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Studies on variability, heritability and genetic advance for quantitative characters in finger millet genotypes

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Abstract

Finger millet (*Eleusine coracana*) is one of the underutilized crop which is known for its high nutritional value. Finger millet is having substantial genetic variation for various traits and can be exploited for crop improvement. The present study was aimed to know about genetic variability and heritability of grain yield and yield related traits in 18 finger millet genotypes obtained from all over India. Analysis of Variance revealed significant variation for all traits studied. Grain yield and fodder yield ranged from 22.6 to 42.7 and 59.0 to 95.4 q/ha respectively. Keeping in view of both grain yield and fodder yield, VR 1101 is the best culture which suitable for dual purpose.

Keywords: Finger millet, variability, heritability, correlation

Introduction

Finger millet (*Eleusine coracana* L. Gaertn.), is an important small millet grown extensively in diverse regions of India and Africa. Among small millets, finger millet ranks first in area and production. Finger millet occupies sixth position in production after wheat, rice, maize, sorghum and bajra. Out of the total minor millets produced, finger millet known as ragi accounts for about 85% of production in India (Sakamma *et al.*, 2017) ^[14]. Finger millet is grown in India, Srilanka, Nepal, parts of Africa, Madgaskar, Malaysia, Uganda and Japan (http://agritech.tnau.ac.in). India is the major producer in Asia. In India ragi is grown in an area of 2.0 million hectares with a production of 2.15 million tonnes, which accounts for 45 per cent of the world's cultivated area and 55 per cent of the world's production. Ragi is widely grown in the states of Karnataka, Tamil Nadu, Andhra Pradesh, Maharashtra, Orissa, Gujarat, Jharkhand, Uttar Pradesh, Madhya Pradesh and Uttarakhand (Ministry of Agriculture, 2012).

Finger millet consumption has wide range of advantages because of its high nutritive values. Finger millet is highly nutritious as its grains contain 65-75% Carbohydrates, 5-8% protein, 15 -20% dietary fiber and 2.5-3.5% minerals. It contains 5-8% good quality protein, *eleusinin* which our body can easily absorb. It also has key essential amino acids, tryptophan, methionine, threonine, valine, isoleucine and cystine which are required for good health. It is lower in fat content (1.3%) and majority is unsaturated fat. It is the richest source of calcium (344 mg/100 g), iron (3.9 mg/100 g) and other minerals. It is also rich in phosphorus (283 mg/100 g) and potassium (408 mg/100 g). It is highly valued as a reserve food in the times of famine.

To explore health benefits of finger millet consumption, cultivation of this crop is needed. Farmers tend to grow the crop when they can make profit by growing this crop. For making profits, high yielding varieties in finger millet are needed. To develop high yielding varieties by a plant breeder, Exploitation of genetic variability existing in the economic traits is the first principle in the improvement of any crop. In pursuit, to develop such high yielding varieties, a breeder has to know how much variability is present in the existing gene pool and the heritability of traits to be enhanced. Also to predict genetic gain under selection genetic advancement along with heritability estimates are needed (Johnson *et al.*, 1955) ^[8]. Interrelationship between different traits can be studied by knowing the association of characters with one another which provides a scope for better response to selection of traits (Bezaweletaw *et al.*, 2006; Singamsetti *et al.*, 2018) ^[4, 15].

genetic variability, heritability of various quantitative traits and to assess the importance of characters for selection of high yielding lines in finger millet genotypes.

Material and Methods

In the present investigation, 18 finger millet genotypes including one local check variety, Sri Chaitanya were evaluated at Agricultural Research Station, Vizianagaram, Andhra Pradesh during *kharif*, 2018. Genotypes were sown in a randomized complete block design (RCBD) in three replications with a spacing of 22.5×10 cm per each entry. Each genotype was grown in 10 lines of 3 m length. Fertilizers, 50-40-25 NPK kg/ha and need based plant protection measures were taken to raise a healthy crop. Observations were recorded on plant height (cm), ear length (cm), finger length (cm), finger width (cm), flag leaf length (cm), flag leaf width (cm), productive tillers per plant, days to 50% flowering & maturity, fodder yield (q/ha) and grain yield (q/ha).

Analysis of variance and summary statistics was calculated as per Panse and Sukathme (1967)^[12]. Phenotypic and genotypic coefficients of variation (PCV and GCV) were computed as per Burton and Devane (1953)^[6]. Heritability in broad sense was computed as per Allard (1960)^[11]. Genotypic and phenotypic correlations were calculated according to Falconer (1981)^[7]. Heritability and genetic advancement were categorized into low, medium and high as per Johnson *et al.*, (1955)^[8].

