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Genetic variability studies in fodder drumstick (*Moringa oleifera* L.)

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Abstract
The present investigation was conducted at Grass Breeding Scheme, Mahatma Phule Krishi Vidyapeeth, Rahuri, Dist. Ahilyanagar, Maharashtra during *kharif* 2023.The experimental material used for the study consisted of 52 fodder drumstick genotypes. The analysis of variance showed existence of considerable variability for all eleven characters. A wide range of variability was observed for almost all the characters studied. The genotypes RMO-2023-09, RMO-2023-18, RMO-2023-19, RMO-2023-21 and RMO-2023-25 recorded higher green forage yield plant^{-1}, dry matter yield plant^{-1} and simultaneously other characters. All the characters under study showed high estimates of broad sense heritability. High heritability estimates accompanied with high genetic advance was observed for the characters *viz*., plant height, plant spread and green forage yield plant^{-1} indicating inheritance of these characters due to additive gene action and direct selection of such traits are necessary for crop improvement.

Keywords: Variability, heritability, genetic advance, yield

Introduction

Moringa originated in sub-Himalayan tracts of the Indian sub-continent. It is a fast growing, evergreen, deciduous medium sized perennial tree of about 10 m to 12 m height. *Moringa oleifera* L. is a tropical plant belonging to family Moringaceae (Kantharajan and Dodd, 1991) [7]. Himalayan northern parts of India and is cultivated throughout tropical and sub-tropical areas of the world, where it is known by various vernacular names (Ramachandran *et al*., 1980) [11]. Drumstick is a fast-growing and drought-tolerant tree and can be effectively adjusted for various environmental and farming conditions. Drumstick is also known as 4F Plant (food, fodder, fuel and fertility). Drumstick leaves have a rich source of β-carotene, protein, vitamin C, calcium and potassium and acts as good source of natural antioxidants; and thus, increase the shelf life of fat-rich foods due to the presence of various types of antioxidant compounds such as ascorbic acid, flavonoids, phenolis and carotenoids. In Philippines, it is known as 'Mother's best friend' and is sometimes prescribed for anemia and due to its use to increase female milk production. (Siddhuraju and Becker, 2003) [12]. Fahey (2005) [4] referred to Moringa as a nutrient dense food source of its high nutritional value of leaves, pods and seeds.

India is the prevalent prime producer of Moringa crop, with an annual production of 2.2 million tonnes of tender fruits from an area of 38,000 ha. Among the states, Andhra Pradesh leads in both area and production followed by Karnataka and Tamil Nadu. Tamil Nadu is the pioneering state as it has broad genetic diversity (annual and perennial Moringa) from diversified geographical areas, as well as few introductions from Srilanka (Balakumbahan *et al.*, 2020) [2].

India possesses the highest livestock population in the world, which is growing at the rate of 4.8% per year. Accordingly, the country's feed requirement to feed such a large livestock population is also increasing. Regular supply of adequate and nutritious feed and fodder is essential for the development of livestock sector. Fodder crops are the main and cheapest source of roughage feed for livestock. However, shortage of quality fodder, particularly during lean periods is major factor contributing to lower livestock productivity. Currently, the country faces a net deficit of 35.6% green fodder, 10.95% dry fodder and 44%

concentrate feed ingredients. The demand for green and dry fodder will reach to 1012 and 631 million tons by 2050. Therefore, to meet out this deficit, fodder supply has to grow at 1.69% annually to sustain livestock husbandry. Since last two decades, static area under cultivated fodder is only 8.4 m ha (less than 5%). Forage has an important role to play in ruminant nutrition in providing energy, protein and minerals and fiber for chewing. Tree fodders could be a good option to meet the fodder demand of livestock in areas having a perennial shortage of green fodder. Research efforts have confirmed the potentiality of browsing plants to provide alternate source of nutrition for ruminants in tropics. There is a huge list of such browse trees and shrubs with potential use as fodder, which may go even up to more than 300 species. This fast- growing tree is grown throughout the tropics for multi-purpose use viz. human food, livestock forage, medicine values, dye, water purification, and for its wide adaptability and ease of establishment (Subrahmanya *et al*., 2016) [13].

