisture, 38.4per cent crude protein, 34.17per cent fatty oil, 3.5 per cent fibre and 3.2 per cent mineral matter.

Germplasm evaluation and characterization for economically important traits are basic prerequisite for crop improvement. For any crop improvement programme, evaluation of germplasm to assess the existing variability is the first step. Greater the variability present in the initial material better would be the chances for evolving desired types. A clear understanding of variability of various characters of the breeding materials is an asset to the plant breeder for selecting superior genotypes on the basis of their phenotypic expression. The diversity in moringa genotypes presents an opportunity for selection of superior types and improvement of different quantitative and qualitative characters. The determination of genetic variability and its partitioning into various components is necessary to have an insight into the genetic nature of yield and its components. In this regards, estimates of genotypic and phenotypic variance for various quantitative characters along with heritability and genetic advance expected by selection for yield and its components are useful in designing an effective breeding programme.

MATERIALS AND METHODS

The study has taken up in the education and research block of Department of biotechnology and crop improvement, College of horticulture, University of horticultural sciences, Bagalkot. Twenty-one genotypes of *Moringa oleifera* used in the present study were collected from different eco-geographical locations covering different states of India were studied in Randomized block design in three replications (Table 1). The observation were recorded for twenty one different quantitative morphological parameters viz., plant height, tree girth, number of primary branches, leaf length, petiole length, days to

flower initiation, inflorescence length, number of branches per inflorescence, flower size, number of pods per plant, pod length, pod girth, number of pods per cluster, number of pods per branch, days to pod initiation, days to pod maturity, single pod weight, number of seeds per pod, seed size, hundred seed weight and pod yield per plant. The data collected on all the characters were subjected to standard methods of analysis of variance (ANOVA) (Panse & Sukhatme, 1985). Genotypic and phenotypic co-efficient of variation were estimated according to Burton (1952) GCV and PCV were classified by Sivasubramanian and Madhamenon (1973). Heritability and genetic advance as per cent of mean was calculated based on Johnson et al. (1955).

Table 1: Details of the drumstick genotypes used in the experiment

Sr. No.	Name of the accession	Code	Area of collection	State of collection
1	PKM-01	MO_1	Periyakulam	Tamil Nadu
2	PKM-02	MO_2	Periyakulam	Tamil Nadu
3	Dhanraj	MO_3	Dharwad (UASD campus)	Karnataka
4	Bhagya (KDM-01)	MO_4	Bagalkot(UHSB campus)	Karnataka
5	Karwar-01	MO_5	Kumburda village, Karwar	Karnataka
6	Badami-02	MO_6	Badami	Karnataka
7	Mysore-01	MO_7	Mysore	Karnataka
8	Mysore-02	MO_8	Mysore	Karnataka
9	Mysore-03	MO_9	Mysore	Karnataka
10	Yelwala-01	MO_10	Shettinayakanahalli, Mysore	Karnataka
11	Shirdi-01	MO_11	Shirdi	Maharashtra
12	Tangi-01	MO_12	Tangi village	Orissa
13	Bhubaneshwar-01	MO_13	Bhubaneshwar	Orissa
14	Cuttack-01	MO_14	Cuttack	Orissa
15	Bagalkot-01	MO_15	Bagalkot	Karnataka
16	Thar-harsha	MO_16	Vejalpur, Godhra	Gujarat
17	Mandya-01	MO_17	Mandya	Karnataka
18	BG-1	MO_18	Bagalkot	Karnataka
19	BG-2	MO_19	Bagalkot	Karnataka
20	BG-3	MO_20	Bagalkot	Karnataka
21	BG-4	MO_21	Bagalkot	Karnataka

RESULT AND DISCUSSION

The analysis of variance revealed the existence of significant differences among the genotypes for all the traits, indicating the presence of considerable genetic variability among the experimental material under study (Table 2). Thus, there is a plenty of area and scope for the improvement of different quantitative and qualitative traits through selection. The tendency of individual genetic characteristics in a population to vary from one another. Similarly highly significant variation for all characters studied was reported by Raja and Bagle (2003), Selvakumari et al. (2013), Varma et al. (2019), Priya et al. (2019) and Balaguru et al. (2020). The mean performance, range and general mean of twenty one genotypes of drumstick for twenty one quantitative characters studied are presented in Table 3. Range of variation observed for all

the traits in the present study indicated the presence of sufficient amount of variation among the genotypes for all the characters studied.

