Genetic Variability Studies for Grain Yield and Yield Components in Little Millet (*Panicum sumatrense* Roth ex Roem. & Schult.)

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ABSTRACT: Little millet is a small seeded nutri-cereal, whose demand is gaining importance in recent days. So, it is important to estimate the extent of variability present in available germplasm which could be applied in selection procedures to develop consumer preferable varieties. Based on this, the present research was conducted at Agricultural Research Station, Perumallapalle during *Rabi*, 2022-23 for 30 little millet genotypes by considering a total of 14 yield and yield components to study genetic parameters *viz.*, genetic variability, heritability (broad sense) and genetic advance as percent of mean. From the observations, the analysis of variance was recorded significant differences for all the traits studied except for SCMR at both 50 DAS and 80 DAS. High GCV and PCV was recorded for leaf area index at both 50 DAS and 80 DAS along with number of productive tillers plant^{-1}, main panicle weight, grain yield plot^{-1} and fodder yield plot^{-1}, indicating that these characters were governed by additive gene action and simple selection could be rewarding. High heritability was observed for the traits leaf area index at 50 DAS followed by days to maturity, leaf area index at 80 DAS, days to 50% flowering, 1000 seed weight, number of productive tillers plant^{-1}, panicle length, plant height, harvest index, grain yield plot^{-1} and fodder yield plot^{-1}. High heritability coupled with high genetic advance as percent of mean was recorded for all the characters except for days to maturity and SCMR at both 50 and 80 DAS, which concluded the better scope of these traits improvement through selection, as these characters are predominately governed by additive gene effects.

Keywords: Little millet, genetic variability, heritability, genetic advance.

INTRODUCTION

Little millet (*Panicum sumatrense* Roth ex Roem. & Schult.) is one of the most important small millet crops consumed in the place of rice and popularly known as sama, samo, vari or kutki. It is also called an Indian millet as it is native to India. It is a self-pollinated, chasmogamous (Nandini *et al*., 2019), allotetraploid crop with chromosome number of 36 (2n=4x=36) belongs to poaceae family, panicoideae subfamily and tribe paniceae. It is cultivated as a cereal across Nepal, India and Western Myanmar. The wild relative of little millet is *Panicum psilopodium* (Ganapathy, 2017). It forms an important role in tribal agriculture in Eastern Ghats of India. Little millet is grown on temperate and tropical climate and it can give consistent yields on marginal lands in drought-prone arid and semiarid regions as it is least water demanding crop and it is important crop for regional food stability (Dwivedi *et al.,* 2012). Little millet is an annual tuffed grass having slender culms, soft leaves and panicle as

inflorescence with erect hairy branches, paired spikelets with two glumes (Natesan *et al*., 2020) and two florets with lower one as sterile and other is fertile one. The grains can be preserved for several years as they are least affected by storage pests and therefore, the crop is recognized as an important reserve food crop during famines (Venkataratnam *et al.,* 2019).

In India, little millet is cultivated in an area of 4.44 Lakh hectares with an annual production of 3.47 Lakh tonnes and productivity of 781 Kg ha^{-1} (Ministry of Agriculture, 2021). In Andhra Pradesh, little millet is grown in an area of 22,000 ha with production of 19,010 t and productivity of 864 Kg ha^{-1} (Ministry of Agriculture, 2021).

In any breeding programme, the basic step is exploitation of genetic variability among the genotypes and targeting the improvement of desirable traits. If there is greater the variation in the base population, there is high chance for selecting the better and promising individuals for developing improved

varieties. Yield is the polygenic trait and is highly influenced by environment and effect of other traits. However, selection based on the highly heritable yield attributes is most effective in improving yield and which in turn used to calculate the breeding value of individuals. Among the genetic parameters, heritability coupled with genetic advance as per cent of mean leads more advantage in the prediction of expected genetic gain in the trait with selection of best genotypes from base population.

