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Genetic variability and association studies of pearl millet genotypes for yield contributing traits under rainfed conditions of Andhra Pradesh

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Abstract

Pearl millet (*Pennisetum glaucum* (L.) R. Br.) is an important cereal in semi-arid tropics in Africa and India. Conventionally, pearl millet has good amounts of grain minerals compared to other cereals. Estimation of genetic parameters would be useful in developing appropriate breeding and selection strategies. In the present study the performance of 16 pearl millet genotypes, including popular varieties and released hybrids, was examined in RBD with three replications during the rainy season of 2019. An investigation of phenotypic and genotypic variance, heritability, genetic advance, correlation coefficients and path analysis for yield and its attributing traits revealed that genotypes had a lot of genetic variability particularly for grain yield to be exploited. Grain yield and productive tillers per plant had high variation, heritability and genetic advance as a *per cent* of mean reveals a presence of additive genetic variance and these traits are very important for selection criteria for yield improvement. Character association studies at both phenotypic and genotypic levels indicated that panicle diameter, 1000-grain weight and dry fodder yield had displayed significant and positive correlations among themselves as well as with grain yield. The path coefficient analysis at genotypic level indicated dry fodder yield, panicle length, days to maturity, 1000-grain weight all had positive direct effects on grain yield. Hence, these traits were taken into consideration while developing yield-related selection criteria.

Keywords: Pearl millet, grain yield, genetic parameters, correlation coefficients and path analysis

Introduction

Pearl millet (*Pennisetum glaucum* (L.) R. Br.) is the primary source of nutritious food for millions of people in semi-arid areas of tropical and sub-tropical countries of the world. It's a nutrient-dense staple food grain that's also utilized as a feed, fodder, construction material and even a biofuel source (Singh and Chhabra, 2018) ^[19]. In India, it is the fourth most frequently cultivated food crop, after rice, wheat and maize. It occupies an area of 6.93 m ha with a production of 8.61 million tonnes and has a productivity of 1243 kg/ha (Anonymous, 2019) ^[1]. This is mainly due to cultivation of pearl millet in rainfed situation in marginal soils of poor fertility and improper management. The main constraint in this situation is moisture stress at different stages of crop growth with no fixed pattern due to erratic distribution of rainfall. In some years, excess moisture at later stages especially at grain filling phase affects quality of the produce. In arid areas, landraces/OPVs (open pollinated varieties) that are low yielders are mostly cultivated during *Kharif* season. The low production of pearl millet in India demands the development of more adaptable, stable, high-yielding varieties and hybrids. Genetic variability is the basic requirement for crop improvement as this provides wider scope for selection. Thus, effectiveness of selection is dependent upon the nature, extent and magnitude of genetic variability present in material and the extent to which it is heritable. However, the assessment of variation made on truly diverse germplasm provides the correct picture of the extent of variation which would help in assessing the variability and factors for limited progress made in pearl millet. The pre-requisite for bringing yield improvement is to identify the genotypes with high variability. Genetic variability among traits is important in selecting desirable types. Genetic parameters such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) are useful in detecting the amount of variability present in the germplasm. Heritability coupled with high genetic advance would be more useful tool in predicting the resultant effect in selection of the best genotypes for yield and its attributing traits. Progress in any crop improvement programme depends on accurate assessments of genetic variability, heritability and genetic advance in the base material are essential for finding traits that responsive to selection. Furthermore, using correlation and path coefficient studies, it is possible to design an appropriate breeding strategy for the target environment by understanding the relationships between yield related traits.

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Whereas, path analysis aids breeders in grading genetic traits based on their contribution by demonstrating the direct and indirect effects of each contributing character on the trait under consideration. The purpose of this study was to assess genetic variability for yield and related traits, as well as to evaluate and compare the character-to-grain yield correlations and to partition the genotypic correlation coefficients into direct and indirect effects that might be useful as an index of selection.

