



Research Article

GENETIC VARIABILITY OF DIVERSE CULTIVATED FINGER MILLET [*ELEUSINE CORACANA* (L.) GAERTN] GENOTYPES

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Abstract: The genetic variability of 33 selected finger millet genotypes were assessed for magnitude of genetic variability, heritability and genetic mean advance for yield and yield contributing traits. Significant genotypic difference was observed among genotypes for all the 15 yield and yield contributing characters. The traits such as main earhead weight recorded the highest estimates of GCV (57.87 %) followed by grain yield per plant (33.90 %) and shoot dry weight (33.56 %). All the characters except test weight, number of fingers per main ear, number of tillers per plant and number of earheads per plant recorded high heritability in the present study indicated the relatively lower influence of environmental factors on these characters and where, phenotypic selection would be effective. The grain yield per plant recorded significant low differences between GCV and PCV coupled with high heritability and high genetic mean advance. Therefore, grain yield per plant could be potentially used in the genetic improvement of finger millet through selection and hybridization.

Keywords: Finger millet, Genetic variability, Heritability, Genetic advance

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Introduction

Finger millet [*Eleusine coracana* (L.) Gaertn] is one among potential food and nutritional security crop for future because of its wider adaptability to changing environmental cues. The high nutritive value of finger millet coupled with its ability to thrive under low rainfall conditions makes it a climate-smart crop [1-2]. It is a self-pollinating, allotetraploid (AABB) with basic chromosome number of 9 ($2n=4x=36$). It ranks 4th in the world among millets after the sorghum, pearl millet and foxtail millet [3]. In India, finger millet accounts for about 85 percent of the total millet production and cultivated over 1.19 million hectares [4]. The cultivation of finger millet in India is mainly confined to regions of Karnataka, Tamil Nadu, Andhra Pradesh, Odisha, Maharashtra, Uttar Pradesh, Uttaranchal, Bihar and Gujarat. The evolution of crop plant is primarily depending on the existence of variability and the diversity in the population. Variability in broad sense refers to the presence of differences among the individuals in a population, which may arise due to differences either in the genetic constitution of an individual within a population or in the agro-climatic environment in which they are grown. The basic knowledge on such existing variability and diversity within a population is essential for effective selection of an individual in successful crop improvement programme. Since, the beginning of the systematic plant breeding, the existence of natural genetic variability and diversity between individuals within a population has been extensively studied and harnessed in the improvement of crop species for its wider adaptability, higher yield as well as resistance to biotic and abiotic factors [5]. Therefore, insights into the enormity of genetic variability present in a population are of paramount importance for a judicious breeding programme. In the present investigation, an attempt was made to estimate the extent of genetic variation for yield and yield related traits in different cultivated finger millet genotypes.

Materials and Method

Thirty three genotypes of finger millet were obtained from the All India

Coordinated Research Project on Small Millets (AICRPSM), GKVK, Bengaluru [Table-1]. Fifteen yield contributing characters were evaluated for analysis of variance (ANOVA), genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability [$h^2_{(bs)}$] and genetic advance as a percent mean (GAM) to assess the magnitude of genetic variability. The 33 finger millet genotypes were grown in randomized block design with two replications at the experimental field of Department of Plant Biotechnology, UAS, GKVK, Bengaluru during Kharif, 2018. Each genotype was grown in single row of 2 meters length with spacing of 22.5 cm between the rows and 10 cm between the plants. Five randomly selected competitive plants from each genotype in each replication were used to record observations of fifteen yield contributing characters.

Table-1 List of genotypes selected for genetic variability studies

SN	Genotypes	SN	Genotypes
1	GE156	18	GE3510
2	GE4201	19	GE4963
3	GE1377	20	PS1
4	GPU67	21	GE4568
5	GE4983	22	GE4832
6	GE2963	23	GE492
7	GE1200	24	GE4547
8	GE4731	25	GE12
9	GE1681	26	GPU28
10	GE113	27	GE4596
11	GE2866	28	GE4738
12	GE3461	29	GE4995
13	GE2735	30	GE292
14	GE1264	31	GE2358
15	L-5	32	GE1050
16	GE5118	33	PR202
17	GE199		

