

Original Research Article

Genetic Variability Studies of Grain Yield and its Attributes in Proso millet (*Panicum miliaceum* L.)

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ABSTRACT

Understanding the amount and nature of genetic variation is vital for any crop enhancement. Hence, seventeen proso millet advanced breeding lines developed across the country were evaluated during *kharif*, 2019 at Agricultural Research Station, Vizianagaram to assess genetic variability, heritability and genetic advance for seven yield contributing traits. The characters included under study were days to 50 % flowering, plant height, days to maturity, number of productive tillers per plant, panicle length, grain yield and fodder yield per plant. The ANOVA revealed significant differences among seventeen genotypes for all the characters included under study. Fodder yield and grain yield showed high variability indicating the scope of improvement of these characters by simple direct selection. Narrow range of variations for PCV and GCV were observed for days to 50% flowering, days to maturity, indicating less variation for these traits. High heritability and high GAM were recorded for grain yield, fodder yield and plant height indicates preponderance of additive gene action and additive gene action is very much selection responsive.

Keywords

Proso millet,
Variability

Introduction

Proso millet (*Panicum miliaceum* L.), also called as common millet or broomcorn millet, is an annual herbaceous plant from the genus *Panicum* with chromosome number of $2n = 36$. It 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). Moreover, 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). The protein content accounts for 12% and the essential amino acid index (EAAI) of proso millet was higher (51%) compared to wheat (Kalinova and Moudry, 2006). Although it is found to be a hardy crop, it is also affected by many diseases. The major constraint in the profitable production of all proso millet growing areas of the world is banded sheath blight (*Rhizoctonia solani*) has been increasing problem and reported to cause considerable loss in grain yield (Patro *et al.*, 2019).

In any crop improvement programme knowledge 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 (Anuradha *et al.*, 2017). 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.

Materials and Methods

The experiment was conducted with 17 proso millet lines and they were evaluated at Agricultural Research Station, Vizianagaram, Andhra Pradesh during *kharif*, 2019. Genotypes were planted in a randomized complete block design (RCBD) with three replications and a spacing of 30 × 10 cm. per each entry. Every genotype was grown in 10 lines each of 3 m length. Fertilizers, DAP (87 kg/ha), MOP (42 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). Correlations were calculated as suggested by (Johnson *et al.*, 1955).

Results and Discussions

Analysis of variance showed significant differences among the genotypes for all the characters included under study (Table 1). Similar variations were reported by Anuradha *et al.*, (2020) in browntop millet, Anuradha *et al.*, (2014) in barnyard millet and Anuradha *et al.*, (2013) in finger millet. 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 were presented in Table 2.

The values of PCV obtained for yield and its attributing characters ranged from 5.58 for days to maturity to 36.88 for fodder yield. The values of GCV ranged from 5.23 for days to maturity to 31.72 for fodder yield. These results are in consonance with earlier studies of Manoharan (1978) and Hawlader (1991). Phenotypic coefficient of variability is higher than genotypic coefficient of variability for all the characters indicating that the interaction of genotypes with environment.

Table.1 Analysis of variance of seven characters for 17 genotypes of Proso millet (*Panicum miliaceum* L.)

Mean sum of squares									
S.no	Sources	Df	Days to 50 % Flowering	Plant height	Days to Maturity	Number of Productive Tillers	Panicle length	Grain Yield	Fodder Yield
1	Treatments	17	36.093**	1202.232**	43.686**	1.398**	79.259**	34.840**	709.235**
2	Replication	2	3.353	119.416	2.176	0.010	12.785	0.707	6.802
3	Error	34	1.145	58.788	1.947	0.165	7.311	2.474	74.421

Table.2 Estimates of genetic variability parameters of yield component attributes in proso millet (*Panicum miliaceum*)

S.no	Characters	Mean	Min (Range)	Max (Range)	GCV	PCV	ECV	H ²	GA	GAM
1	Days to 50% flowering	40.94	34.67	45.33	8.34	8.74	2.61	91.05	6.71	16.39
2	Plant height	113.00	76.73	141.60	17.28	18.56	6.79	86.64	37.43	33.13
3	Days to maturity	71.35	64.00	75.67	5.23	5.58	1.96	87.72	7.20	10.09
4	Number of productive tillers	3.56	2.53	5.00	18.01	21.32	11.41	71.33	1.12	31.33
5	Panicle length	29.91	20.92	37.43	16.37	18.70	9.04	76.64	8.83	29.53
6	Grain yield	12.72	8.07	22.02	25.83	28.64	12.37	81.35	6.10	47.99
7	Fodder yield	45.86	23.21	90.87	31.72	36.88	18.81	73.98	25.77	56.20

High PCV and GCV was observed for characters fodder yield and grain yield indicating that there is great scope for improvement of these characters by direct selection among the genotypes whereas moderate variations were recorded for plant height, panicle length and number of productive tillers per plant. Narrow range of variations between PCV and GCV were observed for days to 50% flowering, days to maturity, indicating less variation for these traits.

Presence of variability implies possibility of selections. To have reliable selection one has to depend on heritability studies. Highly heritable traits are governed by genotypic variances rather than with environmental variances. 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 and high GAM were recorded for grain yield, fodder yield and plant height indicated preponderance of additive gene action and additive gene action is very much selection responsive. Similar results were reported by Panwar and Kapila (1992). Moderate GAM were observed for days to 50 % flowering, days to maturity.

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