MATERIALS AND METHODS

Thirty diverse little millet genotypes (Table 1) were raised in Randomized Block Design (RBD) in three replications with spacing of 22.5 cm between rows and 7.5 cm within the row at Agricultural Research Station, Perumallapalle during *rabi*, 2022-23. Each genotype was grown in two lines of three meter length. Data was collected for 14 yield and yield components *viz.*, days to 50% flowering, days to maturity, number of productive tillers plant[-1], main panicle weight (g), thousand seed weight (g), panicle length (cm), plant height (cm), leaf area index at 50 DAS and 80 DAS, SCMR readings at 50 DAS and 80 DAS, fodder yield plot[-1] (kg), grain yield plot[-1] and harvest index (%).

Analysis of variance was conducted by using the technique described by Panse and Sukhatme (1964). Phenotypic and genotypic coefficients of variation (PCV and GCV) were computed according to Burton (1952). Heritability in broadsense was estimated as per the formula proposed by Allard (1960). Genetic advance as per cent of mean by using the formula suggested by Johnson *et al.* (1955). Statistical analysis was carried by using WINDOSTAT 9.2.

RESULTS AND DISCUSSION

Analysis of variance revealed the significant differences for all the characters studied except for SCMR, indicating the presence of substantial magnitude of genetic variability among the genotypes, suggesting greater scope for improvement of yield and yield components through simple selection (Table 2).

High GCV and PCV (Table 3) was recorded for leaf area index at 80 DAS (GCV = 75.58%; PCV= 77.42%) followed by leaf area index at 50 DAS (GCV = 34.72%; PCV = 35.21%), grain yield plot[-1] (GCV = 23.13%; PCV = 27.58%), number of productive tillers plant[-1] (GCV = 21.75%; PCV = 22.51%), fodder yield plot[-1] (GCV = 20.21%; PCV = 25.99%) and main panicle weight (GCV = 20.10%; PCV = 26.49%). It indicated the presence of large variation among the genotypes for these characters. Therefore, simple selection can be practiced for further improvement of these characters. The obtained results were in agreement with Nirmalakumari *et al.* (2010) in little millet, Wolie *et al.* (2013) in finger millet, Ashok *et al.* (2016 b) in foxtail millet, Ashok *et al.* (2016 a) in little millet, Anuradha *et al.* (2020) and Madhavilatha *et al.* (2020) in little millet for grain yield plot[-1] and number of productive tillers plant[-1]; Anuradha *et al.* (2017, 2020) in little millet for fodder yield plot[-1] and

Suthediya *et al.* (2021) for number of productive tillers plant[-1] in kodo millet.

Moderate coefficient of variation was recorded for harvest index (GCV = 17.96%; PCV = 19.74%), panicle length (GCV = 16.38%; PCV = 18.86%), plant height (GCV = 14.56%; PCV = 15.25%), 1000 seed weight (GCV = 12.15%; PCV = 12.53%) and days to 50% flowering (GCV = 10.37%; PCV = 10.65%). It indicates the existence of comparatively moderate variability for these traits, which could be exploited for improvement through selection in advanced generations. The results were in accordance with Katara *et al.* (2019); Nagar *et al.* (2020) in little millet, Suthediya *et al.* (2021) in kodo millet for plant height; Ashok *et al.* (2016 a) in little millet, Anuradha *et al.* (2020) in little millet for days to 50% flowering; Arya *et al.* (2018) in barnyard millet and Nagar *et al.* (2020) in little millet for 1000 seed weight.

Low coefficients of variation was recorded for days to maturity (GCV = 6.03%; PCV = 6.16%), SCMR at 50 DAS (GCV = 2.58%; PCV = 8.03%) and SCMR at 80 DAS (GCV = 2.37%; PCV = 8.70%). It indicated that there is very low chance of improvement of these characters due to low range of variation. The results were in line with Anuradha *et al.* (2020) in little millet, Suthediya *et al.* (2021) in kodo millet, Matere *et al.* (2022) in little millet for days to maturity.