Results and Discussion

Crop improvement depends on the genetic variability studies and utilisation of the same for breeding purpose by choosing proper lines. These studies are required to assess the amount of role played by the environment in determining a character and also to judge how much easily a choosen character can be transformed to the next generation.

The results from ANOVA (Table 1) revealed significant variability (p < 0.01) in 18 finger millet genotypes studied for days to 50% flowering, days to maturity, finger length, finger width, leaf length, leaf width, grain yield and fodder yield. Similar variations were reported by Anuradha *et al.*, (2017, 2018) ^[2-3]; Singamstti *et al.*, (2018). The summary statistics and mean values (Table 2) indicated that days to 50% flowering ranged from 66 to 96.3 days while days to maturity from 101 to 127 days. In the present study two were early varieties (VL 352 and GPU 45) while remaining were having longer duration for maturity. Leaf length ranged from 33 to 41 cm, where longest booting leaf was observed in OEB 601

(40.9 cm). Grain yield also varied from 22.6 to 42.7 q/ha. Highest yielder was VR 1101 with an yield of 42.7 q/ha, while in early maturing types, the highest yield was obtained in GPU 45 (25.4 q/ha). VR 1101 can be suggested as a better culture for getting higher yields and GPU 45 can be suggested as best fit intensive cropping system. Fodder yield ranged from 59 q/ha to 95.4 q/ha while the mean fodder yield was 75.3 q/ha. After observance of fodder yield and grain yield, VR 1101 is the best culture which serves as dual purpose.

Phenotypic Coefficient of Variation (PCV) was higher than Genotypic Coefficient of Variation (GCV) for all traits studied GCV (Table 3). GCV ranged from low to moderate (4.21 to 14.35). Highest GCV and PCV were observed for finger length, grain yield and fodder yield indicating large variability of these two traits among finger millet genotypes. GCV and PCV are low for leaf length and plant height indicating lesser variability for these two traits among 18 genotypes studied.

Highest heritability estimates were observed for days to 50% flowering and days to maturity followed by finger length. Other characters, plant height, number of fingers/ear, finger length, finger width, leaf length and leaf width, fodder yield and grain yield were observed to have moderate heritability. Genetic Advance as per cent Mean (GAM) ranged from low to high. High GAM were observed for finger length (24.51%) while low GAM was observed for leaf length (6.17%). Similar results were reported earlier by Lal *et al.*, (1996) ^[10]; Patil *et al.*, (2013) ^[13]; Jyothsna *et al.*, 2016 ^[9], Mahanthesha *et al.*, 2017 ^[11]; Anuradha *et al.*, 2017& 2018 ^[2-3]; Singamsetti *et al.*, 2018 ^[15].

High heritability with high GAM was recorded for finger length indicating predominance of additive gene action which can be easily improved through direct selection provided it is not controlled by enormous number of genes with very less effect. Moderate heritability with moderate GAM were observed for days to 50% flowering, days to maturity, indicating presence of both additive and non additive gene action. Grain yield, fodder yield and few other traits like No. of fingers/ear, ear length, finger width and flag leaf width scored moderate heritability with moderate GAM indicating both additive and non additive gene action. Predominance of non additive gene action is expected for plant height, No. of productive tillers/plant and flag leaf length as they recorded moderate broad sense heritability coupled with low GAM. This study suggests that selection for grain yield directly is not worthier but it can be selected via other traits on which it is associated with which are mostly controlled by additive gene action.

Table 1: ANOVA of 18 finger millet genotypes.

	Mean Squares													
Source of Variations	df	Days to 50% flowering	Days to Maturity	Plant Height (cm)	No. of Prod. Tillers	No. of fingers/ Ear	Ear Length (cm)	Finger Length (cm)	Finger width (cm)	Leaf Length (cm)	Leaf width (cm)	Grain Yield (q/ha)	Fodder Yield (t/ha)	
Treatments	17	162.47**	196.55**	98.08**	0.30*	1.22**	2.55**	2.95**	0.03*	15.61*	0.03**	307.15**	63.44**	
Replications	2	4.50	0.24	50.73	0.11	1.10	2.14	1.46	0.05	32.63	0.22	25.61	14.42	
Error	34	1.97	1.65	24.08	0.15	0.26	0.54	0.40	0.02	7.96	0.01	82.41	16.94	

