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Genetic Variability Studies for Quantitative Traits in a Pool of Maintainer (B) and Restorer (R) Lines in Pearl Millet (*Pennisetum glaucum* (L.) R. Br.)

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A B S T R A C T

The present investigation was carried out at Agricultural Research Station, Perumallapalle, Tirupati, A.P. with 10 maintainer (B) and 27 restorer (R) lines of pearl millet during *summer,* 2020 in randomized block design with three replications to estimate genetic parameters *viz.,* genetic variance, heritability (broad sense) and genetic advance as per cent of mean for 15 quantitative traits. The analysis of variance revealed highly significant differences among the genotypes for all the characters studied. The phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) and the difference between PCV and GCV was narrow for most of the characters, implying little influence of environment on expression of the traits. High values of PCV, GCV and heritability estimates coupled with maximum genetic advance over mean were obtained for panicle length, green fodder yield per plant, dry fodder yield per plant, panicle weight, 1000 grain weight, harvest index and grain yield per plant indicating the preponderance of additive gene action and selection based on these characters could be effective.

Introduction

Pearl millet (*Pennisetum glaucum* (L.) R. Br.) is diploid (2n=14) and highly cross pollinated, annual C_4 crop which belongs to the family of poaceae. It is originated in central tropical Africa and is cosmopolitan within arid and semi-arid topics of Africa and India. It is commonly known as cumbu or dark millet or spiked millet or candle millet. It has protogyny and anemophily mechanisms which fulfils the essential biological requirements for hybrid development.

In India, pearl millet is cultivated in a total area of 6.93 million hectares with a production of 8.61 million tonnes and productivity of 1243 kg/ha (Anonymous, 2019). It is the fifth most widely cultivated staple grain crop in India next to rice, wheat, maize and sorghum.

It is an outstanding multipurpose coarse cereal crop for grain, fodder and stover across wide range of environments around the world. It can adapt well to drought and adverse agro-ecological conditions, capable of rapid and vigorous growth, hence it is grown under

marginal lands of low and erratic rainfall with high temperature and low soil fertility.

Pearl millet is rightly termed as poorman's food and nutri-cereal as it is a good source of carbohydrates (67.1%), proteins (11.6%), fat (5.2%) and minerals (2.7%). Protein content of pearl millet is higher than barley (11.5%), maize (11.1%), sorghum (10.4%) and rice (7.2%). It is having a low glycemic index, rich source of vitamins (thiamine, riboflavin and niacin) and minerals (P, K, Mg, Fe, Zn, Cu and Mn). It supports weight loss and helps in reducing cholesterol levels (Pearl millet news, 2019).

Devolopment of superior hybrids mainly depends on nature and magnitude of genetic variability for different characters present in experimental material. Heritability measures the degree of resemblance between the parents and the off-springs, while genetic advance aids in exercising the necessary selection pressure. Heritability in conjunction with genetic advance has a major role in determining the effectiveness of selection for a character.

Hence in the present study a pool of maintainers (10) and restorers (27) were evaluated for presence of variability, heritability and expected genetic advance for various quantitative characters with a view to identify the parental lines with best potentiality for enhancing yield and its component characters.

Materials and Methods

Experimental material consisted of 10 maintainer (B) lines and 27 restorer (R) lines received from ICRISAT, Patancheru and were sown during *summer,* 2020 in a Randomized Block Design (RBD) with three replications at Agricultural Research Station, Perumallapalle, Tirupati, A.P.

Recommended package of practices were followed to raise the crop. Each germplasm line was sown in a single row of 5 m length with inter and intra row spacing of 45×15 cm. The observations were recorded on plot basis for days to 50% flowering and days to maturity. Five plants were randomly selected from centre of row in each genotype of each replication and data was recorded for yield, yield attributing and water use efficiency traits *viz.,* plant height (cm), number of productive tillers per plant, panicle length (cm), panicle girth (cm), green fodder yield per plant (g), dry fodder yield per plant (g), panicle weight (g), 1000 grain weight (g), threshing (%), harvest index (%), grain yield per plant (g), SPAD chlorophyll meter reading at 45 DAS and specific leaf area at 45 DAS ($cm^2 g^{-1}$).

The various genetic parameters *viz.*, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), heritability (h^2_{bs}) in broad sense and genetic advance as per cent of mean were calculated as suggested by Burton (1952), Lush (1940) and Johnson *et al.,* (1955). The data analysis was carried out with WINDOWSTAT 9.2 software.