Table 2: One- factor analysis of variance across 21 quantitative characters in drumstick genotypes

Sl. No.	Traits	MSS (genotypes)	Error	F-Value (Genotypes)
	d. f	20	40	
1	Plant height (cm)	9849.001	300.0813	32.82111*
2	Tree girth (cm)	52.52569	4.18565	12.54899*
3	Number of primary branches	1.337714	0.529429	2.526713*
4	Leaf length (cm)	92.09041	3.177532	28.981743*
5	Petiole length (cm)	4.734206	0.316497	14.95814*
6	Days to flower initiation	208.9549	6.403143	32.63317*
7	Inflorescence length (cm)	10.18029	2.799306	3.63672*
8	Number of branches per inflorescence	6.603302	0.276063	23.9195*
9	Flower size (mm)	6.11591	0.996367	6.138211*
10	Number of pods per plant	717.4665	20.51368	34.97502*
11	Pod length (cm)	612.8009	10.92919	56.07009*
12	Pod girth (mm)	14.73018	0.440962	33.40467*
13	Number of pods per cluster	0.577206	0.020063	28.76899*
14	Number of pods per branch	13.6313	0.971111	14.03681*
15	Days to pod initiation	17.89349	1.449302	12.34629*
16	Days to pod maturity	59.09283	8.577206	6.889519*
17	Single pod weight (g)	4283.26	32.17838	133.1099*
18	Number of seeds per pod	27.20971	2.041619	13.32752*
19	Seed size (mm)	1.745071	0.375123	4.651999*
20	Hundred seed weight (g)	4.41905E-05	1.23582E-05	3.575819*
21	Pod yield per plant (Kg)	31.59736	0.770268	41.02127*

***5 per cent significance**

Comparative variability of traits is evaluated by estimating the genotypic coefficient of variation (GVC) and the phenotypic coefficient of variation (PCV). Greater the variability in a population, there are the greater chances for effective selection for desirable types. The estimates of variances due to these three components for twenty one quantitative characters are represented in table 4. In the present study, the phenotypic variance ranged between 0.206 (number of pods per cluster) to 3483.055 (plant height). The genotypic variance ranged between 0.186 (number of pods per cluster) to 3182.973 (plant height). The environmental variance ranged between 0.020 (Number of pods per cluster) to 300.081 (plant height). In general, phenotypic variance was higher in magnitude than genotypic variance for all characters and the genotypic variances were higher in magnitude over respective environmental variances for all the characters. The magnitude of phenotypic coefficient of variation was higher than corresponding genotypic coefficient of variation for all the 21 quantitative parameters, which indicated prime role of environment on the character expression. With respect to the genetic variability components such as PCV and GCV, the value of 0-10 per cent indicate low genetic variation which is represented by the traits flower size (9.176) and days to pod maturity (8.791) (Table 4). 10-20 per cent indicates moderate variation which is present in most of the traits under study. The value of >20 per cent indicate higher genetic variation which is present in the traits like number of primary branches (20.269), pod length (27.643), number of pods per cluster (28.636), single pod weight (34.858) and pod yield per plant (37.144). This showed similarity with the studies of Raja and Bagle (2003), Selvakumari et al. (2013), Varma et al. (2019), Priya et al. (2019) and Balaguru et al. (2020).

Heritability is the portion of phenotypic variation which is transmitted from parent to the progeny. High heritability was recorded for all the characters except number of primary branches, inflorescence length, seed size and hundred seed weight (Table 3). The higher broad sense heritability was recorded for pod length (94.8 per cent) followed by pod yield per plant (93.0 per

cent), number of pods per plant (91.9 per cent), pod girth (91.5 per cent), plant height (91.4 per cent), days to flower initiation (91.3 per cent) etc., Higher heritability in broad sense showed that large proportion of phenotypic variance was attributable to the genotypic variance and these traits were less affected by the environment. The least heritability was reported for number of primary branches (33.7 per cent) followed by hundred seed weight (46.2 per cent) and inflorescence length (46.8 per cent).

