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Genetic Variability and Diversity Studies on Yield and Quality Traits in Finger Millet (*Eleusine coracana* (L.) Gaertn.)

Ravikanth Bendi, N. D. R. K. Sarma

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Abstract The present study aims to reveal the importance of some yield and quality traits, genetic variability and diversity existing in the 55 genotypes of finger millet. The coefficient of variation at phenotypic (PCV) and genotypic (GCV) levels were high for number of basal tillers, peduncle length, inflorescence length, inflorescence width, length of finger, grain yield plant^{-1}. High heritability coupled with high genetic advance observed in days to 50% flowering, plant height, number of basal tillers, peduncle length, inflorescence exertion, inflorescence length, inflorescence width, length of finger, number of fingers ear^{-1}, grain yield plant^{-1} which indicates the predominance of additive gene effects. Mahalanobis D^2 analysis grouped the 55 genotypes into eight clusters. Clustering pattern failed to indicate any relationship between genetic diversity and geographic diversity. Cluster 1 (29) has the maximum number of genotypes followed by II (11), III (9), IV (2) and remaining four were solitary clusters. Among the characters studied calcium content followed by days to 50% flowering contributed maximum towards the total divergence.

Keywords Finger millet, Genetic divergence, D^2 statistic.

Introduction

Finger millet (*Eleusine coracana* (L.) Geartn.) also known as birds foot millet, ranks first both in area and production among the small millets grown in India. Early maturity, low input requirements, freedom from major pest and diseases have made it an important crop of dry land farming. The nutritional quality of finger millet grain makes it an ideal food for infants and invalids. Finger millet grain is nutritious with high quality protein, rich in minerals, dietary fiber, phytochemicals and vitamins. It is the richest source of calcium (358 mg/100 g) which is eight to ten times more than that of wheat or rice [1].

Improvement of any crop depends upon the presence of wide spectrum of variability in the germplasm and its utilization in the breeding program. Besides genetic variability, knowledge on heritability and genetic advance plays a predictive role in breeding. Since many quantitative characters are highly influenced by environment, there is a need to partition the overall variability into its heritable and non-heritable components with the help of suitable genetic parameters such as genetic coefficient of variation, heritability estimates and genetic advance. Estimates of both heritability and genetic advance as per cent of mean are more useful in the choice of selection method, rather than heritability or high genetic advance alone.

The knowledge of characters influencing divergence is an important aspect for a breeder. Information on the nature and degree of genetic divergence would help the plant breeder to choose right parents for breeding programs. Genetic improvement through

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R. Bendi*, N.D.R.K.Sarma
Department of Genetics & Plant Breeding, Agricultural College, Naira,
Acharya N. G. Ranga Agricultural University 532185 (AP), India
e-mail: bendi.ravikanth@gmail.com
*Correspondence

Table 1. Analysis of variance for 14 characters in 55 finger millet genotypes.

Sl. No.	Character	Replications (df:2)	Treatments (df : 54)	Error (df : 108)
1	DTF	9.382	580.904**	4.153
2	PH	12.314	892.180**	41.015
3	NBT	0.122	1.847**	0.076
4	FLL	407.05	4748.623**	526.594
5	PL	162.087	1820.468**	153.469
6	IE	107.487	1563.864**	82.542
7	IL	20.396	1393.205**	31.420
8	IW	16.771	537.604**	32.234
9	NFE	0.059	2.602**	0.342
10	FL	28.382	1257.155**	29.784
11	FW	0.213	2.450**	0.486
12	GYP	1.943	23.739**	0.587
13	SPC	0.111	4.464**	0.170
14	CC	2.142	4601.933**	3.989

conventional breeding approaches depends mainly on the availability of the diverse germplasm and the amount of genetic variability present in the population [2].

Materials and Methods

The experimental material consists of 55 finger millet genotypes obtained from Agricultural Research Station, Vizianagaram (AP). The material was grown in randomized block design with three replications at Agricultural college farm, Naira (AP). Each entry was grown in two rows of three meter length with a spacing of 30 × 10 cm. The data was recorded on five randomly selected plants for 14 quantitative traits viz., days to 50% flowering (plot basis), plant height (cm), number of basal tillers, flag leaf length (mm), peduncle length (mm), inflorescence exertion (mm), inflorescence length (mm), inflorescence width (mm), length of finger (mm), width of finger (mm), number of fingers ear^{-1}, seed protein content (%) (estimated by Microkjeldahl method), calcium content (mg/100g) (estimated by Versenate titration method) and grain yield plant^{-1} (g).

