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RESEARCH PAPER

Genetic Variability for Grain Yield and its Component Traits in Little Millet [*Panicum sumatrense* L.]. Breeding Lines

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ABSTRACT

Twenty little millet breeding lines along with two checks were evaluated for grain yield and its component traits to study genetic variability, heritability and genetic advance at Agricultural Research station, Vizianagaram, ANGRAU. Analysis of variance revealed existence of significant differences between the genotypes. The genetic variability parameters like PCV and GCV were low to moderate for all the eight traits studied. High heritability was witnessed by days to 50% flowering, days to maturity, plant height, panicle length and test weight. High genetic advance as per cent of mean was exhibited by days to 50% flowering, days to maturity and test weight, indicating the existence of non-additive gene action controlling the traits.

HIGHLIGHTS

- Highest grain yield was recorded by VS 60 (2018 kg/ha) and highest fodder yield by VS 75 (6203 kg/ha).
- Days to 50% flowering, days to maturity and test weight exhibited high heritability and genetic advance as per cent of mean indicating additive gene action and might respond to simple selection.

Keywords: Little millet, heritability, genetic advance, variability

Little millet (*Panicum sumatrense* L.) is self-pollinated crop belonging to the family Poaceae (Graminae), sub family Panicoideae and genus Panicum. Little millet is a domesticated form of the weedy species *Panicum psilopodium* (De Wet *et al.* 1983). It is a quick growing, short duration cereal which can withstand both drought and water logging. Little millet is cultivated to a limited extent in India, Sri Lanka, Pakistan, Myanmar, and other South East Asian countries (Hiremath *et al*. 1990). The crop is less affected by pests, diseases, and environmental stresses than other grains. It can also adapt to a wide range of growing conditions and require less water. Little millet is a nutrient-rich crop, high in protein, fiber, and minerals like iron, calcium, and potassium. It is also gluten-free, making it an excellent option for people with gluten intolerance. This crop is widely cultivated in India, particularly in the states of Tamil Nadu, Andhra Pradesh, and Karnataka. It is a drought-tolerant crop and can thrive in poor soil conditions, making it an ideal crop for small-scale farmers and marginal lands. Little millet has been a part of traditional Indian cuisine for centuries, particularly in the southern states. It is used to make a variety of dishes, including porridges, bread, and desserts.

Information on genetic variability, heritability, and genetic advance is crucial for crop improvement programs as it helps breeders identify genetic differences, understand genetic control, and predict selection gains. By knowing the genetic variability,

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heritability, and genetic advance of a trait, breeders can develop effective selection schemes, improve breeding program efficiency, and ultimately enhance crop improvement. Limited work has been previously done on little millet after the crop has come to the light. Therefore, the present investigations were undertaken to determine genetic variability, heritability and genetic advance in little millet breeding lines.

MATERIALS AND METHODS

The present investigation was carried out with 18 little millet breeding lines and two national checks, BL 6 and OLM 203 at Agricultural Research Station, Vizianagaram, ANGRAU, Andhra Pradesh during kharif, 2023. The entries were laid out in Randomized complete block design with three replications. The data was recorded on eight parameters *viz*., days to 50% flowering (DFF), days to maturity (DM), plant height (PH; cm), number of productive tillers (NPT), panicle length (PL; cm), grain yield (GY; q/ha), fodder yield (FY; q/ha) and 1000 seed weight (TW; g). Data analysis was done using Indostat software for analysing Analysis of variance, genetic variability, heritability, genetic advance and genetic advance as per cent of mean.

RESULTS AND DISCUSSION

Analysis of variance presented in Table 1 shows there is significant differences among the 20

Table 1: Analysis of variance (ANOVA) for eight traits studied in little millet genotypes

Source of variation	Df	DFF	DM	PH	NPT	PL	GY	FY	TW
Genotypes	19	356.54**	419.72**	246.18**	2.78*	14.98**	99317.87*	1040922.14	0.59**
Replications	2	2.07	5.60	54.20	0.54	0.84	236570.34*	2146347.74*	0.01
Error	38	4.36	4.67	43.85	1.05	2.42	42857.17	525977.37	0.05

*At 5% level of significance; ** at 1% level of significance.*

Table 2: Mean values of 18 little millet breeding lines along with two checks evaluated during *kharif*, 2023