Table-2 Analysis of variance of fifteen traits in 33 genotypes of finger millet

MSS	Replication	Genotypes	Error	S. Em.±	CV (%)	CD at 5%	CD at 1%
Days to 50 % flowering	1.22	88.69**	1.07	0.73	1.31	2.11	2.83
Plant height (cm)	1.2	524.22**	22.41	3.35	6.64	9.64	12.97
No. of tillers	0.57	5.97**	1.72	0.93	26.63	2.67	3.6
Productive tillers	6.22	3.76**	1.68	0.92	28.9	2.64	3.55
No. of earheads plant ⁻¹	4.66	5.89**	2.11	1.03	26.14	2.96	3.98
Main earhead length (cm)	0.04	6.33**	0.51	0.5	10.95	1.45	1.95
No. of Fingers/ main ear	0	5.80*	3.04	1.23	27.17	3.55	4.78
Finger length (cm)	0	7.33**	0.22	0.34	8.28	0.97	1.3
Finger width (cm)	0	0.06**	0.01	0.08	12.45	0.22	0.29
Peduncle length (cm)	3.13	25.33**	2.62	1.15	7.67	3.3	4.43
Weight of main earhead (g)	1.87	9.78**	0.45	0.48	18.04	1.37	1.84
Total earhead weight/plant (g)	0.96*	104.98*	0.66	0.57	3.65	1.65	2.22
Shoot dry weight (g)	29.94	106.99**	17.71	2.98	21.13	8.57	11.52
Test weight (g)	0.08	0.49**	0.23	0.34	12.69	0.97	1.31
Grain yield/plant (g)	1.71	74.03**	0.46	0.48	3.78	1.38	1.85

**significant at P=0.05; * significant at P=0.01

Table-3 The Estimates of mean, range, variability (GCV and PCV), heritability [$h^2_{(bs)}$] and genetic advance mean (GAM) of all the characters in 33 finger millet genotypes

Characters	Mean	Range		GCV (%)	PCV (%)	H ² (%)	GAM
		Min.	Max.				
Days to 50 % flowering	78.86	61	96	8.39	8.5	97.61	13.47
Plant height (cm)	71.33	36.6	97.2	22.21	23.18	91.8	2.23
No. of tillers	4.93	2	10.25	29.57	39.79	55.21	1.3
Productive tillers	4.49	2.2	9.67	22.72	36.76	38.2	1.3
No. of earheads plant ⁻¹	5.56	2.6	11.67	24.75	35.99	47.27	6.26
Main earhead length (cm)	6.52	3.17	11	26.19	28.39	85.11	1.14
No. of Fingers/ main ear	6.42	2.8	17.17	18.3	32.76	31.2	3.77
Finger length (cm)	5.73	2	9.88	32.93	33.95	94.06	0.27
Finger width (cm)	0.86	0.5	1.42	18.51	22.31	68.86	4.25
Peduncle length (cm)	21.1	14.2	30.8	15.97	17.72	81.24	12.42
Weight of main earhead (g)	3.73	0.55	10.2	57.87	60.61	91.14	1.95
Total earhead weight/plant (g)	22.17	11.6	40.82	32.58	32.79	98.76	0.46
Shoot dry weight (g)	19.91	3.9	39.9	33.56	39.66	71.6	3.24
Test weight (g)	3.77	3	6.52	9.71	15.98	36.93	11.65
Grain yield/plant (g)	17.89	8.96	31.98	33.9	34.11	98.77	31.26

Result and Discussion

Genetic variability studies provide fundamental information on genetic parameters of genotypes, on which breeding practices are constituted for further crop improvement. The analysis of variance representing mean sum of squares due to replication, treatment (individual genotype) and error components for all the fifteen characters were presented in [Table-2]. The genotypic differences were highly significant for all the fifteen characters indicating the genotypes evaluated were highly variable for all the fifteen characters under observation. The amount of genetic variability observed among the genotypes suggested ample scope for utilizing these genotypes for in the crop improvement programme for yield and yield related traits. The estimates of range, mean, GCV, PCV, heritability and genetic advance as percentage of mean for all the fifteen characters evaluated were summarized in [Table-3]. The values of GCV and PCV for various yield and yield related traits were ranged between 8.39 percent to 57.87 percent and 8.50 percent to 60.61 percent respectively. The value of GCV and PCV of weight of main earhead (57.87 % and 60.61 %) was recorded to be highest among all the 15 characters followed by grain yield per plant (33.90 % and 34.11 %) and shoot dry weight (33.56 % and 39.66 %) and the values of GCV and PCV were least in days to 50 percent flowering (8.39 % and 8.50 %). Meanwhile, it is essential to mention the performance of difference genotypes for different characters of economic importance such as grain yield per plant, weight of main earhead, days to 50 percent flowering. The variability among genotypes for grain yield per plant was ranged between 8.96 g to 31.98 g, the genotypes such as GE4568 (31.98 g), GE4983 (27.82 g) and GE5118 (27.58 g) were the highest grain yielder. Likewise, other characters were also showed wide range of variation such as variation among days to 50 percent flowering was ranged from 61 days to 96 days, the genotypes such as GE1200 was found to be early flowering type (61 days) followed by GE1377 (68 days) and the genotype GE492 was the late flowering type (96 days). Similarly, the weight of main earhead displayed a variation ranging

