

Genetic Variability Studies for grain yield and its attributes in Proso millet (*Panicum miliaceum* L.)

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ABSTRACT

Evaluation of 20 proso millet breeding lines was attempted during *kharif*, 2021 at Agricultural Research Station, Vizianagaram to assess genetic variability, heritability and genetic advance for ten yield contributing traits. Number of productive tillers per plant and number of leaves per plant recorded high variability indicating much scope of improvement for these characters with simple selection. High heritability coupled with high GAM were recorded for number of productive tillers per plant, leaf length and number of leaves per plant indicating preponderance of additive gene action which is very much selection responsive. Narrow range of variations for PCV and GCV were observed for days to 50% flowering, days to maturity, indicating less environmental influence for these traits. They also recorded high heritability with low GAM indicating that these two traits may be governed by few genes with non additive gene action. Hence, selection for these traits may be attempted through heterosis breeding. VP008 and VP 033 were found to be promising for earliness and VP021 for higher grain yield.

Key words: *Heritability and genetic advance, Proso millet and Variability.*

Small millets are the hitherto staple food for millions of people residing in arid and semiarid regions of Asian and African countries and are currently restricted to certain traditional growing areas. Increased health problems, due to changes in lifestyle, have driven people to pay attention to their food habits and deliberately shift toward nutritional crops, such as small millets (Anuradha *et al.*, 2022). Proso millet (*Panicum miliaceum* L.) also called as common millet or broomcorn millet is one of the oldest cultivated millet crop and consumed as a staple food among the majority of people who live in arid and semiarid tropics of the world, such as Asia, Africa, and parts of Europe (Lu *et al.*, 2009). Several reports have shown that millet is superior to other major cereals in nutritional value (Pathak *et al.*, 2000). Proso millet-based products own a lower glycemic index (GI) than corn, appears to be a good ingredient for producing low-GI products (McSweeney *et al.*, 2017). For any crop improvement programme knowing about genetic variability among the population is a prerequisite. Genetic improvement through traditional breeding approaches depends mainly on the availability of diverse germplasm and the presence of variability. An

insight into the nature and magnitude of genetic variability present in the gene pool is of immense value for starting any systematic breeding programme because, the presence of considerable genetic variability in the base material ensures better chances of evolving desirable plant type. Hence, an attempt was made to estimate the extent of variation for yield contributing traits in the germplasm accessions by studying PCV, GCV, Heritability and Genetic advance which may provide suitable selection indices for improvement of the crop.

MATERIAL AND METHODS

The experimental was conducted with 20 proso millet lines including check (Co 5) and they were evaluated at Agricultural Research Station, Vizianagaram, Andhra Pradesh during *kharif*, 2021. Genotypes were planted in a Randomized Complete Block Design (RCBD) with two replications and a spacing of 22.5 × 10 cm per each entry. Every genotype was grown in 10 lines each of 3 m length. Fertilizers, DAP (87 kg/ha) and Urea (22 kg/ha) were applied basally at the time of land preparation and remaining 22 kg/ha Urea was applied three weeks

after sowing. Standard management practices were followed to maintain a healthy crop. Observations were recorded on five plants for plant height (cm), number of productive tillers per plant and panicle length (cm). Days to 50% flowering, days was recorded by visualizing the entire plot. Fodder yield and grain yield were recorded on per plot basis and then converted into per hectare.

The mean of all the plants for each trait under each replication was subjected to ANOVA as per the method suggested by (Panse and Sukhathme, 1967). The estimates of GCV and PCV were worked out according to the method suggested by (Burton, 1952). Heritability in broad sense was calculated as per the formula given by (Lush, 1940). Range of heritability was categorized as suggested by (Robinson *et al.* 1949). Genetic advance was estimated according to the method suggested by (Johnson *et al.* 1955).

RESULTS AND DISCUSSION

Analysis of variance showed significant differences among the genotypes for all the characters included under study (Table 1). The extent of variability in respect of range, mean, phenotypic coefficient of variability, genotypic coefficient of variability, heritability, genetic advance and genetic advance as percent of mean presented in (Table 3). In the present study VP 033 was the earliest with 64 days to maturity followed by VP 008 with 66 days to maturity (Table 2). These two genotypes can be utilized for breeding early varieties in proso millet. VP 008 was 8 days earlier compared to the check, Co 5 and also had yield advantage of 111kg/ha over the check, hence it may be used as a variety after multilocation evaluation. VP 024 can be used for breeding non-lodging genotypes since it was observed to be the shortest (100 cm) among all the genotypes studied followed by VP 033 with (101 cm). The entry, VP 033 with short plant height and early duration and on par yield with check also appears to be promising and it also has to be tested in multilocation trials. Highest grain yield was recorded by VP 031 (2111 kg/ha) which had out yielded the check variety Co 5(1695 kg/ha) by 416kg/ha though statistically not significant.