Heritability estimates along with genetic advance is more useful than the heritability value alone for selecting the best individual. Higher value of heritability associated with high genetic advance as percent mean was observed for pod yield per plant, single pod weight, pod length, plant height, leaf length, pod girth, number of pod per cluster and number of branches per inflorescence. This is attributed to the additive gene action. Heritability values were high than those of genetic advance for most of the traits which indicated that they were least influenced by the environment and shows that the phenotypes were true representative of their genotypes and selection based on phenotypic performance would be reliable genotypes which is in line with the findings of Karunakar et al. (2018), Lakshmi Narayana Priya et al. (2019) and Varma et al. (2019).

Table 3: *Per se* performance of 21 genotypes for quantitative traits

Genotypes	PH (cm)	TG (cm)	NPB (No. s)	LL (cm)	PeL (cm)	DFI	IL (cm)	NBI (No. s)	FS (mm)	NPP (No. s)	PL (cm)
MO_1	300.20	33.95	4.47	45.13	11.97	74.13	20.85	7.73	14.83	101.73	66.62
MO_2	281.00	33.02	4.00	35.20	12.45	64.87	20.31	7.13	16.04	99.47	94.28
MO_3	399.27	38.20	5.13	47.33	11.81	85.87	21.19	11.20	16.70	105.33	29.89
MO_4	421.00	33.63	5.07	40.81	11.16	67.33	19.91	7.33	17.52	96.60	53.89
MO_5	303.67	38.64	3.87	41.50	10.09	87.73	21.98	6.73	15.62	90.60	44.28
MO_6	307.00	36.03	3.40	28.62	9.87	88.13	20.15	4.93	16.95	91.73	45.31
MO_7	352.40	44.93	5.67	45.21	10.03	74.47	18.55	7.07	17.47	90.87	41.19
MO_8	323.33	39.63	5.00	39.41	10.33	82.13	20.27	6.53	18.49	83.73	47.29
MO_9	394.07	38.03	3.87	48.27	12.59	88.93	17.88	8.27	18.11	88.40	68.17
MO_10	400.40	34.64	4.40	39.43	10.79	71.13	22.05	9.80	19.52	77.73	45.26
MO_11	378.93	32.44	3.40	38.70	8.99	78.73	20.80	10.40	17.22	74.53	46.52
MO_12	294.93	35.21	3.93	49.31	12.73	83.87	23.18	8.20	19.55	62.67	44.15
MO_13	382.67	45.80	4.93	35.33	9.63	84.00	20.36	7.07	16.24	41.07	40.38
MO_14	391.33	39.00	5.60	40.33	10.51	83.60	23.01	8.20	18.82	72.93	57.56
MO_15	205.93	33.63	3.40	47.51	12.11	74.67	20.70	9.33	19.06	59.00	71.72
MO_16	409.33	45.53	4.20	42.00	11.74	96.73	17.19	6.13	18.94	79.60	47.57
MO_17	320.00	36.20	4.47	32.04	9.52	70.13	19.32	7.13	19.12	90.73	38.70
MO_18	316.00	37.54	4.53	41.47	9.46	89.33	17.57	7.00	19.96	89.27	54.31
MO_19	413.80	42.03	4.33	46.28	12.85	76.73	19.01	9.20	18.37	89.73	47.86
MO_20	289.00	35.20	4.13	43.03	12.71	81.67	16.92	8.00	18.78	93.93	65.27
MO_21	385.93	42.47	4.80	35.41	10.95	72.00	22.51	7.27	18.95	91.00	54.75
Mean	346.20	37.89	4.41	41.06	11.06	79.82	20.18	7.84	17.92	84.32	52.62
SE(m)	10.00	1.18	0.42	1.03	0.32	1.46	0.97	0.30	0.58	2.61	1.91
C.V %	15.003	15.399	16.5011	14.3409	15.0862	13.1702	8.2924	16.7007	15.5709	15.3716	16.2829
C.D @5%	28.58	3.38	1.20	2.94	0.93	4.18	2.76	0.87	1.65	7.47	5.46
Min.	205.93	32.44	3.40	28.62	8.99	64.87	16.92	4.93	14.83	41.07	29.89
Max.	421.00	45.80	5.67	49.31	12.85	96.73	23.18	11.20	19.96	105.33	94.28