Results and Discussion

Analysis of variance revealed highly significant differences for all the characters under study, thereby indicating the presence of ample amount of genetic variation among the genotypes (Table 1). The estimates of variability parameters for yield and its component characters in 37 pearl millet inbred lines were presented in Table 2. Phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) for all the characters under study suggesting the role of environment in the expression of these characters (Fig. 1).

High estimates of phenotypic and genotypic coefficient of variation were registered for grain yield per plant (GCV = 51.48%; PCV = 58.52%) followed by panicle weight (GCV = 42.97%; PCV = 47.80%), dry fodder yield per plant (GCV = 42.04%; PCV = 49.14%), green fodder yield per plant (GCV = 36.25%; PCV = 42.18%), number of productive tillers per plant (GCV = 23.54%; PCV = 35.13%), 1000 grain weight (GCV = 22.62%; PCV = 23.95%), panicle length (GCV = 21.40%; PCV = 23.87%) and harvest index (GCV = 21.34%; PCV = 26.60%) indicating the existence of immense inherent variability that remained unaltered by environmental conditions among the genotypes, which in turn was more useful for exploitation in hybridization and/or selection.

Likewise, high estimates of variability were reported by Dehinwal *et al.,* (2016), Nehra *et al.,* (2017) and Talawar *et al.,* (2017) for number of productive tillers per plant, 1000 grain weight and grain yield per plant;

Bhasker *et al.,* (2017) and Kumar *et al.,* (2014) for panicle length and dry fodder yield per plant; Vinodana *et al.,* (2013) and Kumar *et al.,* (2017) for green fodder yield per plant; Sumathi *et al.,* (2010) and Vagadiya *et al.,* (2013) for panicle weight which corroborates with the findings of the present study.

Moderate estimates of coefficient of variation were observed for plant height (GCV = 14.69%; PCV = 17.13%) followed by panicle girth (GCV = 14.66%; PCV = 17.09%), threshing percentage (GCV = 12.02%; PCV = 17.02%), specific leaf area at 45 DAS (GCV = 11.32%; PCV = 18.77%) and SPAD chlorophyll meter reading at 45 DAS (GCV = 10.35%; PCV = 12.18%). This indicated the existence of sufficient variability for attempting selection to improve these traits in the genotypes studied. These findings were in consonance with Sathya *et al.,* (2013) and Sowmiya *et al.,* (2016) for both plant height and panicle girth and Priyanka (2019) for specific leaf area at 45 DAS.

Table.1 Analysis of variance for yield and yield attributes in 37 inbred lines of pearl millet

S. No.	Characters	Mean sum of squares		
		Replications (df = 2)	Treatments (df = 36)	Error (df = 72)
1	Days to 50 % flowering	4.225	40.964**	1.753
2	Days to maturity	4.622	35.842**	2.149
3	SPAD chlorophyll meter reading at 45 DAS	25.680	73.938**	8.398
4	Specific leaf area at 45 DAS ($cm^2 g^{-1}$)	2440.944	2445.743**	900.872
5	Plant height (cm)	272.421	1434.744**	153.430
6	Number of productive tillers per plant	0.387	0.573**	0.166
7	Panicle length (cm)	14.280	66.846**	5.046
8	Panicle girth (cm)	0.085	0.345**	0.037
9	Green fodder yield per plant (g)	1249.730	4012.531**	423.272
10	Dry fodder yield per plant (g)	52.680	361.445**	39.331
11	Panicle weight (g)	82.256	472.473**	34.626
12	1000 grain weight (g)	0.929	13.322**	0.515
13	Threshing (%)	8.314	208.203**	52.260
14	Harvest index (%)	22.276	167.086**	26.047
15	Grain yield per plant (g)	48.215	264.725**	23.514

*Significant at 5% level; ** Significant at 1 % level

Table.2 Estimates of mean, range and genetic parameters for yield and yield attributes in 37 inbred lines of pearl millet