Materials and Methods

The field experiment was carried out at Agricultural Research Station, Anantapuramu, and Andhra Pradesh during *khariif* 2019. The experimental material consisted of 16 pearl millet genotypes including eleven released hybrids (HHB 299, AHB 1200, 86M01, NBH 5767, Pratap, GHB 558, NBH 4903, NBH 5061, 86M86, Kaveri Super Boss and 86M64) and five popular open-pollinated varieties (Dhanshakti, ICMV 221, ICMV 155, Pusa Comp. 612 and ABV 04). The genotypes were evaluated in rainy seasons of 2019 at the Agricultural Research Station, ANGRAU, Ananthapuramu, (latitude: 14° 41' N, longitude: 77° 40' E and 373 m above mean sea level) located in the scarce rainfall zone of Andhra Pradesh, India. Each entry was sown in a six rows plot of 4.0 m length keeping row-to-row and plant-to-plant distance of 50 cm and 15 cm, respectively. Thinning was performed after 20 days of germination when the plant height was 10-15 cm, to ensure single plant per hill. The field was uniformly fertilized with recommended dose of 30 kg Nitrogen, 20 kg P₂O₅ and 20 kg K₂O per hectare as basal *i.e.*, just before seeding and 30 kg Nitrogen per hectare at 35 days after seeding. To achieve good crop growth, standard cultural and agronomic practices were used. Five competitive plants per genotype in each replication were selected randomly for recording observations on different characters *viz.*, plant height (cm), number of productive tillers per plant, panicle length (cm) and panicle diameter (cm), while observations on days to 50% flowering, days to maturity, dry fodder yield (kg/ha) and grain yield were recorded on plot basis. 1000-grain weight, a sample of 1000 grains were counted randomly from the threshed seed and the weight is recorded in grams.

The analysis of variance (ANOVA) method, as described by Singh and Chowdary (1985) [18], was used. Burton's method (1952) [5] was used to calculate the variability parameters, genotypic and phenotypic coefficients of variation (GCV and PCV). The method proposed by Lush (1940) [12] was used to calculate estimates of broad sense heritability. Johnson *et al.*, (1955) [10] proposed a method for calculating expected genetic progress. PCV and GCV (Robinson *et al.*, 1949) [16] and GA and GAM (Johnson *et al.*, 1955) [10] were classified into three groups: low (0-10%), moderate (10.1-20%) and high (>20%). Heritability was classified into three categories: low (0-30%), moderate (30.1-60%) and high (>60%). The genotypic correlations between yield and its component traits, as well as among themselves, were calculated using Falconer (1981) [9] methodology. Path coefficient analysis was carried out as suggested by Dewey and Lu (1959) [8]. The simple correlation coefficients already estimated at genotypic level were utilized for this purpose. By keeping yield as dependent variable and other eight yield attributing characters as independent variables, various direct and indirect effects were estimated.

Results and Discussion

In the current study, the analysis of variance indicated significant variations in all traits between genotypes,

suggesting that there is enough variability and potential for additional selection to breed superior genotypes. The mean, range of variation and the estimate of genetic parameters such as heritability, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) and genetic advance as *per cent* of mean (GAM) are presented in Table 1. The estimates of the PCV were greater than the GCV for all the traits under study, suggesting the influences of the environmental forces on the expression of these characters.

High to moderate co-efficient of variation was observed for no. of Productive tillers (18.28, 24.53) and grain yield (18.73, 22.54), whereas moderate to low co-efficient of variation was observed for panicle length (10.07, 13.11), plant height (8.57, 10.08), panicle diameter (7.85, 10.15) and dry fodder yield (7.51, 12.02). Which is in agreement with the findings of Patil *et al.*, (2018) [15] for panicle diameter; Sowmiya *et al.*, (2016) [20] for both plant height and panicle diameter. Low GCV and PCV was noticed for 1000-grain weight (4.37, 7.13), days to 50% flowering (2.45, 2.81) and days to maturity (2.90, 3.20) indicating a limited range of variability for these traits, limiting the possibilities for easy selection. Similar kind of findings were also reported by Sharma *et al.*, (2018) [17] for days to flowering and days to maturity.

The amount of variation present in a given character is measured by the genotypic coefficient of variation. However, it does not define the fraction of heritable variation in overall variance. Hence, heritability which represents the heritable variation existing in the character was computed. High heritability was recorded by days to maturity (82.06) followed by days to 50% flowering (75.96), plant height (72.22) and grain yield (69.04).

