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Studies on genetic variability in little millet (Panicum sumatrense)

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Abstract

Genetic parameters were studied for yield, yield attributing and physiological traits in 50 little millet genotypes. The genotypic coefficient of variation (GCV) for all the traits studied were lesser than the phenotypic coefficient of variation (PCV) indicating that interaction of genotypes with environment. High GCV, PCV coupled with high heritability and genetic advance as per cent of mean was observed for leaf area index at panicle initiation, specific leaf weight at panicle initiation, harvest index, main panicle weight and fodder yield plot⁻¹ and moderate heritability coupled with high genetic advance as per cent of mean was found in grain yield plot⁻¹ indicating the role of additive gene action in governing the inheritance of these traits. Phenotypic selection based on these traits can be improved through simple selection.

Keywords: Genetic parameters, Little millet, Physiological and Yield attributing traits

Introduction

Little millet (*Panicum sumatrense*; 2n=4x=36) is one of the most important small millet crop cultivated in dry land areas. Little millet is a hardy crop, well known for its drought tolerance and will survive under water logged conditions. Being a rich source of fibre, nutrients, vitamins and minerals it provides food and nutritional security for human beings. In India, little millet is cultivated in Tamil Nadu, Karnataka, Andhra Pradesh, Maharashtra, Orissa, Bihar, Madhya Pradesh, Uttar Pradesh, Jharkhand, Chhattisgarh and Gujarat. In India it is cultivated in an area of 2.34 lakh hectares with annual production of 1.27 lakh t and productivity of 544 kg ha⁻¹ (Annual report, AICPMIP, 2017-2018).

Crop improvement mainly depends on the existence of genetic variability, heritability and genetic advance as per cent of mean in the population. An estimate of the extent of variability present in the germplasm could be useful in application for selection procedures in breeding programme. Heritability along with genetic advance were useful for predicting the gain under selection (Johnson *et al.*, 1955)^[5, 6]. The relative magnitude of these parameters helps us in deciding the breeding programme. The fore the present study was undertaken to explore genetic variability, heritability and expected genetic gain in little millet genotypes for various yield, yield attributing and physiological traits.

Materials and Methods

In the present study, 50 little millet genotypes including improved lines developed from different research centres and released varieties were evaluated at Agricultural Research Station, Perumallapalli, during *Kharif* 2018. The experiment was conducted in randomized block design with three replications. Each genotype were raised in 2 rows of 3 m length with a spacing of 22.5×7.5 cm and all the recommended packages of practices were followed to raise healthy crop. Observations were recorded on five randomly selected plants from each entry in three replications for 9 yield attributing traits *viz.*, days to 50% flowering, days to maturity, plant height (cm), number of productive tillers per plant, panicle length (cm), main panicle weight (g), 1000 seed weight (g), grain yield plot⁻¹ (kg), fodder yield plot⁻¹ (kg) and 8 physiological traits *viz.*, leaf area index at both panicle initiation and 15 days after panicle initiation, specific leaf weight at panicle initiation and 15 days after panicle initiation, harvest index (%) and relative injury (%) at 15 days after panicle initiation. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated by the formula given by Burton (1952) ^[3]. Heritability in broad sense [h²_(b)] was calculated by the formula given by Lush

(1940)^[7]. Genetic advance as per cent of mean was estimated by the formula given by Johnson *et al.* (1955)^[5, 6]. The information on such aspects will help in formulating appropriate breeding method for crop improvement.

Results and discussions

The mean square estimates in 50 little millet genotypes were significant for all the characters indicating the presence of sufficient variability among genotypes. The details of little millet genotypes were presented in Table1. The range of variation and genetic parameters estimated are presented in Table 2. The values of PCV was higher than the GCV for all the traits studied (Fig 1) indicating the variation is not only due to the genotypes but also influence of environment. The genetic parameters viz., phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in broad sense and genetic advance as percent mean were estimated for all the traits under study. Genotypic coefficient variation (GCV) ranged from 7.86 (plant height) to 41.86 (leaf area index at panicle initiation). Phenotypic coefficient of variation (PCV) ranged from 9.19 (plant height) to 45.04 (leaf area index at panicle initiation). PCV and GCV were high for leaf area index at panicle initiation stage (41.86, 45.04) followed by leaf area index at 15 days after panicle initiation stage (31.07, 35.28), specific leaf weight (30.67, 36.56), harvest index (28.51, 35.02) specific leaf weight at 15 days after panicle initiation (26.62, 33.77), fodder yield plot⁻¹ (23.17, 26.97), main panicle weight (21.53, 24.58) and grain yield plot⁻¹ (20.24, 27.58) indicating the presence of considerable amount of variation among the germplasm. Hence, simple selection could be effective for further improvement of these characters. Similar results were also reported by Selvi *et al.* (2014) ^[11] Ashok *et al.* (2016) ^[2] Anuradha et al. (2017), Geetha et al. (2018)^[4] and Patel et al. $(2018 a)^{[10]}$ in little millet.