Sl. No.	Entry	DFF	DM	PH	NPT	PL	GY	FY	TW
1	VS 43	65.7	98.3	142.4	6.3	32.4	1906	5648	2.02
2	VS 49	54.7	86.3	136.5	7.0	28.2	1638	4907	1.89
3	VS 54	48.7	78.3	142.9	6.5	29.7	1935	5926	2.18
4	VS 56	54.0	83.3	154.0	6.5	32.4	1800	5093	1.70
5	VS 57	83.0	114.7	147.5	8.5	27.5	2019	5833	2.28
6	VS 60	85.7	118.0	145.3	8.3	27.4	1367	4167	2.41
7	VS 61	54.3	84.3	148.3	6.3	25.1	1798	4907	1.77
8	VS 64	53.7	83.0	146.7	7.7	27.2	1658	5463	1.79
9	VS 65	67.0	98.7	151.5	7.2	29.6	1683	5463	1.97
10	VS 66	64.0	94.0	144.0	8.4	23.5	1509	4074	2.81
11	VS 68	65.3	97.0	143.1	6.8	28.1	1685	5370	1.67
12	VS 72	80.0	112.7	110.4	6.7	23.9	1477	4444	2.58
13	VS 73	59.3	89.7	145.9	5.5	28.6	1601	5185	2.42
14	VS 74	50.0	80.0	137.7	5.8	27.5	1808	5000	2.90
15	VS 75	61.3	91.7	149.5	7.7	28.4	1951	6204	2.78
16	VS 76	62.3	92.7	143.5	6.9	26.8	1844	5093	1.73
17	VS 77	60.7	90.7	148.3	8.8	28.4	1442	4259	2.68
18	VS 78	66.7	99.0	142.5	6.9	26.8	1589	5185	2.87
19	OLM 203	81.0	113.7	146.9	7.7	27.9	1844	5648	2.57
20	BL 6	65.0	96.0	152.4	7.9	27.6	1790	4815	2.77
Mean		64.12	95.10	143.96	7.14	27.85	1717.13	5134.26	2.29
Min		48.67	78.33	110.40	5.53	23.48	1366.67	4074.07	1.67
Max		85.67	118.00	154.00	8.80	32.43	2018.52	6203.70	2.90
CD (5%)		3.45	3.57	10.94	1.70	2.57	342.13	1198.58	0.35
CD (1%)		4.62	4.78	14.66	2.27	3.44	458.27	1605.43	0.47
CV (%)		3.26	2.27	4.60	14.38	5.58	12.06	14.13	9.30

Table 3: Genetic parameters for eight traits studied in little millet breeding lines

Character	DFF	DM	PH	NPT	PL	GY	FY	TW
GCV	16.90	12.37	5.70	10.64	7.35	7.99	8.07	18.56
PCV	17.21	12.58	7.33	17.89	9.23	14.46	16.27	20.76
ECV	3.26	2.27	4.60	14.38	5.58	12.06	14.13	9.30
H^2	96.42	96.73	60.60	35.39	63.39	30.51	24.60	79.92
GA	21.92	23.83	13.17	0.93	3.36	156.11	423.35	0.78
GAM	34.18	25.06	9.15	13.04	12.05	9.09	8.25	34.18

GCV- Genotypic co-efficient of variation; PCV- Phenotypic co-efficient of variation; ECV- Environmental co-efficient of variation; H^2- Heritability; GA- Genetic advance; GAM- Genetic advance as per cent of mean.

genotypes studied in this experiment, which implies that there is a good scope for selection of the studied characters. The mean values of all the six traits for little millet genotypes were presented in Table 2.

Days to 50% flowering and days to maturity recorded a mean value of 64.12 and 95.10 respectively. The genotype VS 54 recorded minimum number of days to 50% flowering and days to maturity (48 DFF; 78 DM) whereas VS 60 took highest days to flower and mature (85 DFF; 118 DM) The overall mean of plant height was 143.96 cm and it ranged from 110.40 cm in VS 72 to 154.00 cm in VS 56. Number of productive tillers ranged from 5.53 (VS 73) to 8.80 (VS 77) with a mean value of 7.14. Panicle length has ranged from 23.48 cm (VS66) to 32.43 cm (VS 43) with a mean value of 27.85 cm. Grain yield has recorded a mean value of 1717.13 kg/ha and ranged from 1366.67 kg/ha in VS 60 to 2018.52 kg/ha in VS 57. VS 66 recorded minimum of 4074.07 kg/ha and VS 75 recorded 6203.70 kg/ha of fodder yield and it recorded a mean value of 5134.26 kg/ha. Test weight has recorded a mean value of 2.29 g and ranged from 1.67 g (VS 68) to 2.90 g (VS 74).

Genetic variability is the basis for any selection strategy because the larger the genetic variability in the existing population, the greater will be the scope of selection for the improvement of genotypes for the given traits (Mohamed *et al*. 2012; Hussain *et al*. 2021). Table 3 presents the values of genetic variability, heritability, genetic advance and genetic advance as per cent of mean. The results of genetic variability indicated that moderate GCV and PCV were observed by days to 50% flowering, days to maturity, number of productive tillers, and test weight indicating the existence of moderate genetic variability and demonstrated little scope for effective selection for the given traits. Low values of GCV and PCV were recorded by plant height and panicle length, whereas low GCV and moderate values of PCV were observed for grain yield and fodder yield, which exhibited a huge impact of environment on these traits.

The results of heritability and genetic advance as per cent of mean revealed that days to 50% flowering, days to maturity and test weight exhibited high heritability and genetic advance as per cent of mean indicating the presence of additive gene action controlling the traits. Selection will be effective in improving these traits. High heritability and moderate genetic advance as per cent of mean was recorded by panicle length and plant height recorded high heritability and low genetic advance as per cent of mean, indicating the existence of both additive and non-additive gene action. Number of productive tillers recorded moderate heritability and genetic advance as per cent of mean whereas grain yield has recorded moderate heritability and low genetic advance as per cent of mean but fodder yield recorded low heritability and genetic advance as per cent of mean. Direct selection is ineffective for grain yield and fodder yield as these traits are influenced by environment. Earlier investigators, such as Jyothsna *et al*. (2016) and Matere *et al*. (2022) studied genetic variability for similar traits in little millet.

CONCLUSION

In conclusion, the material chosen differed in their genotypic make up as evidenced by the significant differences among them in respect of all the quantitative characters studied. Phenotypic coefficients of variations estimate was slightly higher than the genotypic coefficients of variation

for all the traits, indicating low environmental influence on the expression of all the traits.

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