PH- Plant height, TG- Tree girth, NPB- Number of primary branches, LL- leaf length, PeL- Petiole length, DFI- Days to flower initiation, IL- Inflorescence length, NBI-Number of branches per inflorescence, FS- flower size, NPP-Number of pods per plant, PL- Pod length

Genotypes	PG (mm)	PPC (No. s)	PPB (No. s)	DPI	DPM	SPY (g)	NSP (No.s)	SS (mm)	HSW (g)	PYP (Kg)
MO_1	14.12	1.53	13.40	19.87	65.20	166.27	20.07	10.21	37.80	16.20
MO_2	15.37	1.60	8.87	17.47	51.33	179.73	24.27	9.11	27.53	14.56
MO_3	8.52	1.80	16.07	21.60	57.40	64.87	13.67	8.89	31.27	7.19
MO_4	13.16	1.27	12.27	15.27	47.80	107.00	22.67	8.49	23.73	10.33
MO_5	14.11	1.27	11.27	18.33	56.40	91.27	16.20	7.97	25.67	8.07
MO_6	8.94	2.13	14.13	18.07	58.53	94.60	20.67	10.00	36.67	9.25
MO_7	13.55	1.27	12.60	23.43	60.27	88.07	19.80	9.18	27.80	7.97
MO_8	8.21	2.53	11.27	20.87	58.00	102.47	18.87	8.18	25.20	7.78
MO_9	14.19	1.27	10.93	14.47	62.87	133.13	25.53	8.25	29.00	11.01
MO_10	11.21	1.33	8.87	18.27	57.87	74.73	19.00	8.81	26.80	5.68
MO_11	12.69	1.87	15.80	19.87	54.13	79.40	18.33	8.49	31.53	5.26
MO_12	13.92	2.00	14.07	24.00	52.33	73.27	18.93	9.09	33.53	4.51
MO_13	15.12	1.13	8.20	22.67	57.13	94.47	18.27	8.49	29.60	4.74
MO_14	13.24	2.20	14.20	18.33	60.80	86.60	19.80	8.23	27.33	6.58
MO_15	12.95	2.07	10.13	19.20	49.60	183.67	25.27	9.71	31.93	10.44
MO_16	12.34	2.07	10.73	20.80	61.00	95.13	24.00	10.20	35.20	8.39
MO_17	15.63	1.13	12.80	18.87	56.73	67.73	18.47	7.82	27.87	6.62
MO_18	9.21	1.20	12.87	21.27	54.80	123.87	21.87	9.03	29.53	10.13
MO_19	11.95	1.20	11.87	18.47	60.47	81.07	22.47	10.07	34.40	7.39
MO_20	13.65	1.07	13.13	16.87	59.87	166.20	23.00	8.00	28.07	14.30
MO_21	12.79	1.33	12.80	19.87	61.73	139.87	18.87	8.60	32.00	11.46
Mean	12.61	1.58	12.20	19.42	57.35	109.21	20.48	8.90	30.12	8.95
SE(m)	0.38	0.08	0.57	0.69	1.69	3.27	0.82	0.35	2.02	0.51
C.V %	15.2645	18.9416	18.0753	16.1989	15.1070	15.1942	16.9781	16.8841	11.6724	9.8101
C.D @5%	1.09	0.23	1.63	1.99	4.83	9.36	2.36	1.01	0.01	1.45
Min.	8.21	1.07	8.20	14.47	47.80	64.87	13.67	7.82	23.73	4.51
Max.	15.63	2.53	16.07	24.00	65.20	183.67	25.53	10.21	37.80	16.20