Moderate values of GCV and PCV was observed for number of productive tillers plant⁻¹, days to 50% flowering, relative injury at 15 days after panicle initiation days to maturity thousand seed weight and panicle length. Similar results were reported by Nirmalakumari et al. (2010)^[9] Selvi et al. (2010) ^[11] Anuradha et al. (2017) ^[1] Geetha et al. (2018) ^[4] Patel et al. (2018 a) [10] and Suryanarayana and Sekhar (2018) [12] in little millet. Hence direct selection for these traits might be misleading if adopted for improvement programme through these traits. Low GCV and PCV were recorded for plant height, SCMR at panicle initiation stage and SCMR at 15 days after panicle initiation indicating the narrow range of variability for these traits there by restricting the scope for further improvement of these traits through simple selection. Lower coefficients of variation was observed earlier by Nirmalakumari et al. (2010)^[9] Selvi et al. (2010)^[11] Jyothsna et al. (2016 a), Anuradha et al. (2017)^[1] and Patel et al. (2018 a)^[10] in little millet.

The consideration of genetic variability alone will not be much use in crop improvement unless supplemented with the information on heritability estimates which gives a measure of the heritability portion of the total variation.

In the study, estimates of higher heritability was observed for all the characters except grain yield and it ranging from 53.90 (grain yield plot⁻¹) to 89.50 (days to 50% flowering). High heritability was recorded for days to 50% flowering, days to maturity, leaf area index at panicle initiation, thousand seed weight, number of productive tillers plant, SCMR at panicle initiation, leaf area index at 15 days after panicle initiation, fodder yield plot⁻¹, panicle length, plant height, relative injury at 15 days after panicle initiation, specific leaf weight at 15 days after panicle initiation, SCMR at 15 days after panicle initiation, harvest index and specific leaf weight at panicle initiation suggested that these traits were less influenced by environment and selection would be effective for these traits. These results were in agreement with the findings of Nandini et al. (2016)^[8], Ashok et al. (2016)^[2] Anuradha et al. (2017) ^[1] Geetha et al. (2018) ^[4] Patel et al. (2018) ^[10] and Survanaravana and Sekhar (2018)^[12] in little millet.

In addition to genetic variability and heritability and genetic advance will help in predicting the gain under selection. In the present study genetic advance as per cent of mean ranged from 13.84 (plant height) to 78.94 (leaf area index at panicle initiation). Higher genetic advance as per cent of mean was recorded for all the characters except plant height, panicle length and SCMR at both panicle and 15 days after initiation. High genetic advance as per cent of mean indicated that these characters governed by additive gene action and selection will be rewarding for improvement of these traits. Similar findings were reported by Selvi *et al.* (2014), Nandini *et al.* (2016)^[8], Anuradha *et al.* (2017)^[1] Geetha *et al.* (2018)^[4] Patel *et al.* (2018 a)^[10] and Suryanarayana and Sekhar (2018)^[12] in little millet.

In the present investigation, high heritability coupled with high genetic advance as per cent of mean were recorded for days to 50% flowering, days to maturity, number of productive tillers plant¹, main panicle weight, thousand seed weight, fodder yield plot⁻¹, leaf area index both at panicle initiation and 15 days after panicle initiation stages, specific leaf weight at both panicle initiation and 15 days after panicle initiation stages, harvest index and relative injury at 15 days after panicle initiation stage indicating that additive gene action involved in the inheritance of these characters which can be improved by pure line selection and mass selection. Selvi et al. (2014)^[11] and Ashok et al. (2016)^[2] reported similar results for days to 50% flowering days to maturity and number of productive tillers plant⁻¹. High heritability coupled with moderate genetic advance as per cent of mean was recorded for plant height, panicle length, SCMR at both panicle and 15 days after panicle initiation stage indicating that both additive and non-additive gene effects were involved in the genetic control of these traits. Improvement of these traits can be done effectively through simple pedigree method and phenotypic selection.

Table 1: List of pedigree details of 50 little millet genotypes used for study

S. No	Genotypes	Pedigree	Centre	
1	BL-2	$CO-2 \times OLM-56$	Jagdalpur	
2	BL-4	$CO-2 \times TNAU-97$	Jagdalpur	
3	BL-8	$CO-2 \times OLM-56$	Jagdalpur	
4	BL-41-3	Paiyur-2 × TNAU-97	Jagdalpur	
5	BL-150	Paiyur-2 × DLM-369	Jagdalpur	
6	CO-2	Pure line selction	Coimbatore	
7	DhLtMV-10-2	$CO-4 \times Paiyur-2$	Hanumanamatti	