The genetic variability, Heritability and genetic advance are important selection parameters for any crop. Heritability estimate along with genetic advance are more helpful in predicting the gain under selection. So the variability study provides base for improvement and selection for good fodder yield among various Moringa genotypes. The manuscript focus on determining variability of various genotype to be utilized in breeding program.

Materials and Methods

The present investigation was conducted at Grass Breeding Scheme, Mahatma Phule Krishi Vidyapeeth, Rahuri, Dist. Ahilyanagar, Maharashtra during *kharif* 2023. The Mahatma Phule Krishi Vidyapeeth, Rahuri comes under semi-arid, sub-tropical region with annual rainfall ranges between 310-620 mm with an average rainfall 520 mm.

The experimental material used for the study consisted of 52 fodder drumstick genotypes which were obtained from Grass Breeding Scheme, M.P.K.V., Rahuri. The list of fodder drumstick genotypes is given in Table 1. During *Kharif* 2023, fifty-two genotypes of fodder drumstick were evaluated in a Randomized Block Design (RBD) with two replications. Each genotype was sown in double rows with spacing 90 cm between row and 60 cm within rows

The fertilizer @ 30 kg N/ha in the form of urea and 60 kg P/ha in the form of single super phosphate were applied as a basal dose before sowing and mix well in soil. All necessary intercultural operations are carried out as per requirement. The observation of various qualitative as well as quantitative characters are recorded with proper scale and instrument.

Table 1: Sources of fodder drumstick genotypes

Sr. No.	Genotypes	Area of Collection	Sr. No.	Genotypes	Area of Collection
1	RMO-2023-01	KANCHERI	27	RMO-2023-29	BELAPUR
2	RMO-2023-02	BABHULGAON	28	RMO-2023-30	DEVLALI
3	RMO-2023-03	SHEDGE VASTI	29	RMO-2023-31	DIGRAS
4	RMO-2023-04	HAREGAON	30	RMO-2023-32	PADHEGAON
5	RMO-2023-05	RAHURI KHURD	31	RMO-2023-33	DEVLALI
6	RMO-2023-06	BARGAON	32	RMO-2023-34	DHAMORI
7	RMO-2023-07	DIGRAS	33	RMO-2023-35	SHRIRAMPUR
8	RMO-2023-08	DIGRAS	34	RMO-2023-36	BABHULGAON
9	RMO-2023-09	MULANAGAR	35	RMO-2023-37	MALUNJE
10	RMO-2023-10	MULANAGAR	36	RMO-2023-38	UNDIRGAON
11	RMO-2023-12	MULSHI	37	RMO-2023-39	MALUNJE
12	RMO-2023-13	DEVLALI	38	RMO-2023-41	HAREGAON
13	RMO-2023-15	MPKV,RAHURI	39	RMO-2023-42	MIRKHEL
14	RMO-2023-16	MULANAGAR	40	RMO-2023-43	NIMGAON WAGHA
15	RMO-2023-17	VAMBORI	41	RMO-2023-44	VAMBORI
16	RMO-2023-18	DEVLALI	42	RMO-2023-45	SHIRDI
17	RMO-2023-19	DEVLALI	43	RMO-2023-46	BALSA KHURD
18	RMO-2023-20	GOTUMBE AAKHADA	44	RMO-2023-47	SAYLA
19	RMO-2023-21	RAHURI KHURD	45	RMO-2023-48	MPKV,RAHURI
20	RMO-2023-22	BHINGARDE VASTI	46	RMO-2023-49	MPKV,RAHURI
21	RMO-2023-23	DIGRAS	47	RMO-2023-50	MPKV,RAHURI
22	RMO-2023-24	MPKV,RAHURI	48	RMO-2023-51	NANDED
23	RMO-2023-25	MPKV,RAHURI	49	RMO-2023-52	KATALA
24	RMO-2023-26	SADE ROAD	50	RMO-2023-53	RAWLGAON
25	RMO-2023-27	DAM PHATA	51	RMO-2023-55	HIGOLI
26	RMO-2023-28	UNDIRGAON	52	RMO-2023-56	VNMKV,PARBHANI

Results and Discussion

On the basis of observation taken the analysis was done regarding the variability parameters. The analysis of variance revealed significant genotypic differences for all eleven characters (Table 2).