High heritability was observed for leaf area index at 50 DAS (97.20%) followed by days to maturity (96.00%), leaf area index at 80 DAS (95.30%), days to 50% flowering (94.80%), 1000 seed weight (94.10%), number of productive tillers plant[-1] (93.30%), plant height (91.10%), harvest index (82.80%), panicle length (75.40%), grain yield plot[-1] (70.30%) and fodder yield plot[-1] (60.50%). It indicated that expression of all these traits is mainly by genetic constitution, there is less environmental influence. It explains that the phenotypes are the true representative of their genotypes for these traits and selection based on phenotypic value could be reliable. So, for improving these traits direct selection would be more effective.

These results were in conformity with the findings of Ashok *et al.* (2016 b) in foxtail millet; Ashok *et al.* (2018) in finger millet; Ashok *et al.* (2016 a); Anuradha *et al.* (2017); Madhavilatha *et al.* (2020); Matere *et al.* (2022) in little millet for days to 50% flowering, plant height and number of productive tillers plant[-1]. High heritability for days to 50% flowering by Anuradha *et al.* (2020); Nagar *et al.* (2020) in little millet. Nagar *et al.* (2020) for 1000 seed weight, number of productive tillers plant[-1], plant height and grain yield plot[-1] in little millet.

The moderate heritability was observed for main panicle weight (57.60%) which indicated the involvement of additive gene action in the inheritance of this traits. Low heritability was observed for SCMR at 50 DAS (10.30%) followed by SCMR at 80 DAS (7.50%). Indicated that, this trait is highly influenced by environmental conditions especially moisture availability.

Most of the traits were having high GAM. High GAM was recorded for leaf area index at 80 DAS (152.00%) followed by leaf area index at 50 DAS (70.53%),

number of productive tillers plant^{-1} (43.28%), grain yield plot^{-1} (39.96%), harvest index (33.68%), fodder yield plot^{-1} (32.39%), main panicle weight (31.44%), panicle length (29.31%), plant height (28.62%), 1000 seed weight (24.28%) and days to 50% flowering (20.81%). Similar results were recorded by Madhavilatha *et al.* (2020) in little millet for plant height, number of productive tillers plant^{-1} and grain yield plant^{-1}; Nagar *et al.* (2020) for days to 50% flowering, plant height and number of productive tillers plant^{-1} in little millet; Matere *et al.* (2022) in little millet for number of productive tillers plant^{-1}, main panicle weight. Moderate GAM was observed for days to maturity (6.77%). Whereas, low GAM was found for SCMR at 50 DAS (1.71%) and at 80 DAS (1.33%).

Heritability along with the genetic advance is the powerful tool in estimating the resultant effect of selecting the best individuals from the wide population. In the present study, high heritability along with high GAM was recorded for days to 50% flowering, plant height, panicle length, number of productive tillers plant^{-1}, 1000 seed weight, leaf area index both at 50 DAS and 80 DAS, fodder yield plot^{-1}, grain yield plot^{-1} and harvest index. It indicated that these traits are largely governed by genes, the source of variation is genetic factor itself. There is predominance of additive genes over these traits which responds well to simple selection.

Table 1: List of 30 little millet genotypes used in the present study along with their parentage.