8	DhLtMV-14-1	$CO-2 \times TNAU-110$	Hanumanamatti
9	DhLtMV-21-1	$CO-2 \times TNAU-26$	Hanumanamatti
10	DhLtMV-28-4	$CO-2 \times TNAU-26$	Hanumanamatti
11	DhLtMV-36-3	$CO-4 \times Paiyur-2$	Hanumanamatti
12	DhLtMV-39-1	$CO-4 \times Paiyur-2$	Hanumanamatti
13	DLM-8	Pure line selection from Local Germplasm	Dindori
14	DLM-14	Pure line selection from Local Germplasm	Dindori
15	DLM-89	Pure line selection from Local Germplasm	Dindori
16	DLM-95	Selection from Local Germplasm	Rewa
17	DLM-103	Pure line selection from Local Germplasm	Dindori
18	RLM-186	Selection from Local germplasm of Rewa	Rewa
19	DhLt-28-4	$CO-2 \times TNAU-26$	Hanumanamatti
20	GPUL-1	$JK-8 \times Peddasame$	Banglore
21	GPUL-2	Pure line selection from Peddasame	Banglore
22	GPUL-3	$JK-8 \times Peddasame$	Banglore
23	GPUL-4	$JK-8 \times Peddasame$	Banglore
24	GPUL-5	$JK-8 \times Peddasame$	Banglore
25	GV-2-1	Mutant of Guiarat Vari-1	Waghai

Table 1 Cont....

S. No	Genotypes	Pedigree	Centre	
26	IIMRLM-7012	Selection from IPMR-699	IIMR, Hydrabad	
27	IIMRLM-7162	Selection from GPMR-1153	IIMR, Hydrabad	
28	KADIRI-1	Selection from Kadiri local	Bangalore	
29	KOPLM-53	IPS from local germplasm	Kolhapur	
30	NALLASAMA	Selection from Local	ARS, Perumallapalle	
31	OLM-217	Selection from Udayagiri Local	Berhampur	
32	OLM-233	Selection from L55	Berhampur	
33	RLM-37	Selection from Local germplasm No 37	Rewa	
34	RLM-238	Selection from Local germplasm of Rewa	Rewa	
35	RLM-367	Selection from Local germplasm No. 367	Rewa	
36	TNAU-152	Paiyur-1 × PM-29	Coimbatore	
37	TNAU-159	TNAU-81 × TNAU-25	Coimbatore	
38	TNAU -160	TNAU-91 × MS-4729	Coimbatore	
39	TNPsu-167	$CO-2 \times TNAU-26$	Coimbatore	
40	TNPsu-170	$CO-4 \times IPM-113$	Coimbatore	
41	TNPsu-171	$CO-2 \times TNAU-28$	Coimbatore	
42	TNPsu-174	$CO-2 \times IPM-113$	Coimbatore	
43	TNPsu-183	CO-2 × MS-4729	Athiyandal	
44	TNPsu-186	MS-507 × MS-1211	Athiyandal`	
45	WV-125	Local collection from Waghai	Waghai	
46	WV-126	Local collection from Dangas	Waghai	
47	WV-167	Local selection from Subir	Waghai	
48	BL-6	Paiyur-1 × OLM-29	Jagdalpur	
49	JK-8	Selection from Local germplasm	Rewa	
50	OLM-203	Pure line selection from Lakshmipur local Berhampur		

Table 2: Estimates of variability and genetic parameters for yield, yield attributing and physiological traits Little millet

S.	Character	Range		Moon	Coefficient	of Variation	Heritability	Genetic Advance as
No	Character	Minimum	Maximum	wiean	Genotypic	Phenotypic	(Broad sense) (%)	per cent of Mean (%)
1.	Days to 50% flowering	46.0	82.0	58.33	17.26	18.24	89.50	33.63
2.	Days to maturity	76.0	110.0	88.34	11.74	12.41	89.40	22.87
3.	Plant height (cm)	95.0	143.0	119	7.86	9.19	73.10	13.84
4.	Number of productive tillers plant-1	5.2	9.4	7.0	19.71	21.80	81.70	36.70
5.	Panicle length (cm)	21.4	32.80	26.8	10.84	12.63	73.60	19.16
6.	Main panicle weight (g)	1.17	3.82	1.84	21.53	24.38	78.00	39.19
7.	Thousand seed weight (g)	1.50	2.91	2.24	13.72	15.16	81.90	25.58
8.	Fodder yield plot ⁻¹ (kg)	0.78	1.84	1.15	23.17	26.97	73.80	41.01
9.	Grain yield plot ⁻¹ (kg)	0.08	0.31	0.20	20.24	27.58	53.90	30.60
10.	Leaf area index (PI)	0.45	2.38	1.31	41.86	45.04	83.50	78.94
11.	Leaf area index (15 days after PI)	0.53	2.66	1.72	31.07	35.28	77.06	56.37
12.	SCMR (PI)	32.66	45.46	37.42	8.84	10.12	76.20	15.90
13	SCMR (15 days after PI)	23.71	37.18	29.55	9.03	10.83	69.50	15.51
14	SLW $(g \text{ cm}^{-2})$ (PI)	0.02	0.06	0.04	30.67	36.56	70.40	53.01
15	SLW (g cm ⁻²) (15 days after PI)	0.01	0.06	0.03	26.62	33.77	62.10	43.21
16	Relative injury (%) (15 days after PI)	21.05	49.06	32.34	16.34	19.17	72.80	28.77
17	Harvest index (%)	8.25	29.50	18.58	28.51	35.02	66.00	47.81

SCMR: SPAD Chlorophyll meter reading; SLW: Specific leaf weight; PI: Panicle initiation



Fig 1: Comparison of GCV, PCV, heritability and genetic advance as per cent of mean in Little millet genotypes

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