from 0.55 g to 10.20 g and it was highest in GE156 (10.20 g) followed by PR202 (9.20 g), GE4596 (8.34 g) and least in GE12 (0.55 g). Such existence variation in finger millet genotypes for grain yield per plant and Days to 50 percent flowering were also observed in earlier studies [6-10]. Genetic variability for different quantitative characters can be directly measured on the basis of GCV [11]. Higher estimates of GCV was observed for weight of main earhead (57.87 %), grain yield per plant (33.90 %), shoot dry weight (33.56 %), total earhead weight per plant (32.58 %), finger length (32.93 %), number of tillers (29.57 %), main earhead length (26.19 %), number of earheads (24.75 %), productive tillers per plant (22.72 %), plant height (22.21 %). The traits such as peduncle length (15.97 %), number of fingers per main ear (18.30 %) and finger width (18.51 %) reported moderate estimates of GCV whereas, days to 50 percent flowering (8.39 %), test weight (9.71 %) reported the lower estimates of GCV. The estimates of difference between GCV and PCV was ranged between 0.11 percent to 14.46 percent. The lower differences between GCV and PCV were observed for traits such as days to 50 percent flowering (0.11 %), total earhead weight per plant (0.20 %), grain yield per plant (0.21 %), plant height (0.97 %), finger length (1.02 %), peduncle length (1.75 %) and earhead length (2.20 %). The lower differences between GCV and PCV observed for most of the traits in the present study were also reported by earlier studies indicating the good correspondence between the phenotypic and genotypic expression of these trait with lower influence of environment [7, 9, 12-15]. The heritability and genetic advances are two important parameters, heritability identifies the proportion of phenotypic variance that is due to genotype, as it measures the transmission of character from parent to offspring i.e., heritable and genetic advance provides an insight into the expected gain for particular character after the selection [16-17]. In the present investigation, the estimates of heritability in broad sense [$h^2_{(bs)}$] and genetic advance as a percent mean were also analyzed for all the fifteen characters under observation [18] [Table-3]. The estimates of heritability observed for all the yield and yield contributing characters

