Assessment of Variability, Heritability and Genetic Advance for Quantitative Characters in Finger millet [*Eleusine coracana* (L.) Gaertn] Germplasm

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ABSTRACT

The experimental material comprised 30 finger millet (*Eleusine coracana* (L.) Gaertn) germplasm accessions. The data collected on twelve quantitative traits to know the genetic variability, heritability and genetic advance existing in the material. The analysis of variance (ANOVA) revealed highly significant differences (P <0.01) among the accessions for all twelve characters, except for leaf width, number of productive tillers per plant and finger width. The genotypic coefficient of variation for all the characters studied was lesser than the phenotypic coefficient of variation indicating the effect of environment. High PCV and GCV was recorded for leaf width, finger width, ear length and finger length. High heritability coupled with high genetic advance as percent of mean was recorded for all the characters except for plant height, number productive tillers per plant, days to 50 % flowering and days to maturity. Thus, these traits are predominantly under the control of additive gene action and hence these characters can be improved by selection.

Finger millet (*Eleusine coracana* L. Gaertn.) is one of the small millets valued for food, fodder and nutritional security. It is an allotetraploid with $2n = 4x = 36$ chromosomes and is highly self-pollinated annual crop which is cultivated in arid and semi-arid regions of Central Africa and India. It belongs to the family poaceae, sub-family, chloridoideae (Anuradha *et al*., 2020). In India, it occupies sixth position after wheat, rice, maize, sorghum and bajra and is mainly grown in the states of Karnataka, Tamil Nadu, Andhra Pradesh, Maharashtra, Orissa, Gujarat, Jharkhand, Uttar Pradesh, Madhya Pradesh and Uttarakhand.

Finger millet is a drought-hardy crop can grow well under low moisture and hot environmental conditions, because it has an effective carbon assimilating mechanism through C_4 pathway (Huang *et al*., 2017). The grains are highly nutritious as it contains 65-75% carbohydrates, 7-10% high quality protein, 15-20 % dietary fibre (Chetan and Malleshi, 2007). It is the richest source of calcium (344 mg/100 g), iron (3.9 mg/100 g), phosphorus (283 mg/100 g), potassium (408 mg/100 g) and other minerals. It is highly valued and serves as a food reserve in the times of famine (Mahanthesha *et al*., 2017). Being rich in protein and calcium, it serves as 'nutritious millet'

for rural populations. Like other major cereals (rice and wheat), finger millet has been suggested as a way to support in improving the nutritional security in developing nations of Asia and Africa (Puranik *et al*., 2017). It also has key essential amino acids like tryptophan, methionine, threonine, valine, isoleucine and cystine which are required for good health.

Exploitation of genetic variability existing in the working germplasm is the first principle in the improvement of any crop. Knowledge on the magnitude of variability present in a crop species for different traits is of utmost importance as it provides the basis for effective selection. The phenotype of a character is the result of interaction between genotype and environment. Partitioning of phenotypic variability into heritable and non-heritable components is essential to get a true indication of the genetic variation of the trait. Heritability measures the relative amount of the heritable portion of variability. Consistency in the performance of selection in succeeding generations depends on the magnitude of heritable variation present in relation to phenotypic variation. Basic information on heritability is a pre-requisite for planning any breeding programme. Genetic advance indicates the amount of progress that could be

expected with selection for a particular character. Estimates of heritability along with estimates of genetic advance are more useful in selection method rather than heritability or genetic advance alone (Johnson *et al*., 1955)

MATERIAL AND METHODS

The experimental material of finger millet consists of thirty germplasm which includes minicore lines, elite varieties, elite germplasm, exotic lines, mutants, breeding materials, and genetic stocks collected from Indian institute of millets research, Hyderabad. The experiment was laid out in alpha lattice with two replications at agricultural research station, Vizianagaram during *Kharif* 2022. By adopting a spacing of 22.5 cm between rows and 10 cm between plants respectively. All recommended package of practices were followed to raise good and healthy crop stand. Data were collected on twelve yield and yield contributing characters *viz*., days to 50% flowering, days to maturity, plant height (cm), number of productive tillers per plant, ear head length (cm), number of fingers per ear head, finger length (cm), finger width (cm), flag leaf length (cm), flag leaf width (cm), grain yield (q/ha) and fodder yield (t/ha).