The values of PCV obtained for yield and its attributing characters ranged from 6.44 for days to maturity to 34.37 for number of productive tillers per

plant. Similarly, the values of GCV ranged from 6.08 for days to maturity to 31.03 for number of productive tillers per plant. High PCV and GCV for number of productive tillers per plant and low values for days to 50% flowering was also reported earlier by Salini *et al.* (2010), Anuradha *et al.* (2020). Phenotypic coefficient of variability is higher than genotypic coefficient of variability for all the characters. The difference between PCV and GCV were wider for grain yield, fodder yield and plant height while it was narrower for days to 50% flowering and days to maturity indicating higher GE interaction for former traits and lesser GE for later traits. Number of productive tillers per plant and number of leaves per plant with high GCV and PCV has a greater scope for improvement and selections can be performed between genotypes. Whereas moderate variations recorded for panicle length, leaf length and narrow variation for all other traits indicates less scope for selection of these traits among genotypes.

Presence of variability implies possibility of selections. For reliable selection one has to depend on heritability studies. Highly heritable traits are governed by genotypic variances rather than with environmental variance. Hence, there is more chance for success in selection of genotypes based on heritability. However, heritability informs whether the variation is genetic or non genetic while Genetic Advance as Percent Mean (GAM) enlightens the aspect of gene action. Heritability along with GAM studies are meaningful. In the present investigation, high heritability was recorded for days to 50% flowering, days to maturity, number of productive tillers per plant, leaf length and number of leaves per plant. Similarly high heritability for all characters were reported by Salini *et al.* (2010) while high heritability was reported for number of leaves, tillers, plant height and days to maturity during both years of their study by Calamai *et al.* (2020). High GAM were recorded for number of productive tillers per plant, leaf length, leaf width and number of leaves per plant. High heritability coupled with high GAM was recorded for number of productive tillers per plant, leaf length and number of leaves per plant indicating preponderance of additive gene action is very much selection responsive. Whereas high heritability with moderate GAM was recorded for plant height and panicle length indicating both additive and non additive gene action. Grain yield and fodder yield recorded moderate

heritability with moderate GAM indicating the importance of both gene actions while for days to 50% flowering and days to maturity it is preponderance of non additive gene action because of its high heritability with low GAM. Days to 50% flowering and days to maturity may have dominant and epistatic gene action which can be improved by heterosis breeding. Salini *et al.* (2010) recorded high heritability with moderate GAM for days to 50% flowering. Calamai *et al.* (2020) also recorded

moderate heritability for grain yield. Conversely high heritability and high GAM was reported by Anuradha *et al.* (2020) for grain yield and fodder yield.

The study reveals that VP021, VP008, VP033 are promising genotypes for one or the other traits. Ample variation existed among genotypes for the characters studied. Selection for number of productive tillers per plant, leaf length and number of leaves per plant may be rewarding while selection for grain yield and maturity requires breeding efforts.

Table 1: ANOVA of twenty proso millet (*Panicum miliaceum* L.) genotypes.

Source of Variations	Df	Mean Sum of Squares									
		DFF	DM	PH	NPT	PL	LL	LW	NL	GY	FY
Treatments	19	27.65**	41.68**	322.18**	4.58**	52.52**	64.03**	0.21**	5.24**	102764*	569463*
Replications	1	0.22	0.4	1.37	0.68	4.49	4.9	0.45*	0.26	9364	394463
Error	19	0.7	2.4	83	0.47	16.22	14.02	0.08	0.75	42456	251229

**Significant at 1% and * significant at 5% level

Note: Df: Degrees of freedom; DFF: Days to 50% flowering; DM: Days to maturity; PH: Plant height (cm); NPT: No. of productive tillers per plant; PL: Panicle length (cm); LL: Leaf Length; LW: Leaf Width; NL: Number of leaves per plant; GY: Grain yield (kg/ha); FY: Fodder yield (kg/ha)

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Table 2: Performance of twenty proso millet (*Panicum miliaceum* L.) genotypes