S. No.	Characters	Mean	Range		Variance		Coefficient of Variation		Heritability (Broad sense) (%)	Genetic advance (GA)	Genetic advance as percent of mean (%)
			Min.	Max.	Genotypic	Phenotypic	Genotypic	Phenotypic			
1.	Days to 50 % flowering	49.23	43.33	59.00	13.07	14.82	7.34	7.82	88.17	6.99	14.21
2.	Days to maturity	84.68	78.33	93.33	11.23	13.38	3.96	4.32	83.94	6.33	7.47
3.	SPAD chlorophyll meter reading at 45 DAS	45.15	33.07	53.93	21.85	30.24	10.35	12.18	72.23	8.18	18.12
4.	Specific leaf area at 45 DAS ($cm^2\ g^{-1}$)	200.43	155.84	252.63	514.95	1415.82	11.32	18.77	36.37	28.19	14.07
5.	Plant height (cm)	140.65	101.27	185.47	427.10	580.53	14.69	17.13	73.57	36.52	25.96
6.	Number of productive tillers per plant	1.56	1.00	2.67	0.14	0.30	23.54	35.13	44.92	0.51	32.51
7.	Panicle length (cm)	21.21	13.87	33.07	20.60	25.65	21.40	23.87	80.32	8.38	39.50
8.	Panicle girth (cm)	2.19	1.62	2.95	0.10	0.14	14.66	17.09	73.58	0.57	25.90
9.	Green fodder yield per plant (g)	95.41	32.93	197.20	1196.42	1619.70	36.25	42.18	73.87	61.24	64.19
10.	Dry fodder yield per plant (g)	24.65	8.87	59.87	107.37	146.70	42.04	49.14	73.19	18.26	74.09
11.	Panicle weight (g)	28.11	10.40	73.27	145.94	180.58	42.97	47.80	80.83	22.37	79.58
12.	1000 grain weight (g)	9.13	4.55	14.96	4.27	4.78	22.62	23.95	89.23	4.02	44.02
13.	Threshing (%)	59.99	32.87	69.65	51.98	104.24	12.02	17.02	49.87	10.49	17.48
14.	Harvest index (%)	32.13	13.91	47.87	47.01	73.06	21.34	26.60	64.35	11.33	35.26
15.	Grain yield per plant (g)	17.41	5.40	51.33	80.40	103.92	51.48	58.52	77.37	16.25	93.28

Fig.1 Estimates of GCV and PCV for yield and yield attributes in pearl millet
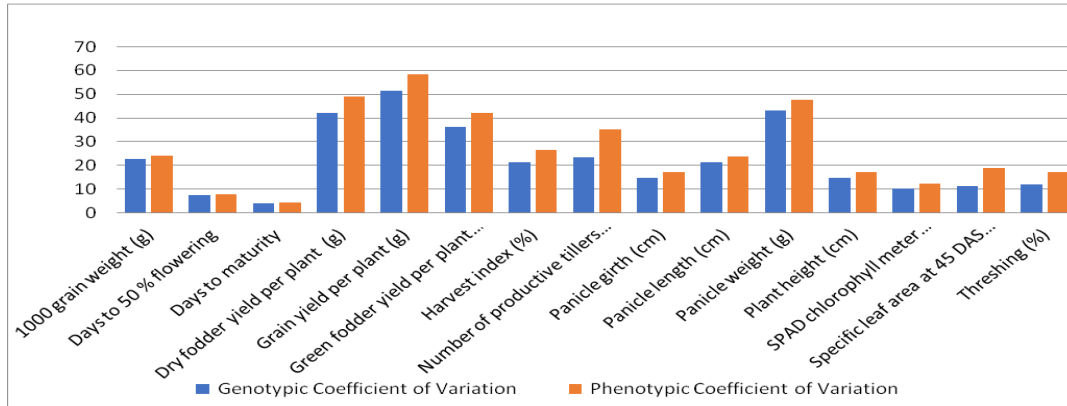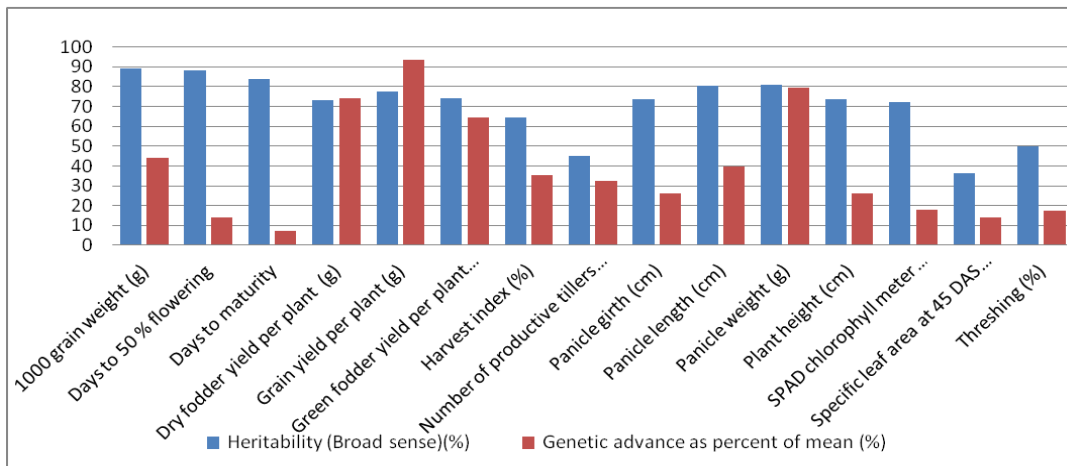