Sr. No.	Genotypes	Parentage	Source
1.	BL 6	Paiyur-1 × OLM-29	S.G. College of Agricultural Research Station, Jagdalpur
2.	CLMV-1	Pureline selection from Germplasm GPmr 1153	Indian Institute of Millet Research, Hyderabad
3.	DH LM 22-3	DHLM 36-3 × DHLM 28-4	Dharwad
4.	DHLM 36-3	Co-4 × Paiyur-2	Agricultural Research Station, Hanumanamatti
5.	DLM 14	Pureline selection from Local germplasm	Tribal Agricultural Research Station, Dindori
6.	DLM-8	Pureline selection from Local germplasm	Tribal Agricultural Research Station, Dindori
7.	GLM 368	Pureline selection from Local germplasm	Tribal Agricultural Research Station, Dindori
8.	GPUL 11	CO 4 × TNSu221-4	Project Co-ordinate Unit, GKVK, Bengaluru
9.	GPUL 12	OLM 203 × TNPsu 219-9	Project Co-ordinate Unit, GKVK, Bengaluru
10.	GPUL 6	JK 8 × Peddasame	Project Co-ordinate Unit, GKVK, Bengaluru
11.	GPUL 7	JK 8 × Peddasame	Project Co-ordinate Unit, GKVK, Bengaluru
12.	GPUL 9	Pureline selection from Local germplasm	Project Co-ordinate Unit, GKVK, Bengaluru
13.	GV2-1	Mutant of Gujarat Variety-1	Hill Millet Research Station, Waghai
14.	IE 6332	Pureline selection from Local germplasm	Indian Institute of Millet Research, Hyderabad
15.	IIMR LM 4001	Selection from IPmr1075-2	Indian Institute of Millet Research, Hyderabad
16.	IIMR LM 4004	Selection from germplasm line 7093-1	Indian Institute of Millet Research, Hyderabad
17.	IIMR LM 5004	Pureline selection from Local germplasm	Indian Institute of Millet Research, Hyderabad
18.	IIMR LM 8005	Pureline selection from LIT 174	Indian Institute of Millet Research, Hyderabad
19.	JK-8	Selection from local germplasm	College of Agriculture, Rewa
20.	LIT 287	Pureline selection from Local germplasm	Indian Institute of Millet Research, Hyderabad
21.	LMNDL 5	Pureline selection from LMNDL-1 population	Regional Agricultural Research Station, Nandyal
22.	LMNDL-3	Pureline selection from Local germplasm	Regional Agricultural Research Station, Nandyal
23.	OLM 18	Selection from Kandhamal local	Agricultural Research Station, Berhampur
24.	RLM 369	Pureline selection from Sidhi Dt.	College of Agriculture, Rewa
25.	VS 19	Pureline selection from Local germplasm	Agricultural Research Station, Vizianagaram
26.	VS 10	Selection from Dumbriguda collection	Agricultural Research Station, Vizianagaram
27.	VS 13	Selection from local peddasame	Agricultural Research Station, Vizianagaram
28.	VS 6	Selection from Gummalakshmipuram collection	Agricultural Research Station, Vizianagaram
29.	VS-25	Selection from Gummalakshmipuram collection	Agricultural Research Station, Vizianagaram
30.	WV 168	Selection from GV 2 × OLM 56	Hill Millet Research Station, Waghai

Table 2: ANOVA for yield and yield components in 30 Little millet genotypes.

Sr. No.	Characters	Mean Sum of Squares		
		Replications (df: 2)	Genotypes (df: 29)	Error (df: 58)
1.	DFF	7.633	106.540**	1.588
2.	DM	2.844	104.735**	0.720
3.	PH	7.289	554.180**	9.950
4.	PL	6.679	50.480**	4.940
5.	NPTP	0.146	7.202**	0.168
6.	MPW	3.681	24.701**	4.860
7.	TSW	0.004	0.233**	0.005
8.	LAI at 50 DAS	0.007	0.170**	0.001
9.	LAI at 80 DAS	0.010	0.269**	0.005
10.	SCMR at 50 DAS	1.230	13.760	10.220
11.	SCMR at 80 DAS	7.855	12.477	10.040
12.	FYPP	0.040	0.078**	0.013
13.	GYPP	0.003	0.065**	0.008
14.	HI	11.030	213.145**	9.250

** Significant at 1 % level

DFF: Days to 50% flowering; **DM:** Days to maturity; **PH:** Plant height (cm); **PL:** Panicle length (cm); **NPTP:** Number of productive tillers plant^{-1}; **MPW:** Main panicle weight (g); **TSW:** 1000 seed weight (g); **LAI:** Leaf area index; **SCMR:** Soil plant analysis development chlorophyll meter readings; **FYPP:** Fodder yield plot^{-1} (kg); **GYPP:** Grain yield plot^{-1} (kg); **HI:** Harvest index (%)

Table 3: Genetic variability parameters of yield and yield components in Little millet.