Table 2: Analysis of variance for eleven characters of fodder drumstick genotypes

Sr. No.	Characters	Replication	Genotypes	Error
	DF	1	51	51
1	Plant height (cm)	517.53^{*}	11526.84^{**}	124.42
2	Plant spread (cm)	44.46	1832.13^{**}	23.58
3	No. of primary branches plant^{1}	5.08	98.53^{**}	2.73
4	Leaf length (cm)	0.01	1.35^{**}	0.01
5	Leaf breadth (cm)	0.02	0.40^{**}	0.01
6	Leaf to stem ratio	0.01	0.15^{**}	0.01
7	Dry matter content (%)	1.82	37.19^{**}	0.69
8	Dry matter yield plant^{1} (g)	38.28	60.49^{**}	10.11
9	Crude protein content (%)	0.13	0.16^{**}	0.09
10	Crude Protein yield plant^{1} (g)	0.01	6.83^{**}	0.09
11	Green forage yield plant^{1} (g)	773.90	14167.71^{**}	986.20

*, ** significant at 5% and 1% levels respectively.

The mean performance analysis revealed the status of each genotype performance regarding character under study. On that behalf the following result were depicted in Table 3.

The study revealed that the average height of the plants was 189.81 cm. On that basis 16 genotypes *viz*., RMO-2023-01, RMO-2023-09, RMO-2023-10, RMO-2023-15, RMO-2023-17, RMO-2023-18, RMO-2023-19, RMO-2023-20, RMO-2023-21, RMO-2023-22, RMO-2023-23, RMO-2023-25, RMO-2023-30, RMO-2023-35, RMO-2023-42, RMO-2023-45, found to be highly significant for plant height also at par with mean value. Among that 16 genotypes RMO-2023-21 shows highest height (452 cm) so can included in breeding for height. The overall mean for plant spread was found to be 93.02 cm. Additionally, fourteen genotypes *viz*., RMO-2023-01, RMO-2023-09, RMO-2023-15, RMO-2023-18, RMO-2023-19, RMO-2023-21, RMO-2023-22, RMO-2023-23, RMO-2023-25, RMO-2023-30, RMO-2023-33, RMO-2023-41, RMO-2023-42, RMO-2023-45, demonstrated significantly greater plant spread compared to the grand mean. The genotype RMO-2023-25 exhibit larger plant spread (200 cm) than fourteen genotypes. The general mean for number of primary branches per plant was 19.66. The seventeen genotypes had significantly higher number of primary branches plant per plant than grand mean. The genotype RMO-2023-21 having highest branches (34.50) than all others. The leaf length average was 2.15 cm. Twenty genotypes having significantly longer leaves than grand mean. The genotypes RMO-2023-21 shows larger leaf size (4.40 cm) than rest. In case of leaf breadth average leaf breadth was 0.89 cm. Fifteen genotypes produced significantly higher leaf breadth than average. RMO-2023-21 having highest leaf breadth (2.05) as compare to others. The general mean for leaf to stem ratio was 1.06. The twenty two genotypes had significantly higher leaf to stem ratio than grand mean. Among this the genotype RMO-2023-21 have found to be highest ratio (1.72) than others.

The general mean for dry matter yield plant^{-1} was 45.61 gm. The dry matter yield plant^{-1} of the five genotypes *viz*., RMO-2023-33, RMO-2023-08, RMO-2023-13, RMO-2023-35, RMO-2023-02 had significantly higher than grand mean. Out of this five RMO-2023-33 genotype shows higher dry matter yield per plant (57.60 gm). The average dry matter content was 17.93% of fifty two genotypes. The eighteen genotypes had significantly higher dry matter per cent than mean. RMO-2023-28 genotype having highest dry matter content than eighteen genotypes. The general mean for crude protein content was 18.54%. Twenty genotypes had significantly higher crude protein content than average. While genotype RMO-2023-25 exhibit highest crude protein (25.08%). The general mean for crude protein yield plant^{-1} was 8.73 gm. Significantly higher crude protein yield plant^{-1} was produced by eighteen genotypes than grand mean.. Among them genotype shows higher crude protein yield (12.35 gm). The general mean for green forage yield plant^{-1} was 270.15 gm. The nine genotypes recorded significantly higher green forage yield plant^{-1} than grand mean. The genotype have higher green forage yield (478.40 gm) than all others.

