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Genetic Variability, Heritability and Genetic Advance of Grain Yield in Pearl Millet [*Pennisetum glaucum* (L.) R.Br.]

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ABSTRACT

A set of 53 genotypes comprising of 40 F_1s along with four male sterile lines and 12 pollinators were studied for genetic variability, heritability and genetic advance for grain yield and its eight components in pearl millet at R.A.R.S, Palem during kharif 2015. The analysis of variance revealed highly significant differences among the genotypes for all the nine characters studied. These characters, namely, days to 50% flowering, days to maturity, plant height, productive tillers per plant, panicle length, panicle diameter, 1000 grain weight and fodder yield per plot were less affected by environment showing close correspondence between genotypic co-efficient of variation and phenotypic co-efficient of variation. The high values of GCV, PCV and heritability estimates coupled with maximum genetic advance over mean were obtained for the characters like plant height, productive tillers per plant, panicle length and fodder yield indicated that selection for these traits could be effective.

Key words: *GCV, Genetic advance, Heritability, PCV, Pearl millet.*

INTRODUCTION

Pearl mille [*Pennisetum glaucum* (L.)] is an important staple food crop in arid and semi arid regions of India. This crop has high variability because of its cross pollination and tillering nature. Crop improvement depends on the magnitude of genetic variability and the extent to which the desirable characters are heritable. The critical assessment of nature and magnitude of genetic variability, heritability and genetic advance is one of the important prerequisites of plant breeding. The estimates of variability parameters for grain yield and its components in pearl millet could help in planning successful breeding programme.. Grain yield is a complex character being governed by a large number of minor genes with cumulative, duplicate and dominant effect and highly influenced by environment.

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This necessitates a thorough knowledge on variability owing to genetic factors, actual heritable genetic variation present in the progeny and the genetic advance that can be achieved through selection. Therefore, the present investigation was undertaken to estimate the genetic variability, heritability and genetic advance for grain yield and nine component traits in pearl millet during *Kharif*-2015.

MATERIALS AND METHODS

Five cytoplasmic-genetic male sterile lines and 8 diverse restorer lines were crossed following line x tester mating design during summer-2014. The resultant 40 F1s along with fertile counter parts of five male sterile lines and pollinators were evaluated in a randomized block design with three replications at Regional Agricultural Research Station (R.A.R.S), Palem, Professor Jayashankar Telangana State Agricultural University, Telangana, during *Kharif*- 2015. Each entry was grown in a single row of 5.0 m length with inter and intra row spacing of 45 x 15 cm. The recommended agronomic practices and plant protection measures whenever necessary were adopted for raising the good crop. Observations were recorded on five randomly selected competitive plants for each entry, in each replication for nine characters (Table 1), except days to 50% flowering and days to maturity which were recorded on plot basis. Mean values were subjected to standard statistical procedures namely, analysis of variance[7], genotypic and phenotypic co-efficient of variations[4] and heritability and genetic advance[6].

RESULTS AND DISCUSSION

The analysis of variance (Table 1) revealed highly significant differences among the genotypes for all the nine characters studied. The results indicated that vast genetic variability existed among the genotypes for all the characters under study. The range of phenotypic variability was found to be wide. The high phenotypic variation for plant height and grain yield per plant, indicating thereby the possibility of effective selection for these traits. On the other hand, number of productive tillers per plant, panicle length and fodder yield per plot exhibited narrow range of phenotypic variability. The remaining characters showed moderate magnitude of phenotypic variability. In the present study, the higher estimates of genotypic variance over environmental variance in all the characters except grain yield per plant revealed that the variation among the genotypes had a genetic basis. The estimates of phenotypic and genotypic variances were high for plant height, panicle length and grain yield per plant. The phenotypic and genotypic variances were moderate for days to maturity[9] and 1000 grain weight; while, they were low for the remaining characters. Borkhataria *et al*.[3] was also reported high genotypic and phenotypic variances for plant height and grain yield.

The relative amount of variation expressed by different traits was judged through estimates of phenotypic and genotypic co-efficient of variation. The characters like plant height, productive tillers per plant and fodder yield per plot[2], exhibited high magnitude of GCV and PCV indicating the presence of wide genetic variability for these traits and chances for improvement of these characters are fairly high. The moderate values of GCV and PCV were observed for 1000 grain weight[2], panicle diameter, panicle length[9], and grain yield per plant. The remaining characters showed low magnitude of GCV and PCV. Results also revealed that the estimate of PCV values was slightly higher higher than their corresponding GCV value for days to 50 % flowering, days to maturity, plant height, panicle length, panicle diameter and

1000 grain weight, which showed that these traits were less affected by environment. These results are in conformity with the report of Borkhataria *et al*[3], Hepziba *et al*[5] and Saraswathi *et al*[8].