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

RESULTS AND DISCUSSION

The analysis of variance (ANOVA) revealed highly significant differences (P <0.01) among the accessions for all twelve characters, except for leaf width, number of productive tillers per plant and finger width (Table 1), indicating that the presence of high genetic diversity among finger millet accessions. Variations in finger millet genotypes were also reported by Singamsetti *et al*. (2018), Mahanthesha *et al*. (2017), Kumari and Singh (2015) and Kumar *et al*. (2010). The estimates of mean, range, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability in broad sense (h^2)

and genetic advance as percent of mean (GAM) were presented in Table 3.

The existence of wide ranges of variations between minimum and maximum values of each trait (Table 2) indicates the presence of considerable variation among the accessions studied. This variation provides ample opportunities for the genetic improvement of the crop through breeding. Days to 50 % flowering varied from 86 to 103 days with a mean of 95 days. Days to maturity varied from 117 to 135 days with a mean of 128 days. Plant height ranged from 81.1 cm to 124.3 cm with a mean of 106.79 cm. Mean number of productive tillers per plant was 5.54 with ranges of 3.90 to 7.30. Mean fingers per ear head was 9.19 with a range of 6.80 to 11.20. Ear length ranged from 6.73 to 16.77 with a mean of 9.70. Whereas finger length and finger width ranged from 4.75 to 13.10 and 0.42 to 1.25 with a mean of 7.23 and 0.63 respectively. Leaf length ranged from 26.49 to 46.86 with a mean of 35.86. Mean leaf width was 0.92 with a range of 0.48 to 1.49. Mean grain yield and fodder yield and was 31.18 and 45.1 with a range of 22.92 to 48.89 and 32.25 to 62.00 respectively.

Improvement of economic characters like yield through selection is conditioned by the nature and magnitude of variability present in the populations. However the phenotypic expression of complex character like yield is influenced by environment, genotype and their interactions. This suggests the need for partition of overall variability into heritable and non-heritable components by using appropriate statistical techniques. The success of any crop improvement programme largely depends on the magnitude of genetic variability. The genotypic component being the heritable part of the total variability, its magnitude for yield and its component characters which influences the selection strategies to be adopted by the breeders.

Phenotypic Coefficient of Variation (PCV) was higher than Genotypic Coefficient of Variation (GCV) for all traits studied indicating the role of environment in expression of characters. Highest PCV and GCV were observed for leaf width (32.21, 31.09) followed by finger width (30.16, 29.30), ear length (27.04, 25.99) and finger length (23.90, 22.47). Hence, these characters are more suitable for direct selection. Similar findings were reported by Reddy *et al*. (2013) and Priyadharshini *et al*. (2011).

Environment coefficient of variation (ECV) was more than 10% for number of productive tillers per plant, ear length, finger length, finger width, leaf width, grain yield and fodder yield indicating the role of environment in attaining the phenotype for these traits (Table 3). Whereas moderate PCV and GCV were observed for leaf length (14.38, 13.20) and number of fingers per ear head (13.87, 12.14).

For reliable selection on has to depend on heritability studies. Highly heritable traits are governed by genotypic variances rather than with environmental variance. Heritability which is the heritable portion of phenotypic variance is a good index of transmission of characters from parents to offspring (Falconer, 1981). Hence, there is more chance for success in selection of genotypes based on heritability and it informs whether the variation is genetic or non genetic. The heritability estimates alone do not provide reliable information about the gene governing the expression of a particular character and this do not provide the information of the amount of genetic progress that would result from the selection of best individuals. Johanson *et al*. (1995) had pointed about that the heritability estimates along with genetic advance were more useful than heritability estimates alone in predicting the response to selection.

The genotypes under study showed high heritability for all the characters except for number of productive tillers per plant. Highest heritability was recorded for days to 50 % flowering (96.43) followed by finger width (94.35), days to maturity (93.93), leaf width (93.16), ear length (92.38), finger length (88.39), leaf length (84.20), number of fingers per ear head (76.51), grain yield (76.16) and fodder yield (70.15). Heritability estimates were more than 70% for all the characters studied which indicates that these characters were less influenced by environmental conditions and phenotypic selection would be effective for these characters.