High heritability coupled with high genetic advance as *per cent* of mean was observed for grain yield (69.04, 32.05) and moderate heritability with high genetic advance as *per cent* of mean was recorded for no. of productive tillers (55.55, 28.07) indicating presence of additive gene action and selection is effective for these traits. High heritability coupled with low GAM and GCV was observed for days to maturity (82.06, 5.40 and 2.90) and days to 50% flowering (75.96, 4.39 and 2.45), indicating the role of non-fixable genetic variation in the expression of these traits and recurrent selection would be more effective to improve this character. Such confirmatory results were also given by Vidyadhar *et al.*, (2007) [23] and Yaqoob *et al.*, (2015) [23]. Moderate heritability coupled with moderate genetic advance as *per cent* of mean was registered for panicle length (59.02, 15.94) and panicle diameter (59.75, 12.45) 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. Whereas, low heritability coupled with low GAM were observed for 1000-grain weight (37.63, 5.53) and dry fodder yield (39.04, 9.67) indicating that environment is the main role in governing these traits and that selection may be ineffective. Similar results have been reported by Anuradha *et al.*, (2018) [2] and Naoura *et al.*, (2019) [13].

The awareness of correlation coefficients for all conceivable combinations of yield attributes that were assessed at the genotypic and phenotypic levels are presented in Table 2. Genotypic correlation coefficients are a measure of the genetic relationship between traits that may be aids in selecting which characters should be considered for improvement of grain yield. In current investigation, grain yield was positively associated with panicle diameter. (rg=0.834, rp =0.508), dry fodder yield (rg=0.691, rp =0.338) and 1000-grain weight (rg=0.525, rp =0.480) at genotypic as

well as phenotypic level. Similar kind of highly significant positive association of grain yield with dry fodder yield and panicle diameter were reported by Sowmiya *et al.*, (2016)^[20], Dehinwal *et al.*, (2017)^[7] and Anuradha *et al.*, (2018)^[2]; with 1000 grain weight by Naveen *et al.*, (2016)^[14] and Talawar *et al.*, (2017)^[21]. Whereas, grain yield was negatively associated with no. of productive tiller per plant ($rg = -0.365$, $rp = -0.128$). Days to 50% flowering had positive and significant association with days to maturity ($rg = 0.626$, $rp = 0.507$), plant height ($rg = 0.432$, $rp = 0.325$) and panicle length ($rg = 0.544$, $rp = 0.404$) at genotypic as well as phenotypic levels. Which was also confirmed by Vidyadhar *et al.*, (2007)^[23]. Dry fodder yield had positive and significant association with plant height ($rg = 0.438$) and 1000-grain weight ($rg = 0.437$) at genotypic level only. In nutshell, the study of association at both genotypic as well as phenotypic levels of grain yield with its component traits indicated the relevance of 1000-grain weight, panicle diameter and dry fodder yield. Therefore, selection would be efficient, if these attributes are given enough weight throughout the selection process towards yield improvement in pearl millet.

Path coefficient analysis specifies and assesses the relevance of distinct components, whereas genotype selection based just on correlation may be deceptive because it merely measures the mutual association between two variables. The findings of path analysis at genotypic level, which divided the association

of component traits with grain yield into direct and indirect effects (Table 3), revealed that dry fodder yield (7.361) had the greatest positive direct influence on grain yield, followed by panicle length (6.663), days to maturity (3.453) and 1000-grain weight (1.759). These findings were consistent with the earlier reports of Chaudhary *et al.*, (2003)^[6], Arulselvi *et al.*, (2008)^[3], Kumar *et al.*, (2014)^[11], Dehinwal *et al.*, (2017)^[7] and Bhasker *et al.*, (2017)^[4] also reported that at genotypic level the fodder yield per plot had exhibited largest direct effect on grain yield, followed by panicle length and 1000-grain weight. Whereas, highest negative direct effect was recorded for plant height (-11.322), panicle diameter (-9.184), productive tillers per plant (-4.196) and days to 50% flowering (-1.353). These results were similar to findings of Kumar *et al.*, (2014)^[11] for days to 50% flowering and number of productive tillers per plant. Panicle length, panicle diameter showed highly positive indirect effect on grain yield through plant height. Low value of residual effects (2.393) suggested that the contribution of independent characters considered in this study explained about majority of variation for grain yield. The high direct effect of dry fodder yield, panicle length, days to maturity and 1000-grain weight with grain yield reflects a true relationship between them and selection can be practiced for these characters in order to improve grain yield in pearl millet.