The estimates of genotypic variance, phenotypic variances, GCV, PCV, heritability (b.s. %), genetic advance, expected genetic advance as percent of mean for different characters studied are presented in Table 4.

The genotypic and phenotypic coefficient of variation was recorded high for leaf breadth (49.67% and 51.31%), plant height (39.78% and 40.21%), leaf length (38.09% and 38.45%), number of branches plant-1 (35.19% and 36.18%), plant spread (32.32% and 32.32%), green forage yield plant-1 (30.05% and 32.22%), leaf to stem ratio (26.17% and 26.48%), dry matter content % (23.83% and 24.28%), crude protein yield plant-1 (21.03% and 21.30%). Moderate genotypic and phenotypic coefficient of variation was observed for dry matter yield plant-1 (11.00% and 13.02%) and crude protein % (15.41% and 15.49%). The environment had an impact on the traits under study expressed themselves, as seen by the phenotypic coefficients of variation were slightly greater than genotypic coefficients of variation.

The current results were in consistent with reports of Yadav *et al*. (1974) [15] who also reported high to moderate values of PCV and GCV for green forage yield, plant height and leaf breadth and Patel (2002) [10] for green forage yield in *Cenchrus ciliaris*. Bhagirath *et al*. (2011) [3] reported high value of GCV and PCV for green forage yield in *Cenchrus setigerus* genotypes. Whereas, Gore *et al*. (2016) [5] observed high value of GCV and PCV for leaf to stem ratio and green forage yield; Kumar *et al*. (2020) [8] for leaf to stem ratio and green forage yield.

A measure of heritability is the amount of phenotypic variation brought on by the activity of genes. Heritability has been widely accepted by workers as a trustworthy signal for implementing effective improvements in the trait for which selection is used. The proportion of genetic variability, which parents pass down to their offspring, is shown by heritability. In general, heritability is defined by Lush (1949) [9], as the percentage ratio of total genotypic variance to phenotypic variance.

Table 3: Mean performance of fodder drumstick genotypes for green forage yield and its contributing characters

