Genetic Variability Studies for Quantitative Traits in Finger Millet (Eluesine coracana L. Gaertn)

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ABSTRACT: Forty finger millet genotypes were examined for eleven quantitative traits *viz.*, days to 50% flowering, plant height, fodder yield plot⁻¹, days to maturity, main ear length, productive tillers/plant, dry fodder yield per plot, number of fingers per ear, thousand grain weight, harvest index and grain yield per plot to estimate variability parameters. Analysis of variance revealed that significant differences for all studied characters. Grain yield plot⁻¹, fodder yield plot⁻¹, dry fodder plot⁻¹ and thousand grain weight recorded high GCV, PCV, genetic advance as per cent of mean (GAM) and heritability implying that more variation and prevalence of additive gene action for these characters.

Keywords: GCV, PCV, Genetic advance, Heritability, GAM.

INTRODUCTION

Finger millet (*Eleusine coracana* L. Gaertn) belongs to the Poaceae family, sub-family Chloridoideae. It is a self-pollinated, allotetraploid with chromosome number 2n=4x=36. It is believed that finger millet originated in the Ethiopian highlands and was introduced to India about 3000 years ago (Babu *et al*., 2014). Among small millets, finger millet ranks third in terms of area and production in the country after sorghum and pearl millet. In India, finger millet is grown in an area of 11.14 lakh hectares, with a production of 16.69 lakh tonnes and a productivity level of 1497 kg/ha (Directorate of Economics and Statistics 2022-2023). In Andhra Pradesh, finger millet is cultivated in 30,000 hectares of land and produces 35,010 tonnes with a productivity of 1,167 kg/ha (Directorate of Economics and Statistics 2022- 2023).

Genetic variability in the breeding population is key to genetic improvement. Modern breeding programmes mainly focus on genetic variability creation, selection and utilizing that variation present in selected genotypes to develop new breeding materials. Most of the genetic traits are governed by polygenes which are greatly influenced by the environment. For effective selection of the trait, it is important to determine a heritability of that particular character. It is also advantageous to select a certain character based on both genetic advance and high heritability. Various parameters of genetic variability such as genetic advance, heritability (H), PCV and GCV for yield and yield attributing traits are key concerns for plant breeders and any crop improvement programme.

MATERIALS AND METHODS

The study was conducted at ARS, Perumallapalli, ANGRAU during *rabi*, 2022-23. Randomized complete block design (RBD) was used to lay out these genotypes with two replications. In the current study, eleven yield and yield component characters were recorded for GCV, PCV, GAM and heritability for 40 finger millet genotypes consisting of advanced breeding lines and released varieties. The data recorded for days to 50% flowering, main ear length (cm), plant height (cm), days to maturity, productive tillers/plant, fodder yield plot⁻¹ (kg), number of fingers per ear, dry fodder yield per plot (kg), thousand grain weight (g), harvest index (%) and grain yield plot⁻¹ (kg) by randomly selecting five competitive plants. Analysis of variance was calculated as per the procedure followed by Panse and Sukhatme (1957). Genotypic and phenotypic variability coefficients (GCV & PCV) were estimated as per Burton (1952). Broad sense

heritability was computed as per Allard (1960). According to Johnson *et al.* (1955) suggestion, the heritability range was sorted. GAM was estimated as formulated by Johnson *et al.* (1955). Characters were grouped together as high, moderate and low GAM as per the method suggested by Johnson *et al.* (1955).

RESULTS AND DISCUSSION

Analysis of variance revealed significant differences among all the 11 quantitative characters studied indicating that considerable variation was present in experimental material (Table 1).