Heritability and genetic advance are important selection parameters. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection. High heritability coupled with high genetic advance as percent of mean was observed for all the characters except plant height, number productive tillers per plant, days to 50 % flowering and days to maturity. Direct selection for these characters would be effective as heritability and

genetic advance are high due to additive gene interaction. Similar results of high heritability and high genetic advance as percent of mean is observed by Reddy *et al*. (2013) for number of fingers per ear head and earhead length, Kumari and Singh (2015) for grain yield per plant, Devaliya (2018) for fodder yield per plant.

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Table1: Analysis of variance for twelve traits in thirty finger millet germplasm accessions

Source of variation	Df	Mean sum of squares											
		DFF	DM	PH	NPT	NFE	EL	FL	FW	LL	LW	GY	FY
Treatments	29	44.117	33.956	293.555	0.961	3.249	13.758	5.979	0.071	53.195	0.177	80.333	173.095
Replication	1	4.267	3.267	1314.144	1.734	13.067	7.336	0.657	0.034	285.057	0.008	41.076	3.862
Error	29	1.577	2.06	79.027	0.395	0.763	1.048	0.694	0.004	8.403	0.012	19.153	51.661

Note: DFF: Days to 50 % flowering, DM: Days to maturity, PH: Plant height, NPT: Number of productive tillers per plant, NFE: Number of fingers per head, EL: Ear head length, FL: Finger length, FW: Finger width, LL: Leaf length, LW: Leaf width, GY: Grain yield, FY: Fodder yield

Table 2: Mean performance of 30 finger millet germplasm accessions

S.No	Germplasm Accession	DFF	DM	PH	NPT	NFE	EL	FL	FW	LL	LW	GY	FY
1	IE 501	87.5	117	93.6	5.7	8.6	6.73	4.75	0.94	26.49	0.66	24.94	46.42
2	IE- 518	87.5	118.5	90.7	3.9	8.8	7.23	5.44	0.6	28.68	0.65	23.99	34.33
3	IE-2034	102	133	108.3	5.4	6.8	8.03	6.68	0.5	37.48	1.06	35.29	49.84
4	IE-2217	100.5	133	114.1	7.3	8.5	8.5	7.27	0.47	38.24	0.8	25.97	37.2
5	IE-2296	103	134.5	105.5	5.7	7.1	8.72	6.5	0.85	37.32	0.78	41.26	58.21
6	IE-2312	88	121	122.9	4.4	10.5	11.71	8.75	0.42	40.25	0.91	33.23	59.25
7	IE-2430	98.5	127	124	5.2	9.6	8.66	6.87	0.56	37.64	0.53	24.85	39.55
8	IE-2437	93	127	124.3	5.2	10.3	9.16	7.14	0.61	36.96	0.71	23.45	40.29
9	IE-2457	90.5	123.5	123.2	6.3	10.4	8.86	7.54	0.64	34.46	0.58	30.6	42.27
10	IE-2572	98.5	131	118.5	5.4	7.4	16.77	13.1	0.45	46.86	1.44	22.92	38.65
11	IE-2589	95	127.5	119.3	5.4	8.9	10.38	6.19	0.47	29.83	0.62	36.6	60.65
12	IE-2606	96.5	125.5	122.2	5.3	11.2	8.23	6.44	0.63	31.91	0.48	35.14	56.05
13	IE-2619	93	129	98.5	5.3	8	9.58	6.94	0.98	30.32	0.84	28.4	33.17
14	IE-2710	100.5	131.5	101.6	5.5	8.1	9.86	7.08	1.25	36.51	1.37	48.89	58.55
15	IE-2790	99	128.5	118.5	6.1	10.9	14.55	9.8	0.53	43.18	1.49	32.08	42.68
16	IE-2872	93	126	98.8	5.8	9	9.05	6.89	0.46	32.32	0.5	41.54	62
17	IE-2911	95	126.5	109.8	5.8	8.8	12.73	8.87	0.48	37.34	1.2	42.78	60.75
18	IE-2957	97	130.5	110.7	6.6	10.5	14.42	8.32	0.49	38.14	1.37	32.93	49.4
19	IE-3045	101.5	132.5	89.2	5.4	9.6	9.78	7.08	0.59	37.48	1.03	25.97	43.8
20	IE-3077	94.5	129	104.3	5.4	11	7.55	5.93	0.53	37.88	1.02	27.9	37.1
21	IE-3104	85.5	123	102.6	6.2	9.3	7.84	5.97	0.54	28.54	0.75	29.5	33.85
22	IE-3391	94	127	81.3	6.5	8.7	7.2	5.25	0.96	29.05	0.62	29.75	33.5
23	IE-3392	90.5	125.5	85.3	4.8	7	6.79	5.05	0.58	27.96	0.76	27.9	32.25
24	IE-3470	93.5	129	95.4	6.3	9.4	7.97	7.05	0.64	32.64	0.99	26.9	41.11
25	IE-3475	101	130	111.9	4.5	10.7	8.03	6.54	0.67	45.42	1.38	29.03	41.26
26	IE-3721	97.5	129.5	105.2	5.1	9.8	8.9	6.89	0.68	36.42	1.2	26	42.08
27	IE-3952	94	128	97	5.2	9.6	7.68	5.95	0.58	38.22	0.92	37.13	50.05
28	IE-4028	90.5	126.5	110.7	5.9	7.6	8.76	7.2	0.58	37.8	0.9	30.85	45.75
29	IE-4057	95	130.5	102.4	5.6	8.7	13.38	9.93	0.57	39.7	1.13	30.56	43.86
30	IE-4073	97.5	131	113.8	5.1	10.8	13.88	9.59	0.54	40.67	1.04	29.03	39.31
	Mean	95	128	106.79	5.54	9.19	9.7	7.23	0.63	35.86	0.92	31.18	45.1
	CD (5%)	2.57	2.93	18.18	1.28	1.79	2.09	1.7	0.13	5.93	0.23	8.95	14.698
	CD (1%)	3.46	3.96	24.5	1.73	2.41	2.82	2.3	0.18	7.99	0.3	12.06	19.809
	CV (%)	1.32	1.12	8.32	11.33	9.51	10.56	11.52	10.14	8.08	11.91	14.04	15.935