Partitioning of total phenotypic variation into heritable and non-heritable components is very useful, because, only heritable portion of variation is exploitable through selection. The estimates of heritability (broad sense) ranged from 0.35 to 0.99 per cent. High heritability estimates were recorded for the traits, plant height[2], panicle length and fodder yield per plot[2], suggesting the usefulness of selection based on phenotypic observations. The high heritability may be due to additive gene effects hence these traits are likely to respond to direct selection. Moderate heritability estimate was observed for days to 50 % flowering, days to maturity and productive tillers per plant[2]. While, the remaining two characters *viz.* grain yield per plant, panicle diameter[2] and 1000 grain weight[2], recorded low heritability. The results achieved in the present study are in akin with[10, 5, 1, 3,2]. Genotypic coefficient of variability along with heritability estimates provides a better picture for the amount of genetic gain expected to be obtained from phenotypic selection[4]. It was interesting to note that high GCV was accompanied with high heritability estimates for plant height, panicle length, productive tillers per plant and fodder yield per plot in the present material which further revealed that selection could be more effective for the improvement of these traits.

The estimates of genetic advance ranged from 0.59 (number of productive tillers per plant) to 51.16 (plant height). The estimates of genetic advance did not project the actual genetic gain that has been attained in relation to the *per se* performance which obviously is not uniform in different populations and even in the same population under different environments. Therefore, the expected genetic gain as per cent of mean was computed. The estimates of genetic advance as percentage of mean ranged between 2.48 (days to maturity) to 37.52 (plant height). Heritability in coupled with genetic gain was more useful than the heritability values alone in the prediction of the resultant effect for selecting the best individual genotypes[6]. Genetic gain gives an indication of expected genetic progress for a particular trait under suitable selection pressure. In the present study, the characters like fodder yield per plot, plant height, productive tillers per plant and panicle length exhibited high heritability coupled with high genetic advance expressed as percentage of mean. This indicated the predominance of additive gene action in governing the traits and their suitability of selection for further improvement among the genotypes studied. These results are in accordance with those of [2, 3, 8]. Moderate heritability estimates with low to medium genetic gain was manifested for panicle diameter and 1000 grain weight which might be due to preponderance of non-additive gene effects. Hence, it could be suggested that improvement of these characters might be difficult through simple selection. Characters like grain yield per plant, days to 50% flowering and days to maturity showed low heritability and genetic advance as percentage of mean, which indicated the predominance of additive and non-additive gene action in controlling these traits. Hence, direct selection for these traits is not rewarding. Thus, in the present study, the high values of GCV, PCV and heritability estimates coupled with maximum genetic advance over mean were obtained for the characters like plant height, productive tillers per plant, panicle length and fodder yield indicated that selection for these traits could be effective.

Table 1: Analysis of variance showing mean squares, and variability parameters for different traits studied in pearl millet

Character	Mean Sum of Squares			Range			Phenotypic variance	Genotypic variance	environmental variance	PCV (%)	GCV (%)	Heriability (h^2) %	Genetic Advance	Genetic Advance as % of mean
	Replications	Genotypes	Error	Mean	Min	Max								
DFF	1.746	4.299**	0.762	49.394	48	53	1.94	1.17	0.76	2.78	2.17	0.60	1.74	3.48
DTM	1.974	5.928**	1.181	78.781	76	82	2.76	1.58	1.18	2.11	1.59	0.57	1.96	2.48
PH	4.156	1871.7**	5.352	136.13	81.33	172.3	627.51	622.16	5.35	18.40	18.32	0.99	51.16	37.52
NPTP	0.057	0.544**	0.090	2.07	1.33	3.33	0.22	0.13	0.09	23.03	17.87	0.60	0.59	28.56
PL	0.116	22.331**	0.742	21.66	16	26.88	7.93	7.19	0.74	13.00	12.38	0.90	5.26	24.28
PD	0.021	0.188**	0.038	2.11	1.40	2.63	0.088	0.05	0.03	14.08	10.56	0.56	0.34	16.31
1000	3.145	5.594**	3.754	11.73	9.64	14.74	2.793	1.58	1.20	14.24	10.73	0.56	1.95	16.67
GYP	3.433	99.898**	13.669	41.23	35.33	48.77	21.2542	7.59	13.65	11.18	6.68	0.35	3.39	8.23
FP	1.121	3.684**	0.429	3.95	2.31	6.46	1.514	1.08	0.42	31.14	26.35	0.71	1.81	45.95

P = 0.05 and P = 0.01 levels, respectively. GCV= Genotypic coefficient of variation; PCV= Phenotypic coefficient

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