In the current study, GCV was of lower magnitude than PCV in all traits. This indicates that the effect of environment is high on expression of these traits (Table 2). Among 11 quantitative traits studied, high (greater than 20%) GCV and PCV was recorded for four characters such as grain yield plot^{-1} (GCV: 22.78%; PCV: 24.7%), dry fodder yield plot^{-1} (GCV: 21.83%; PCV: 23.76%), fodder yield plot^{-1} (GCV: 21,6%; PCV: 22.53%) and thousand grain weight (GCV: 21.35%; PCV: 22.84%) indicating huge amount of variation present in finger millet genotypes for these characters, therefore selection would be effective and beneficial for the further improvement of these characters. Moderate estimates of GCV and PCV were observed for four characters *viz.,* harvest index (GCV: 13.27%; PCV: 15.51%), main ear length (GCV: 17%; PCV: 18.57%), number of fingers ear^{-1} (GCV: 12.84%; PCV: 15.4%) and plant height (GCV: 10.42%; PCV: 12.12%). Productive tillers/plant (GCV: 18.16%; PCV: 22.34%) recorded moderate GCV and high PCV indicating effect of environment is high on expression of this character. Low estimates of GCV and PCV were recorded in two characters such as days to 50% flowering (GCV: 4.54%; PCV: 4.64%) and days to maturity (GCV: 3.42%; PCV: 3.53%) indicating lesser variation present in finger millet genotypes for the above two characters. These results were in conformity with the reports of Divya *et al.* (2022) for grain yield plot^{-1}, dry fodder yield plot^{-1}, number of fingers ear^{-1}, main ear length; Jyothsna *et al.* (2016) for thousand grain weight; John (2006) for harvest index; Bharathi *et al.* (2022) for plant height, days to 50% flowering and days to maturity.

Broad sense heritability provides an estimate of genetic variance contribution to the phenotypic variance of character. A combination of coefficient of variation and heritability estimates provides the best indication of selection effectiveness. All the quantitative characters studied showed a high broad sense heritability (greater than 60%) *viz.,* days to 50% flowering (95.5%), days to maturity (93.9%), fodder yield plot^{-1} (91.9%), thousand grain weight (87.4%), main ear length (83.9%), grain yield plot^{-1} (85.1%), dry fodder yield plot^{-1} (84.4%), plant height (74.2%), harvest index (73.2%), number of fingers ear^{-1} (69.5%) and productive tillers/plant (66.1%). This indicates the environment had a less significant impact on these characters. Similar findings were reported by Bharathi *et al.* (2022), Divya *et al.* (2022) for grain yield plot^{-1}, days to 50% flowering, main ear length, days to maturity, number of fingers ear^{-1}, productive tillers/plant, John (2006); Saundarya and Satish (2016) for harvest index. High heritability value indicates that the genetic component could have contributed more to these traits and would remain stable under different environmental conditions.

Table 1: Analysis of variance for yield and yield components in finger millet genotypes.

Sr. No.	Characters	Mean sum of squares		
		Replication (df=1)	Treatment (df=39)	Error (df=39)
1.	Days to 50% flowering	0.61	25.51**	0.58
2.	Days to maturity	0.11	33.66**	0.88
3.	Plant height (cm)	17.39	137.3**	20.35
4.	Productive tillers/plant	0.01	0.96**	0.19
5.	Main ear length (cm)	0.2	2.05**	0.14
6.	Number of fingers ear^{-1}	0.46	2.08**	0.37
7.	Fodder yield plot^{-1} (kg)	0.01	1**	0.04
8.	Dry fodder yield plot^{-1} (kg)	0.04	0.27**	0.02
9.	Harvest index	4715	101.6**	15.71
10.	Thousand grain weight (g)	0.02	0.74**	0.05
11.	Grain yield plot^{-1} (kg)	0.02	0.28**	0.02