Table 1: Mean, range, coefficients of variation, heritability and genetic advance as *per cent* of mean for yield attributing traits of pearl millet genotypes

S. No.	Traits	Mean	Range		Coefficient of variation		Heritability (%)	Genetic advance as <i>per cent</i> of mean (%)
			Min.	Max.	Genotypic	phenotypic		
1	Days to 50% flowering	49.83	47.33	52.33	2.45	2.81	75.96	4.39
2	Days to maturity	85.52	81.67	91.00	2.90	3.20	82.06	5.40
3	Plant Height (cm)	166.46	143.47	200.60	8.57	10.08	72.22	15.00
4	Productive tillers (no./ plant)	1.77	1.20	2.87	18.28	24.53	55.55	28.07
5	Panicle Length (cm)	24.30	19.28	28.00	10.07	13.11	59.02	15.94
6	Panicle Diameter (cm)	2.72	2.21	3.11	7.85	10.15	59.75	12.49
7	1000 - grain weight (g)	16.54	14.33	17.67	4.37	7.13	37.63	5.53
8	Dry Fodder Yield (kg/ha)	4211.10	3751.24	5026.47	7.51	12.02	39.04	9.67
9	Grain Yield (kg/ ha)	3205.62	1935.20	4272.05	18.73	22.54	69.04	32.05

Table 2: Genotypic and phenotypic correlation coefficients between different yield attributing traits of pearl millet genotypes

Traits	Days to 50% flowering	Days to maturity	Plant Height (cm)	Productive tillers (no./plant)	Panicle Length (cm)	Panicle Diameter (cm)	1000 - grain weight (g)	Dry Fodder Yield (kg/ha)	Grain Yield (kg/ha)
Days to 50% flowering	0.000	0.626**	0.432**	-0.165	0.544**	-0.01	-0.276	-0.002	-0.176
Days to maturity	0.507**	0.000	0.051	0.134	0.290*	0.281	0.480**	-0.232	-0.044
Plant Height (cm)	0.325*	-0.037	0.000	-0.288*	0.691**	-0.374**	-0.328*	0.438**	0.158
Productive tillers (no./plant)	-0.097	0.092	-0.12	0.000	-0.443**	-0.426**	-0.092	-0.124	-0.365*
Panicle Length (cm)	0.404**	0.127	0.629**	-0.272	0.000	-0.009	-0.217	-0.082	0.064
Panicle Diameter (cm)	-0.135	0.174	-0.135	-0.2	0.088	0.000	0.995**	0.18	0.834**
1000 - grain weight (g)	-0.041	0.227	-0.172	-0.008	-0.279	0.396**	0.000	0.437**	0.525**
Dry Fodder Yield (kg/ha)	0.014	-0.141	0.279	-0.126	0.025	0.123	0.13	0.000	0.691**
Grain Yield (kg/ ha)	-0.092	-0.051	0.163	-0.128	0.047	0.508**	0.480**	0.338*	0.000

Genotypic (above diagonal) and phenotypic (below diagonal) correlation coefficient; *Significant at 0.05 probability, **Significant at 0.01 probability.

Table 3: Direct (diagonal) and indirect (non-diagonal) effects of various yield attributing traits on grain yield in pearl millet genotypes

Traits	Days to 50% flowering	Days to maturity	Plant Height (cm)	Productive tillers (no./ plant)	Panicle Length (cm)	Panicle Diameter (cm)	1000 - grain weight (g)	Dry Fodder Yield (kg/ha)	GY*
Days to 50% flowering	-1.353	0.847	-0.584	0.223	0.736	0.013	0.374	0.003	-0.176
Days to maturity	2.163	3.453	0.175	0.463	1.000	0.969	1.657	-0.803	-0.044
Plant Height (cm)	-4.888	-0.573	-11.322	3.263	-7.820	4.232	3.712	-4.955	0.158
Productive tillers (no./ plant)	0.691	-0.562	1.209	-4.196	1.859	1.787	0.386	0.522	-0.365*
Panicle Length (cm)	3.625	1.930	4.602	-2.952	6.663	-0.063	-1.445	-0.549	0.064

Panicle Diameter (cm)	0.089	-2.578	3.433	3.912	0.087	-9.184	-9.136	-1.658	0.834**
1000 - grain weight (g)	-0.486	0.844	-0.577	-0.162	-0.382	1.750	1.759	0.769	0.525**
Dry Fodder Yield (kg/ha)	-0.017	-1.711	3.222	-0.916	-0.607	1.329	3.218	7.361	0.691**

GY*= Genetic correlation coefficients between grain yield and other component traits; *Significant at 0.05 probability,

**Significant at 0.01 probability.

Conclusion

The current study illustrated the existence of wide range of variations for most of the traits, as well as possibility of genetic gain through selection among the pearl millet genotypes. Based on the correlation and path analysis the traits viz., dry fodder yield, panicle length, panicle diameter, days to maturity and 1000-grain weight is responsible for the grain yield improvement in Pearl millet.

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