Standard statistical procedures were used for the analysis of variance, genotypic and phenotypic coefficients of variation (GCV and PCV), heritability and genetic advance. Genetic divergence was estimated by multivariate analysis using Mahalanobis D^2 statistic. On the basis of D^2 values genotypes were grouped into different cluster, according to Tocher's method.

Results and Discussion

The analysis of variance showed a wide range of varia-

Table 2. Mean, coefficient of variation, heritability (broad sense), genetic advance and GA as per cent of mean for 14 characters in 55 finger millet genotypes. DTF= days to 50% flowering, PH=plant height (cm), NBT=number of basal tillers, FLL=flag leaf length (mm), PL=peduncle length (mm), IE=inflorescence exertion (mm), IL=inflorescence length (mm), IW=inflorescence width (mm), FL=length of finger (mm), FW=width of finger (mm), NFE=number of fingers ear^{-1}, SPC=seed protein content (%), GYP=grain yield plant^{-1}, CC=calcium content.

Character	Mean	Co\erfficient of variation		Variance		h^2 (b) (%)	Genetic advance	Genetic advance as per cent of mean (%)
		Genotypic (%)	Phenotypic (%)	Genotypic	Phenotypic			
DTF	82.22	16.86	17.05	192.25	196.40	98.00	28.26	34.37
PH	113.31	14.87	15.90	283.72	324.74	87.37	32.43	28.62
NBT	2.32	32.98	35.51	0.59	0.67	86.30	1.46	63.13
FLL	336.60	11.15	13.06	1407.34	1933.94	73.00	65.92	19.59
PL	203.15	11.60	13.11	555.67	709.14	78.00	42.98	21.16
IE	107.73	20.63	22.28	493.77	576.32	86.00	42.37	39.33
IL	72.90	29.23	30.22	453.93	485.35	94.00	42.45	58.22
IW	55.55	23.36	25.50	168.46	200.69	84.00	54.50	44.10
NFE	6.76	12.85	15.49	0.75	1.10	69.00	1.48	21.95
FL	74.69	27.08	28.05	409.12	438.91	93.00	40.23	53.86
FW	10.43	7.76	10.24	0.65	1.14	57.00	1.26	12.11
GYP	8.17	30.73	35.32	7.15	9.44	76.00	4.79	55.09
SPC	9.73	12.30	13.01	1.43	1.60	89.38	2.33	23.96
CC	317.97	12.31	12.33	1532.65	1536.64	99.74	80.54	25.33

Table 3. Clustering pattern of 55 finger millet genotypes by Tocher's method.

Cluster No.	No. of genotypes	Name of genotype (s)
I	22	IE 3470, IE 4709, IE 3614, IE 4734, IE 3077, IE 4673, VR (w) 936, IE 4759, IE 3391, IE 3317, VR 762, IE 3618, IE 2217-2, IE 5817, IE 2619, IE 588, PR 202, IE 6421, IE 6473, IE 2217-1, IE 3945, IE 6294
II	11	IE 6337, IE 2590, IE 6082, IE 4795, IE 2884, IE 4163, IE 6350, IE 5537, IE 5367, VR 847, IE 5106
III	6	IE 2093, IE 3543, IE 501, IE 2293, VR 708, IE 4110
IV	10	IE 6326, IE 4646, IE 4570, IE 2457, IE 5736, IE 4671, IE 2296, IE 4329, IE 4816, IE 2652
V	1	IE 2322
VI	2	IE 6154, IE 4545
VII	2	IE 2323, IE 196
VIII	1	IE 2790

tion and significant differences for all the 14 characters under study (Table 1), indicating the presence of adequate variability. The recordings of the means, range, co-efficient of variation, heritability and genetic advance as percent of mean are presented in Table 2. Highest PCV was recorded by number of basal tillers, whereas lowest was recorded by finger width. Genotypic co-efficient of variation (GCV) followed the similar trend as that of PCV. The co-efficient of variation at phenotypic (PCV) and Genotypic (GCV) levels were high for the traits number of basal tillers, inflorescence length and grain yield plant^{-1}. The similar results of high PCV and GCV were reported by Kadam [3] for number of basal tillers, inflorescence length, inflorescence width, length of finger and grain yield plant^{-1}. In the present study, heritability was high for all the characters viz., calcium content, days to 50% flowering, inflorescence length, finger length and seed protein content.

In the present set of materials, all the characters except flag leaf length and finger width expressed moderate to high genetic advance as percent of mean. Similar trend was reported [4]. The highest genetic advance as per cent of mean was expressed by the trait number of basal tillers (63.13%) and the lowest (12.11%) was expressed by the trait finger width.