** Significant at 1 per cent level of probability

The characters *viz.,* grain yield plot^{-1} (43.29%), fodder yield plot^{-1} (42.68%), dry fodder yield plot^{-1} (41.32%), thousand grain weight (41.11%), productive tillers/plant (30.4%), main ear length (32.1%), harvest index (23.4%) and number of fingers ear^{-1} (22.06%) recorded higher estimates of GAM. Lower values of GAM were recorded in days to 50% flowering (9.13%) and days to maturity (6.83%) whereas plant height (18.52%) showed a moderate GAM. High heritability merged with high GAM was observed in grain yield plot^{-1} (h^2_b = 85.1%, GAM = 43.29%), fodder yield plot^{-1} (h^2_b = 91.9%, GAM = 42.68%), thousand grain weight (h^2_b = 87.64%, GAM = 41.11%), main ear length (h^2_b = 83.9%, GAM = 32.1%), dry fodder yield plot^{-1} (h^2_b = 84.4%, GAM = 41.32%), harvest index (h^2_b = 73.2%, GAM = 23.4%), number of fingers ear^{-1} (h^2_b = 69.5%, GAM = 22.06%) and productive tillers/plant (h^2_b = 66.1%, GAM = 30.4%) indicating the traits are governed by additive gene action. Thus, phenotypic selection would improve these characters more effectively. Plant height showed high heritability merged with moderate GAM (h^2_b = 74.2%, GAM = 18.52%). High heritability merged with low GAM was recorded in days to 50% flowering (h^2_b = 95.5%, GAM

= 9.13%) and days to maturity (h^2_b = 93.9%, GAM = 6.83%) indicating the traits are governed by non additive gene effects. Thus, selection is not effective for these characters. These results were similar with the Bharathi *et al.* (2022) and Divya *et al.* (2022) for days to maturity, main ear length, productive tillers/plant,

Jyothsna *et al.* (2016) for dry fodder yield plot[-1], thousand grain weight, grain yield plot[-1], John (2006) and Saundarya and Satish (2016) for harvest index, Divya *et al.* (2022) for plant height, Sao *et al.* (2017) for days to 50% flowering.

Table 2: Genetic parameters for 11 yield and its component traits in finger millet genotypes.

Sr. No.	Character	Mean	Range		Coefficient of variation		Heritability (Broad sense) %	Genetic advance (GA)	Genetic advance as per cent of mean (%) (GAM)
			Min.	Max.	GCV (%)	PCV (%)			
1.	Days to 50% flowering	77.8	70	84	4.54	4.64	95.5	7.1	9.13
2.	Days to maturity	111	101.5	118.5	3.42	3.53	93.9	7.6	6.83
3.	Plant height (cm)	73.3	59.9	96.9	10.43	12.12	74.2	13.57	18.52
4.	Productive tillers/plant	3.4	2.3	5.5	18.16	22.34	66.1	1.04	30.4
5.	Main ear length (cm)	7.51	5.1	10.1	17	18.57	83.9	2.41	32.1
6.	Number of fingers ear[-1]	7.19	5.5	9.75	12.84	15.4	69.5	1.59	22.06
7.	Fodder yield plot[-1] (kg)	3.21	1.32	4.41	21.6	22.53	91.9	1.37	42.68
8.	Dry fodder yield plot[-1] (kg)	1.63	0.74	2.36	21.83	23.76	84.4	0.67	41.32
9.	Harvest index	49.4	37.61	66.26	13.27	15.51	73.2	11.55	23.4
10.	Thousand grain weight (g)	2.75	1.83	4.88	21.35	22.84	87.4	1.13	41.11
11.	Grain yield plot[-1] (kg)	1.58	0.88	2.84	22.78	24.7	85.1	0.69	43.29

Genotypic Coefficient of Variation (GCV); Phenotypic Coefficient of Variation (PCV)

CONCLUSIONS

Grain yield plot[-1] recorded high PCV and GCV implying that greater variation present in the population for this character, providing huge scope for further improvement of this trait among the studied genotypes. High heritability merged with genetic advance as per cent of mean recorded for grain yield plot[-1] indicating selection would be effective based on this character. Other characters *viz.,* fodder yield plot[-1], dry fodder plot[-1] and thousand grain weight also recorded high GCV, PCV, heritability and genetic advance as per cent of mean implying that more variation and prevalence of additive gene action for these characters. Thus, selection of genotypes based on these traits will be rewarding in future breeding programmes.

Conflict of Interest. None.

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