Sr. No.	Character	Mean	Range		Coefficient of Variation (%)		h²(b) (%)	GA	GAM (%)
			Minimum	Maximum	GCV	PCV			
1.	DFF	58.07	50.00	75.67	10.37	10.65	94.80	12.09	20.81
2.	DM	89.04	78.33	100.67	6.03	6.16	96.00	10.84	12.18
3.	PH	91.85	67.73	119.00	14.56	15.25	91.10	26.29	28.62
4.	PL	23.78	16.13	33.27	16.38	18.86	75.40	6.97	29.31
5.	NPTP	7.03	3.66	10.73	21.75	22.51	93.30	3.05	43.28
6.	MPW	12.78	7.67	17.67	20.10	26.49	57.60	4.02	31.44
7.	TSW	2.27	1.69	2.87	12.15	12.53	94.10	0.55	24.28
8.	LAI 50DAS	0.68	0.33	1.46	34.72	35.21	97.20	0.48	70.53
9.	LAI 80DAS	0.45	0.12	1.30	75.58	77.42	95.30	69.10	152.00
10.	SCMR 50DAS	42.01	37.07	45.41	2.58	8.03	10.30	0.72	1.71
11.	SCMR 80DAS	37.86	33.54	41.21	2.37	8.70	7.50	0.51	1.33
12.	FYPP	0.71	0.36	1.05	20.21	25.99	60.50	0.23	32.39
13.	GYPP	0.60	0.23	0.83	23.13	27.58	70.30	0.24	39.96
14.	HI	45.89	21.52	62.06	17.96	19.74	82.80	15.46	33.68

DFF: Days to 50% flowering; **DM:** Days to maturity; **PH:** Plant height (cm); **PL:** Panicle length (cm); **NPTP:** Number of productive tillers plant^{-1}; **MPW:** Main panicle weight (g); **TSW:** 1000 seed weight (g); **LAI:** Leaf area index; **SCMR:** Soil plant analysis development chlorophyll meter readings; **FYPP:** Fodder yield plot^{-1} (kg); **GYPP:** Grain yield plot^{-1} (kg); **HI:** Harvest index (%)
GCV: Genotypic coefficient of variation (%); **PCV:** Phenotypic coefficient of variation (%); **h²**(b)**:** Broad sense heritability; **GA:** Genetic advance; **GAM:** Genetic advance as per cent of mean

Hence, direct selection for these traits is rewarding. High heritability along with moderate GAM was observed for days to maturity. The similar results of high heritability along with high GAM were earlier reported in different crops *viz.*, Katara *et al.* (2019) for harvest index, Venkataratnam *et al.* (2019) for days to 50% flowering, number of productive tillers plant^{-1}, fodder yield plot^{-1}, 1000 seed weight, leaf area index at both 50DAS and 80DAS and harvest index, Anuradha *et al.* (2020) for days to 50% flowering.

CONCLUSIONS

Leaf area index at both 50 DAS and 80 DAS along with number of productive tillers plant^{-1}, main panicle weight, grain yield plot^{-1} and fodder yield plot^{-1} recorded for having high GCV and PCV, indicated that these characters are governed by additive gene action

and simple selection could be rewarding. High heritability coupled with high genetic advance as percent of mean was recorded for all the characters except for days to maturity and SCMR at both 50 and 80 DAS, which concluded the better scope of their improvement through selection, as these characters are predominately governed by additive gene effects.

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