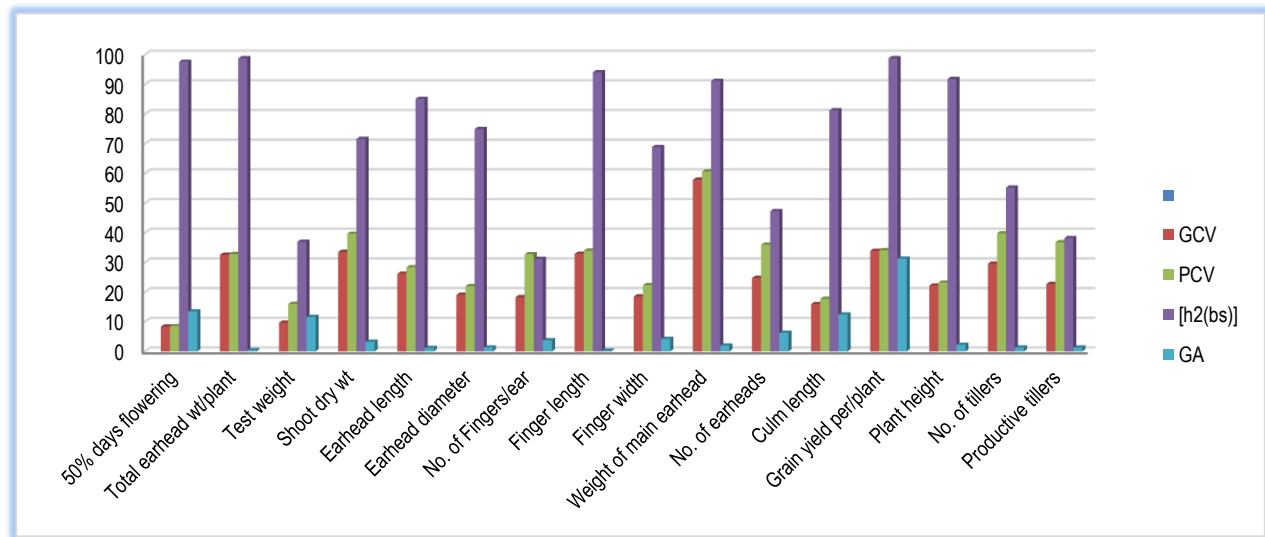


Fig-1 Combinatorial frequency of GCV, PCV, heritability and GAM estimated among 15 yield and yield related traits of finger millet

in the study were categorized as very high. The value of heritability was ranged from 31.20 -98.77 percent. The grain yield per plant recorded highest heritability value of 98.77 percent followed by total earhead weight per plant (98.76 %) and days to 50 percent flowering (97.61 %), finger length (94.06 %) and weight of main earhead (91.14 %) least for number of fingers per main ear (31.20 %). In the present study, all the characters except test weight, number of fingers per main ear, number of tillers and number of earheads showed the high broad sense heritability and later displayed the moderate heritability. High heritability for most of characters studied were also reported in earlier studies [7-10]. However, heritability alone does not necessarily index the genetic gain for the particular trait and it is suggested to consider the genetic advance together with heritability estimates for effective selection [17, 19]. The percent GAM values were ranged from 0.27 percent -31.26 percent [Table-3]. The highest GAM value 31.26 percent was observed for grain yield per plant, whereas days to 50 percent flowering (13.47 %), peduncle length (12.42 %), test weight (11.65 %) were recorded with moderate GAM values and it was least for finger length (0.27 %). In the present study, grain yield per plant was found to have the least difference between GCV and PCV coupled with high heritability and high GAM [Fig-1] and [Table-3]. High rate of heritability combined with moderate GAM was observed for days to 50 percent flowering, test weight and peduncle length.

The higher heritability combined with higher genetic advance can be attributed by additive gene action suggesting the improvement of trait through direct selection [20]. In the present study, higher heritability coupled with higher genetic advance as a percent of mean was observed for grain yield per plant suggesting direct selection of this character would be effective due to substantial contribution of additive gene towards genetic variability [7, 10, 12-14, 21]. The characters such as days to 50 percent flowering, peduncle length displayed high heritability with moderate genetic advance as a percent mean suggesting the possibility of further improvement of these traits. The traits such as total earhead weight per plant, weight of main earhead, shoot dry weight, earhead length, finger length, finger width and plant height displayed high heritability with low genetic advance and moderate heritability with low genetic advance as a percent mean was observed for test weight, number of tillers, productive tillers and number of earheads indicating the profound influence of environment on these traits, where selection would be ineffective [22-23].

Conclusion

The phenotype expression of a specific trait is determined by its genetic composition and the environment in which the plant is grown as well as the interaction between the genotype and the environment. The challenge for successful hybridization programme is to identify and select those divergent germplasm lines those conferring desirable phenotypes, rather than favorable phenotypes generated due to environmental effects.

Application of research: The significant low differences between GCV and PCV coupled with higher heritability and genetic mean advance as a percent mean was observed for single plant grain yield in the present study suggest the greater scope for utilization of this character as a selection criteria and improvement by direct selection of the genotype with high per se mean performance.

Research Category: Crop improvement

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Study area / Sample Collection: Department of Plant Biotechnology, University of Agricultural Sciences, GKV, Bengaluru, 560065, Karnataka, India

Cultivar / Variety / Breed name: Finger Millet [*Eleusine coracana* (L.) Gaertn]

Conflict of Interest: None declared

Ethical approval: This article does not contain any studies with human participants or animals performed by any of the authors.
Ethical Committee Approval Number: Nil

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