Sr. No.	Name of genotype	Plant height (cm)	Plant spread (cm)	No. of primary branches plant^{-1}	Leaf length (cm)	Leaf breadth (cm)	Leaf to stem ratio	Dry matter yield Plant^{-1} (g)	Dry matter (%)	CP%	CPY Plant^{-1} (g)	GFY Plant^{-1} (g)
1	RMO-2023-01	228.00*	124.50*	28.50*	1.35	1.20*	0.71	50.20	14.16	16.70	8.38	297.80
2	RMO-2023-02	160.00	99.00	26.50*	1.80	0.72	1.03	52.60*	15.53	20.00*	11.40*	305.65
3	RMO-2023-03	123.50	83.00	17.50	1.60	0.57	0.77	48.75	16.38	18.40	8.98	298.05
4	RMO-2023-04	108.00	54.00	11.00	0.80	0.41	1.26*	47.50	25.42*	19.98*	10.13*	195.45
5	RMO-2023-05	131.50	72.50	18.50	1.65	0.67	1.54*	44.45	15.43	20.77*	10.23*	304.15
6	RMO-2023-06	146.50	71.00	18.75	1.15	0.87	0.94	46.05	18.38	16.41	7.56	260.30
7	RMO-2023-07	131.00	53.00	12.00	1.45	0.78	0.76	35.60	28.53*	19.65*	8.29	190.15
8	RMO-2023-08	180.00	86.50	24.00*	1.80	1.15*	1.04	55.25*	16.65	21.41*	11.83*	279.20
9	RMO-2023-09	425.00*	133.50*	32.50*	3.50*	1.95*	0.65	48.70	10.70	24.16*	12.35*	455.30*
10	RMO-2023-10	217.50*	98.50	25.50*	1.55	0.85	0.89	44.65	14.23	19.41*	8.66	314.05
11	RMO-2023-12	152.00	80.00	14.00	1.90	1.00	1.08	44.00	19.14	22.58*	10.41*	230.55
12	RMO-2023-13	156.00	79.50	18.00	2.05	1.06	1.13	54.80*	19.15	20.24*	11.09*	307.90
13	RMO-2023-15	229.00*	106.00*	27.00*	2.45*	0.87	1.26*	49.85	14.42	23.84*	11.89*	369.20*
14	RMO-2023-16	165.00	95.50	17.00	1.30	0.71	1.26*	47.90	23.32*	16.29	7.80	151.75
15	RMO-2023-17	218.00*	102.50	22.50	1.60	1.23*	0.91	47.95	21.13*	17.90	8.58	248.50
16	RMO-2023-18	243.50*	112.00*	28.00*	2.55*	1.70*	1.04	39.00	11.17	17.43	7.60	420.20*
17	RMO-2023-19	247.50*	114.00*	30.50*	3.05*	1.65*	1.16*	43.25	10.14	18.51	8.53	433.30*
18	RMO-2023-20	232.00*	101.00	24.00*	1.50	1.20*	1.31*	39.65	13.87	17.66	7.25	277.10
19	RMO-2023-21	452.00*	154.00*	34.50*	4.40*	2.05*	1.72*	44.40	9.28	18.50	7.50	478.40*
20	RMO-2023-22	347.00*	120.50*	32.00*	2.75*	1.60*	0.75	42.35	10.73	16.10	7.27	394.50*
21	RMO-2023-23	225.50*	105.00	22.00	1.90	0.61	0.89	48.10	19.70*	14.50	7.48	318.90
22	RMO-2023-24	150.00	97.50	20.00	2.60*	0.85	0.57	44.95	17.16	14.60	6.57	262.20
23	RMO-2023-25	357.50*	200.00*	33.00*	3.45*	1.80*	1.24*	48.95	11.02	25.08*	12.27*	439.70*
24	RMO-2023-26	180.00	82.00	8.50	2.10	0.64	0.80	49.90	21.67*	16.38	8.17	230.30
25	RMO-2023-27	141.00	47.00	14.00	1.30	0.38	0.82	33.20	18.57	14.51	5.53	120.35
26	RMO-2023-28	202.00	91.00	17.50	1.40	0.44	1.25*	44.55	23.46*	14.40	6.42	189.90
27	RMO-2023-29	212.00	100.00	20.25	1.65	0.53	0.86	43.60	20.29*	15.39	6.46	215.15
28	RMO-2023-30	239.00*	104.00*	21.75	1.20	0.62	0.94	49.10	22.60*	16.09	7.90	217.30
29	RMO-2023-31	90.50	39.00	8.50	2.10	0.81	0.68	42.60	18.96	19.61*	8.36	225.15
30	RMO-2023-32	160.50	81.00	12.50	1.00	0.32	1.33*	40.70	22.17*	18.30	7.45	190.50
31	RMO-2023-33	170.00	107.00*	18.75	2.65*	0.93	0.97	57.60*	18.38	18.95	11.22*	310.35
32	RMO-2023-34	107.00	85.50	10.50	1.40	0.40	0.84	49.55	23.16*	18.31	9.18	214.05
33	RMO-2023-35	221.00*	97.50	18.00	3.00*	1.30*	1.43*	54.80*	17.21	15.67	8.59	320.30
34	RMO-2023-36	168.50	95.00	13.25	1.35	0.80	0.73	35.90	21.54*	20.36*	7.61	178.75
35	RMO-2023-37	130.50	74.00	23.00*	1.00	0.43	0.71	35.40	18.22	16.59	5.88	124.25
36	RMO-2023-38	118.00	58.50	12.00	2.95*	0.31	1.24*	33.45	18.98	17.78	6.51	185.90
37	RMO-2023-39	139.50	88.00	15.50	2.20	0.68	1.16*	45.90	21.83*	19.76*	9.18	210.30
38	RMO-2023-41	180.00	109.00*	23.00*	2.95*	0.86	0.84	51.95	19.57	21.71*	11.28*	265.55
39	RMO-2023-42	273.00*	167.50*	25.25*	1.85	0.35	0.73	47.90	21.17*	21.64*	10.37*	226.30
40	RMO-2023-43	160.00	64.50	13.00	2.00	0.35	1.33*	45.85	22.33*	18.99	8.71	205.40
41	RMO-2023-44	200.00	94.00	20.00	2.10	0.52	1.55*	51.55	21.50*	17.36	9.50*	239.80
42	RMO-2023-45	278.50*	138.00*	29.50*	3.10*	0.84	1.16*	39.70	14.72	21.50*	9.27*	269.75
43	RMO-2023-46	135.00	49.50	8.00	1.50	0.31	1.50*	45.55	24.76*	20.97*	9.36*	184.00
44	RMO-2023-47	116.00	60.50	10.50	2.45*	0.51	0.81	41.40	17.21	18.31	8.30	240.70
45	RMO-2023-48	132.50	89.50	19.00	2.95*	0.54	0.99	48.60	19.28	23.43	11.39*	252.10
46	RMO-2023-49	151.50	90.00	22.00	3.35*	1.25*	1.22*	46.25	14.64	20.69*	10.55*	316.00
47	RMO-2023-50	143.50	57.50	16.50	3.25*	0.82	0.86	46.90	16.11	21.74*	10.65*	291.00
48	RMO-2023-51	104.00	50.50	8.00	1.60	0.80	1.61*	44.50	17.06	17.52	8.21	261.00
49	RMO-2023-52	149.50	82.50	14.50	3.20*	1.30*	1.32*	47.15	14.76	15.57	7.34	319.50
50	RMO-2023-53	178.00	102.00	20.50	3.25*	1.40*	1.13	48.25	14.24	14.51	7.43	339.00*
51	RMO-2023-55	204.00	88.50	17.50	3.35*	1.50*	1.35*	41.35	12.29	11.70	4.84	342.50*
52	RMO-2023-56	159.00	101.00	24.00*	1.50	1.00	1.02	39.50	19.98*	16.53	6.48	130.50
General mean		189.81	93.02	19.66	2.15	0.89	1.06	45.61	17.93	18.54	8.73	270.15
S.E. ±		7.89	3.43	1.17	0.08	0.08	0.03	2.25	0.59	0.21	0.21	22.21
C.D. 5%		22.39	9.75	3.32	0.23	0.23	0.09	6.39	1.67	0.59	0.59	63.05
C.V. %		5.88	5.22	8.40	5.26	12.88	4.07	6.97	4.65	1.58	3.39	11.62