PG- Pod girth, PPC- pods per cluster, PPB- Pods per branch, DPI- Days to pod initiation, DPM- days to pod maturity, SPY- Single Pod weight, NSP- Number of seeds per pod, SS- Seed size, HSW- Hundred seed weight, PYP- Pod yield per plant

Table 4: Genetic variability and heritability parameters for 21 quantitative parameters for drumstick genotypes

Sl. No.	Traits	PV	GV	EV	PCV	GCV	ECV	h^2 (Broad sense)	GA (%)	GAM
1	PH (cm)	3483.055	3182.973	300.081	17.047	16.296	5.004	0.914	111.102	32.092
2	TG (cm)	20.299	16.113	4.186	11.890	10.593	5.399	0.794	7.367	19.443
3	NPB	0.799	0.529	0.269	20.269	16.501	11.771	0.337	0.621	14.083
4	LL (cm)	32.816	29.637	3.178	13.950	13.257	4.341	0.903	10.658	25.954
5	PeL (cm)	1.789	1.473	0.316	12.093	10.971	5.086	0.823	2.268	20.504
6	DFI	73.920	67.517	6.403	10.771	10.294	3.170	0.913	16.177	20.267
7	IL (cm)	5.260	2.799	2.461	11.367	8.292	7.774	0.468	2.210	10.954
8	NBI	2.385	2.109	0.276	19.696	18.521	6.701	0.884	2.813	35.877
9	FS (mm)	2.703	1.706	0.997	9.176	7.290	5.573	0.631	2.138	11.930
10	NPP	252.831	232.318	20.514	18.858	18.077	5.372	0.919	30.098	35.696
11	PL (cm)	211.554	200.625	10.929	27.643	26.919	6.283	0.948	28.415	54.002
12	PG (mm)	5.205	4.764	0.441	18.086	17.303	5.264	0.915	4.302	34.101
13	NPC	0.206	0.186	0.020	28.636	27.204	8.942	0.902	0.843	53.238
14	NPB	5.191	4.220	0.971	18.671	16.834	8.075	0.813	3.816	31.267
15	DPI	6.931	5.481	1.449	13.556	12.055	6.199	0.791	4.289	22.085
16	DPM	25.416	16.839	8.577	8.791	7.156	5.107	0.663	6.881	11.998
17	SPY (g)	1449.206	1417.027	32.178	34.858	34.469	5.194	0.978	76.680	70.213
18	NSP	10.431	8.389	2.042	15.773	14.145	6.978	0.804	5.351	26.133
19	SS (mm)	0.832	0.457	0.375	10.251	7.595	6.885	0.549	1.031	11.590
20	HSW (g)	22.969	12.358	10.611	15.913	11.672	10.816	0.462	4.561	15.143
21	PYP(Kg)	11.044	10.274	0.770	37.144	35.825	9.808	0.930	6.369	71.181

Heritability estimates along with genetic advance is more useful than the heritability value alone for selecting the best individual. Higher value of heritability associated with high genetic advance as percent mean was observed for pod yield per plant, single pod weight, pod length, plant height, leaf length, pod girth, number of pod per cluster and number of branches per inflorescence. This is attributed to the additive gene action. Heritability values were high than those of genetic advance for most of the traits which indicated that they were least influenced by the environment and shows that the phenotypes were true representative of their genotypes and selection based on phenotypic performance would be reliable genotypes which is in line with the findings of Karunakar et al. (2018), Lakshmi Narayana Priya et al. (2019) and Varma et al. (2019).

Selection would be depending on pod yield per plant, the number of pods per plant, single pod weight and pod length may bring out the genetic improvement in the moringa because they showed a high value of GCV, PCV, heritability and genetic gain. Hence the selection will be effective for these traits. These traits can be improved through mass selection, progeny selection, or any other modified selection procedures. It can be concluded that PKM-01, PKM-02, Dhanraj, Shirdi-01 and Bagalkot-01genotypes, performances were outstanding for the traits like pod length, number of pods per plant, single pod weight and pod yield per plant, indicating their utilization in the breeding for development of elite varieties or hybrids in the future and genotypes like Bhagya, Tangi-01 and PKM-02 for better performance in relation to earliness parameters.

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