Note: DFF: Days to 50 % flowering, DM: Days to maturity, PH: Plant height, NPT: Number of productive tillers per plant, NFE: Number of fingers per head, EL: Ear head length, FL: Finger length, FW: Finger width, LL: Leaf length, LW: Leaf width, GY: Grain yield, FY: Fodder yield

Table 3: Genetic parameters of 30 finger millet germplasm accessions

S.No	Parameter	DFF	DM	PH	NPT	NFE	EL	FL	FW	LL	LW	GY	FY
1	Mean	95	128	106.8	5.54	9.19	9.7	7.23	0.63	35.86	0.92	31.18	45.1
2	Minimum	86	117	81.3	3.9	6.8	6.73	4.75	0.42	26.49	0.48	22.92	32.25
3	Maximum	103	135	124.3	7.3	11.2	16.77	13.1	1.25	46.86	1.49	48.89	62
4	GCV	4.85	3.13	9.7	9.6	12.14	25.99	22.47	29.3	13.2	31.09	17.74	17.275
5	PCV	4.94	3.23	11.35	12.5	13.87	27.04	23.9	30.16	14.38	32.21	20.33	20.625
6	ECV	1.32	1.12	8.32	11.3	9.51	10.56	11.52	10.14	8.08	11.91	14.04	15.935
7	H^2	96.4	93.9	73.08	58.9	76.51	92.38	88.39	94.35	84.2	93.16	76.16	70.155
8	Genetic advance	9.33	7.97	18.24	0.84	2.01	4.99	3.15	0.37	8.95	0.57	9.94	13.44
9	GAM	9.81	6.24	17.08	15.2	21.87	51.47	43.53	58.62	24.95	61.82	31.89	29.807

Note: DFF: Days to 50 % flowering, DM: Days to maturity, PH: Plant height, NPT: Number of productive tillers per plant, NFE: Number of fingers per head, EL: Ear head length, FL: Finger length, FW: Finger width, LL: Leaf length, LW: Leaf width, GY: Grain yield, FY: Fodder yield

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