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S.		Days to	Days to	Plant	No. of	No. of	Ear	Finger	Finger	Flag leaf	Flag leaf	Grain	Fodder
No.	Entry	50%	Maturity	height	productive	fingers/	length	length	width	length	width	Yield	Yield
110.		flowering	wiaturity	(cm)	tillers	ear	(cm)	(cm)	(cm)	(cm)	(cm)	(q/ha)	(q/ha)
1	WN 585	77.3	106.7	110.3	2.4	8.9	10.0	6.4	0.9	32.8	1.1	30.4	66.4
2	RAuF	82.3	109.0	118.6	2.6	8.0	9.9	6.6	1.0	36.7	1.2	26.5	59.3
3	VL 352	69.0	100.7	119.7	2.3	8.7	9.2	5.8	1.0	36.2	1.0	22.6	59.8
4	PR 10-35	88.3	117.3	121.5	2.5	8.3	8.6	4.9	1.0	35.3	1.0	24.5	67.0
5	PR 1511	89.3	118.7	120.0	3.1	7.0	11.7	8.3	1.1	40.2	1.1	25.2	75.3
6	KOPN 1059	85.0	115.3	116.5	2.3	7.7	9.5	7.4	1.0	36.7	1.0	26.3	85.6
7	OEB 601	79.7	111.0	126.1	2.7	7.5	9.5	6.0	1.1	40.9	0.9	22.8	86.8
8	PR 202	88.0	125.0	120.9	2.7	7.5	9.0	5.4	1.1	36.0	1.0	27.8	78.8
9	WN 559	95.3	127.3	121.1	2.1	7.3	11.2	8.1	1.1	35.5	1.1	28.9	79.2
10	KOPN 942	85.7	116.0	117.3	2.7	6.9	9.9	7.4	1.2	40.0	1.2	23.5	77.3
11	ML 322	88.0	119.0	110.3	2.7	7.1	9.6	6.9	1.1	40.2	1.1	24.1	59.0
12	WN 550	96.3	127.3	109.5	2.5	7.9	9.3	6.3	1.2	34.6	1.2	28.0	79.1
13	GPU 67	92.0	121.7	108.6	2.3	7.4	8.8	5.7	1.1	38.9	1.3	30.3	76.7
14	OEB 602	75.3	103.3	123.5	1.9	6.9	8.6	5.3	1.1	36.3	1.0	26.2	75.7
15	VR 1101	87.0	114.3	118.8	3.0	8.5	8.8	7.2	1.3	36.7	1.1	42.7	95.4
16	RAuF 13	83.3	115.3	120.5	2.3	8.5	8.9	5.5	1.0	38.3	1.0	31.4	78.1
17	GPU 45	73.7	102.7	112.9	2.3	7.3	8.0	6.3	1.0	35.0	1.2	25.4	85.6
18	Sri Chaitnaya	88.3	118.7	128.3	2.1	7.5	8.7	5.6	1.1	35.1	1.0	27.4	70.8
	GM	84.67	114.96	118.03	2.46	7.71	9.40	6.40	1.07	36.97	1.09	27.44	75.33
	Maximum	96.3	127.3	128.3	3.1	8.9	11.7	8.3	1.3	40.9	1.3	42.7	95.4
	Minimum	69.0	100.7	108.6	1.9	6.9	8.0	4.9	0.9	32.8	0.9	22.6	59.0
	CD (5%)	2.33	2.13	8.14	0.64	0.84	1.22	1.04	0.20	4.68	0.15	6.83	15.06
	CD (1%)	3.13	2.86	10.93	0.87	1.13	1.64	1.40	0.27	6.28	0.21	9.17	20.22
	CV (%)	1.66	1.12	4.16	15.78	6.58	7.83	9.83	11.36	7.63	8.57	15.00	12.05

Table 2: Mean values and Summary Statistics of 18 finger millet genotypes

Table 3: Genetic parameters of 18 finger millet genotypes.

S. No		Days to 50% flower	Days to Maturity	Plant height (cm)	No. of prod. tillers	No. of fingers/ ear		Finger length (cm)	Finger width (cm)	Flag leaf length (cm)	Flag leaf width (cm)	Grain Yield (q/ha)	Fodder Yield (q/ha)
1	GCV	8.64	7.01	4.208	9.057	7.335	8.70	14.40	7.21	4.32	7.59	14.345	11.49
2	PCV	8.80	7.10	5.916	18.195	9.854	11.71	17.44	13.45	8.77	11.45	20.755	16.65
3	ECV	1.66	1.12	4.158	15.781	6.581	7.83	9.83	11.36	7.63	8.57	14.999	12.05
4	H ² (Broad Sense)	96.45	97.52	50.598	24.778	55.403	55.23	68.24	28.72	24.28	43.93	47.771	47.62
5	Genetic Advance	14.80	16.40	7.278	0.229	0.867	1.25	1.57	0.08	1.62	0.11	5.605	12.30
6	GAM	17.48	14.26	6.166	9.287	11.247	13.32	24.51	7.96	4.39	10.36	20.424	16.33

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