* Represents characters showing significantly higher values over the grand mean.

Table 4: Estimates of variability parameters for green forage yield and its contributing characters in fodder drumstick genotypes

Sr. No.	Character	Mean	Range	GCV (%)	PCV (%)	ECV (%)	Heritability h^2 (b.s.) (%)	Genetic Advance	Genetic Advance as % of mean
1	Plant height (cm)	189.80	90.50-452.00	39.78	40.21	5.87	97.90	153.87	81.06
2	Plant spread (cm)	93.01	39.00-200	32.32	32.32	5.22	97.50	61.15	65.74
3	No. of primary branches plant^{-1}	19.66	8.00-34.5	35.19	36.18	8.40	94.60	13.86	70.52
4	Leaf length (cm)	2.15	0.80-4.400	38.09	38.45	5.26	98.10	1.67	77.73
5	Leaf breadth (cm)	0.89	0.31-2.05	49.67	51.31	12.98	93.70	0.88	99.04
6	Leaf to stem ratio	1.06	0.57-1.72	26.17	26.48	4.06	97.60	0.56	53.27
7	Dry matter content (%)	17.93	9.28-28.53	23.83	24.28	4.65	96.30	8.63	48.18
8	Dry matter yield plant^{-1} (g)	45.61	33.20-57.60	11.00	13.02	6.97	71.30	8.73	19.14
9	Crude protein content (%)	18.54	14.40-25.07	15.41	15.49	1.57	99.00	5.85	31.58
10	Crude protein yield plant^{-1} (g)	8.73	4.84-12.35	21.03	21.30	3.39	97.50	3.73	42.78
11	Green forage yield plant^{-1} (g)	270.15	120.35-478.40	30.05	32.22	11.62	87.00	155.97	57.73