The significant estimates of V statistics during the analysis revealed significant differences among mean values of different correlated variables, thus analysis of genetic divergence among the tested germplasm was considered to be relevant. Based on relative magnitude of D^2 values 55 genotypes were grouped into eight clusters (Table 3). Cluster 1 had the maximum of 22 genotypes followed by cluster II (11), cluster IV (10), cluster III (6), cluster VI (2) and cluster VII (2) while cluster V and VII were solitary.

The average intra and inter cluster D^2 values (Table 4) showed that the intra cluster distance ranged from 33.93 (cluster VI) to 107.35 (cluster IV).The clus-

Table 4. Average intra (diagonal) and inter-cluster D^2 values among eight clusters.

	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5	Cluster 6	Cluster 7	Cluster 8
Cluster 1	84.77	398.06	437.01	231.95	121.38	955.02	210.3	378.37
Cluster 2		98.05	235.11	926.85	511.76	222.81	611.22	883.23
Cluster 3			106.69	1003.34	372.3	388.84	365.19	1143.01
Cluster 4				107.35	288.47	1772.37	394.63	304.39
Cluster 5					0	1067.43	91.34	427.72
Cluster 6						33.93	1180.97	1586.19
Cluster 7							51.74	741.97
Cluster 8								0

Table 5. Mean values of eight clusters estimated by Tocher's method. Values in bold indicates maximum and minimum. DTF= days to 50% flowering, PH=plant height (cm), NBT=number of basal tillers, FLL=flag leaf length (mm), PL=peduncle length (mm), JE=inflorescence exertion (mm), IL=inflorescence length (mm), IW=inflorescence width (mm), FL=length of finger (mm), FW=width of finger (mm), NFE=number of fingers ear^{-1}, SPC=seed protein content (%), GYP=grain yield plant^{-1}, CC=calcium content.

	DFF	PH	NBT	FLL	PL	IE	IL	IW	NFE	FL	FW	GYP	SPC	CC
Cluster 1	83.09	120.43	2.35	346.46	208.74	110.63	68.61	55.57	6.78	70.36	10.48	9.63	10.18	305.20
Cluster 2	90.97	111.70	1.76	311.34	196.72	103.57	72.33	52.37	6.47	73.85	10.29	6.58	9.55	361.86
Cluster 3	57.56	84.43	3.10	319.37	213.15	114.88	55.64	46.16	7.51	59.42	9.45	8.08	9.93	350.96
Cluster 4	91.27	118.28	1.97	339.40	188.17	98.08	80.34	56.90	6.40	80.99	11.00	8.07	8.99	270.53
Cluster 5	54.33	110.47	2.62	348.17	205.10	107.83	92.46	72.14	7.60	95.30	10.27	12.40	10.39	299.27
Cluster 6	87.00	130.03	2.07	371.81	214.38	125.75	86.63	56.63	5.94	88.73	12.13	9.77	9.20	402.76
Cluster 7	56.00	79.91	4.33	345.01	235.12	136.37	55.93	47.95	7.78	61.02	9.34	11.09	8.77	293.85
Cluster 8	95.00	133.93	2.13	428.20	152.67	49.78	189.67	129.33	7.13	186.67	9.93	11.08	10.22	289.85

ter means estimated over genotypes for the 14 characters revealed considerable inter cluster variation (Table 5). Cluster VII exhibited higher mean values for flag leaf length, flag leaf width, inflorescence length, inflorescence width and length of finger.

Based on intra and inter-cluster distance among the groups, it is suggested to make crosses, between the genotypes of the clusters V (IE 2323) and VI (IE 6154, IE 4545) for protein content and calcium content; and cluster VI (IE 6154, IE 4545) and VIII (IE 2790) for yield after confirming their general combining ability for evolving transgressive segregants for yield and yield components.

Table 6. Contribution of different characters to total diversity.

Source	Times ranked 1st	Contribution %
Days to 50% flowering	217.00	14.61
Plant height (cm)	3.00	0.20
No. of basal tillers	4.00	0.27
Flag leaf length (mm)	5.00	0.34
Peduncle length (mm)	11.00	0.74
Inflorescence exertion (mm)	7.00	0.47
Inflorescence length (mm)	47.00	3.17
Inflorescence width (mm)	0.01	0.00
Number of fingers ear^{-1}	8.00	0.54
Finger length	0.01	0.00
Finger width	0.01	0.00
Grain yield plant^{-1}	6.00	0.40
Seed protein content (%)	51.00	3.43
Calcium content (mg/100g)	1126.00	75.82

Contribution of different characters towards genetic divergence is presented in Table 6. The traits calcium content (75.82%) contributed maximum towards total diversity followed by days to 50% flowering (14.61%), seed protein content (3.43), inflorescence length (3.17%). The highest contribution of days to 50% flowering for total genetic divergence in finger millet had been reported earlier [5].

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