S.No	Entry	DFF	DM	PH	NPT	PL	LL	LW	NL	GY(kg/ha)	FY(kg/ha)
1	VP 010	43	75	103.3	5.0	31.9	26.8	1.3	8	1917	4819
2	VP 002	40	70	114.7	5.1	37.9	34.9	2.0	10	2056	4417
3	VP 016	41	69	112.9	3.1	40.4	32.9	1.4	7	1778	4389
4	VP 008	38	66	104.2	6.0	32.2	27.1	1.7	5	1806	3625
5	VP 026	41	71	129.6	6.0	39.9	28.0	1.8	8	1528	4083
6	VP 027	42	73	118.2	5.8	34.0	30.7	1.7	7	1389	4250
7	VP 028	43	74	103.2	3.1	22.6	19.9	0.8	6	1584	4806
8	VP 021	49	79	111.3	4.1	31.8	39.9	1.9	6	2069	5111
9	VP 022	47	78	132.4	2.4	39.7	37.0	1.8	6	1834	4722
10	VP 003	46	77	108.7	4.0	33.9	27.2	1.6	9	1306	4139
11	VP 024	45	75	100.0	6.6	37.1	33.1	1.6	7	1972	5028
12	VP 029	43	73	124.9	6.9	36.0	40.2	1.5	5	2000	4917
13	VP 020	42	73	135.3	2.2	34.1	35.0	1.9	10	1639	4417
14	VP 030	41	71	136.0	3.0	42.8	28.9	2.0	5	1750	4306
15	VP 031	53	85	111.6	5.9	30.9	36.8	1.3	6	2111	5500
16	VP 032	41	72	133.9	4.3	42.1	26.9	1.2	8	1695	5250
17	VP 033	36	64	101.0	6.0	31.2	29.2	1.6	8	1722	5014
18	VP034	42	73	133.9	2.5	25.8	39.1	2.0	5	1667	3361
19	VP 035	43	75	109.2	6.0	34.9	33.0	1.2	9	2056	4556
20	CO 5	43	74	123.0	4.4	34.9	41.0	1.7	7	1695	4250
	Mean	42.68	72.95	117.37	4.62	34.71	32.38	1.60	7.10	1777.80	4547.92
	CD (1%)	2.39	4.43	26.06	1.95	11.52	10.71	0.78	2.48	589.40	1433.76
	CD (5%)	1.75	3.24	19.07	1.43	8.43	7.84	0.57	1.82	431.20	1048.92
	CV (%)	1.96	2.12	7.76	14.77	11.60	11.56	17.10	12.22	11.59	11.02

Note: DFF: Days to 50% flowering; DM: Days to maturity; PH: Plant height (cm); NPT: No. of productive tillers per plant; PL: Panicle length (cm); LL: Leaf Length; LW: Leaf Width; NL: Number of leaves per plant; GY: Grain yield (kg/ha); FY: Fodder yield (kg/ha)

Table 3: Genetic parameters of twenty proso millet (*Panicum miliaceum* L.) genotypes

S. No	Parameter	DFP	DM	PH	NPT	PL	LL	LW	NL	GY(kg/ha)	FY(kg/ha)
1	Mean	42.68	72.95	117.37	4.62	34.71	32.38	1.60	7.10	1777.80	4547.92
2	Minimum	36.00	63.50	100.00	2.20	22.60	19.90	0.80	5.00	1305.50	3361.11
3	Maximum	53.00	84.50	136.00	6.90	42.80	41.00	2.00	10.00	2111.00	5500.00
4	GCV	8.60	6.08	9.32	31.03	12.28	15.44	16.25	21.10	9.77	8.77
5	PCV	8.82	6.44	12.13	34.37	16.89	19.29	23.59	24.39	15.16	14.09
6	ECV	1.96	2.12	7.76	14.77	11.60	11.56	17.10	12.22	11.59	11.02
7	H ² (B)	95.07	89.11	59.03	81.53	52.82	64.08	47.45	74.88	41.53	38.78
8	Genetic Advance	7.37	8.62	17.31	2.67	6.38	8.25	0.37	2.67	230.52	511.69
9	GAM	17.28	11.81	14.75	57.72	18.38	25.47	23.06	37.62	12.97	11.25

Note: DFP: Days to 50% flowering; DM: Days to maturity; PH: Plant height (cm); NPT: No. of productive tillers per plant; PL: Panicle length (cm); LL: Leaf Length; LW: Leaf Width; NL: Number of leaves per plant; GY: Grain yield (kg/ha); FY: Fodder yield (kg/ha)
 GCV: Genotypic Coefficient of Variance, PCV: Phenotypic Coefficient of Variance; ECV: Environmental Coefficient of Variance; H² (B): Heritability in Broad sense; GAM: Genetic Advance as Percent Mean

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