Fig.2 Heritability in broad sense and genetic advance as per cent of mean
for yield and yield attributes in pearl millet

On contrary, low estimates of coefficients of variation were recorded for days to 50% flowering (GCV = 7.34%; PCV = 7.82%) and days to maturity (GCV = 3.96%; PCV = 4.32%) indicating narrow range of variability for these traits thereby restricting the scope for simple selection. Similar kind of low estimates of variability was also reported earlier by Bhasker *et al.,* (2017) and Nehra *et al.,* (2017) for days to 50% flowering; Sharma *et al.,* (2018) and Patel *et al.,* (2019) for days to maturity.

Heritability is the heritable portion of phenotypic variance. Genetic advance gives an indication of expected genetic progress for

a particular trait under suitable selection pressure. Heritability (h^2) coupled with genetic advance as per cent of mean (GAM) will bring out the genetic gain expected from selection than heritability alone in accurate prediction of the selection efforts (Johnson *et al.,* 1955).

High heritability coupled with high genetic advance as per cent of mean were recorded for plant height (h^2_{bs} = 73.57%; GAM = 25.96%), panicle length (h^2_{bs} = 80.32%; GAM = 39.50%), panicle girth (h^2_{bs} = 73.58%; GAM = 25.90%), green fodder yield per plant (h^2_{bs} = 73.87%; GAM = 64.19%), dry fodder yield per plant (h^2_{bs} = 73.19%; GAM =

74.09%), panicle weight (h^2_{bs} = 80.83%; GAM = 79.58%), 1000 grain weight (h^2_{bs} = 89.23%; GAM = 44.02%), harvest index (h^2_{bs} = 64.35%; GAM = 35.26%) and grain yield per plant (h^2_{bs} = 77.37%; GAM = 93.28%) indicating the predominance of additive gene effects in controlling these traits. Early and simple selection could be exercised due to fixable additive gene effects.

These results are in line with findings of Bhasker *et al.,* (2017) and Patel *et al.,* (2019) for plant height, panicle length and dry fodder yield per plant; Talawar *et al.,* (2017) and Kaushik *et al.,* (2018) for 1000 grain weight and grain yield per plant; Bika and Shekawat (2015) and Singh *et al.,* (2018) for panicle girth and green fodder yield per plant; Dehinwal *et al.,* (2016) for panicle weight.

High heritability along with moderate genetic advance as per cent of mean recorded for days to 50% flowering (h^2_{bs} = 88.17%; GAM = 14.21%) and SPAD chlorophyll meter reading at 45 DAS (h^2_{bs} = 72.23%; GAM = 18.12%) indicated the presence of non-additive gene action. The high heritability is being exhibited due to favourable influence of environment rather than the genotype and selection for such traits may not be rewarding. These findings were supported by reports of Vinodana *et al.,* (2013) and Bind *et al.,* (2015) for days to 50% flowering. Whereas, high heritability in conjunction with low genetic advance as per cent of mean was observed for days to maturity (h^2_{bs} = 83.94%; GAM = 7.47%) indicating the influence of dominant and epistatic genes in the inheritance and recurrent selection would be more effective to improve this character. Such confirmatory results were also given by Vidyadhar *et al.,* (2007) and Yaqoob *et al.,* (2015).

Moderate heritability coupled with moderate genetic advance as per cent of mean was

registered for specific leaf area at 45 DAS (h^2_{bs} = 36.37%; GAM = 14.07%) and threshing percentage (h^2_{bs} = 49.87%; GAM = 17.48%) which indicated the preponderance of non-additive gene action. Hence, it could be suggested that improvement of these characters might be difficult through simple selection.

Based on present study it can be concluded that the values of PCV were higher than GCV but in a narrow range for almost all the studied characters indicating the least influence of environment. The characters *viz.,* plant height, panicle length, panicle girth, green fodder yield per plant, dry fodder yield per plant, panicle weight, 1000 grain weight, harvest index and grain yield per plant exhibited high heritability coupled with high genetic advance as per cent of mean indicating the role of additive gene action in governing these traits and direct selection would be rewarding for crop improvement.

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