The heritability (b.s.) estimates ranged between 71.30% to 99.00%. The character crude protein content (%) recorded the highest heritability (99.0%) followed by leaf length (98.10%), plant height (97.90%), leaf to stem ratio (97.60%), plant spread and crude protein yield plant^{-1} (97.5%), dry matter content% (96.30%), number of branches plant^{-1} (94.60%), leaf breadth (93.70%), green forage yield plant^{-1} (87.00%) and dry matter yield plant^{-1} (71.30%). All characters showed high heritability (b.s.) estimates.

Present findings were in confirmatory with reports of Bhagirath *et al.* (2011) [3] who additionally revealed significant heritability for dry matter yield, green forage yield in *Cenchrus setigerus*; Babu and Iyanar (2013) [1] for number of leaves and crude protein content in guinea grass; Gore *et al.* (2016) [5] for leaf to stem ratio in marvel grass and Udendra *et al.* (2020) [14] for each of characteristics in grasses species.

Johnson *et al.* (1955) [6] suggested that heritability and genetic advance, when calculated together would prove more useful in predicting the resultant effect of selection on phenotypic expression. It is stressed that genetic advancement and heritability should be used simultaneously since without it; heritability estimates would not be useful. Sufficient improvement though selection in genetically advanced generation cannot be achieved by high heritability alone.

The maximum value of genetic advance was observed for green forage yield per plant (155.97) followed by plant height (153.87) and plant spread (61.15). The moderate value of genetic advance was observed for number of branches plant^{-1} (13.86). All the rest of characters recorded low values for genetic advance of which leaf to stem ratio recorded the least value (0.56). The greatest magnitude of genetic advance as per cent mean was observed for leaf breadth (99.04) followed by plant height (81.06), leaf length (77.73) and number of primary branches plant^{-1} (70.52), plant spread (65.74), green forage yield plant^{-1} (57.73), leaf to stem ratio (53.27), dry matter content (48.18), crude protein yield plant^{-1} (42.78), crude protein content (31.58). The moderate value of genetic advance as per cent mean was observed for dry matter yield plant^{-1} (19.14).

High estimates of heritability along with high genetic advance as percent mean showed by plant height, leaf length, number of branches plant^{-1}, plant spread, green forage yield plant^{-1}, leaf to stem ratio, dry matter content, crude protein yield plant^{-1}, crude protein content. High heritability coupled with moderate estimates of genetic advance as per cent mean was noticed in dry matter yield plant^{-1}. Selection for these traits will be successful since it suggests that additive gene action predominates in the control of these traits.

Comparable outcomes of high estimates of heritability with high genetic advance % of mean were in accordance with Bhagirath *et al.* (2011) [3] for green forage yield and dry matter yield in *Cenchrus setigerus*; Babu and Iyanar (2013) [1] for crude protein content in guinea grass; Gore *et al.* (2016) [5] for leaf to stem ratio and number of leaves in marvel grass.

Conclusion

Analysis of variance revealed that for all the fifty two genotypes studied showed highly significant differences for all the eleven traits studied in fodder drumstick indicating that there is enough variability present among all the genotypes for those traits. Based on mean performance, the genotypes RMO-2023-09, RMO-2023-18, RMO-2023-19, RMO-2023-21 and RMO-2023-25 were found superior for majority of the characters.

There was slightly higher value for the phenotypic coefficient of variation than the corresponding genotypic coefficient of variation for all the eleven characters under study. High genotypic and phenotypic coefficient of variation was observed for leaf breadth, plant height, leaf length, number of primary branches plant^{-1}, plant spread, green forage yield plant^{-1}, leaf to stem ratio and crude protein yield $^{-1}$.

High estimates of heritability combined with high genetic advance as per cent mean showed by all characters except for dry matter yield plant^{-1}. It indicates effect of additive gene action for control of those traits and selection of such traits will be rewarding.

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