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GENETIC DIVERSITY ANALYSIS AMONG RESTORER (R) LINES FOR PRODUCTIVITY TRAITS IN PEARL MILLET [*Pennisetum glaucum* (L.) R. BR.]

P.S. Basavaraj[1*], B.D. Biradar[2] & G. M. Sajjanar[1]
[1]College of agriculture and RARS Vijayapura,
[2]University of agricultural sciences, Dharwad, Karnataka-586101, India.
*Corresponding author: Email:bassuptl@gmail.com

ABSTRACT

In the present study, seventy five genotypes of pearl millet were evaluated for assessing genetic diversity for nine different quantitative characters for exploitation in a breeding programme aimed at improving yield potential of pearl millet by using Mahalanobis D^2 statistics. The intra cluster D^2 value ranged from 0.00 to 5.56 while Inter cluster D^2 value ranged from 6.57 to 15.60 indicated that the selected genotypes were highly divergent. The maximum intra cluster distance was recorded for cluster I (5.56) while cluster III, IV and V (0.00) showed no intra-cluster distance values revealed homogenous nature of the genotype within the cluster. The genetically more divergent genotypes present in cluster II and V as indicated by inter cluster distance value (15.69). Inter cluster D^2 value and mean cluster values for characters indicated that hybridization of clusters II with clusters V genotypes would result in marked heterosis and produce better segregants with improved yield. Among the characters studied panicle weight (43.78%) contributed highest towards genetic divergence followed by panicle girth (20.36%), Selecting parents of these clusters probably provide promising recombinants and better segregants for future breeding strategy. In the R *vs* R combinations, the line LPRT-103 belongs to cluster I showed maximum D^2 values with EMRT-103 and EMRT-142 of cluster II. These lines in top ten R *vs* R pairwise combinations may be useful in development of trait specific heterotic pool of B lines.

KEY WORDS: Pearl millet, Genetic diversity, Cluster and Genotypes inter and intra cluster distance, maintainers.

INTRODUCTION

Pearl millet [*Pennisetum glaucum* (L.) R. Br.] is the fourth most important food crop of the world next to rice, wheat and sorghum. Grown for dual purpose as grain and fodder, its cultivation extends widely from well-irrigated areas to the most arid regions of the world in Asia and Africa. The major constraints to the productivity of crop include lesser area under hybrids and prevalence of different biotic and abiotic stresses. Recently, for genetic improvement of pearl millet, development of hybrids is being preferred over open-pollinated varieties. Hybrid development in pearl millet was facilitated by the availability of a cytoplasmic male-sterility (CMS) system derived from Tift 23A1 cytoplasm in the early 1960s (Burton 1965).

To develop a new variety there is need of the magnitude of genetic variability in the base material and the vast of variability for desired characters. A good knowledge on genetic diversity or genetic similarity could be helpful in long term selection gain in plants (Kumar *et al.,* 2012). Hence, genetic variability and diversity is of prime interest to the plant breeder as it plays a key role in framing and successful breeding programme. The genetically diverse parents are always able to produce high heterotic effects and great frequency of desirable segregants in further generation as already reported by earlier workers (Kumar *et al.*, 1994). The genetic distance between pair of genotypes offers the basis for understanding the structure of the diversity of any intra-species population. It constructs an all-to-all matrix to describe the distance between each sequence pair of genotypes, thereby guiding plant breeder in their selection procedure (Adewale *et al.*, 2011). The multivariate analysis is a useful tool for choosing the parents for hybridization and has been well demonstrated by previous workers (Hazra *et al.*, 1992; Nath *et al.*, 2009). D^2 statistic is a useful tool to measure genetic divergence among genotypes in any crop developed by Mahalanobis (1936). However, the main objective of present study to identify genetic divergent parents, so as to select the potential parents for breeding programme to attain the anticipated improvement in seed yield of pearl millet.

MATERIALS & METHODS

Experimental material consist of 75 diverse restore (R) lines received from ICRISAT, Patencheru (Table. 1) and were sown during *kharif* 2014-15 in Randomized Block Design with two replication at Regional Agricultural Research Station, Vijayapur (Karnataka, India). The recommended packages of practices were followed to raise the crop. Each germplasm line was sown in two rows of 4 m. length with 45 X 15 cm spacing. The observation on days to 50% flowering, plant height (cm), panicle length (cm), panicle girth (cm), panicle weight (g/panicle), grain yield/plot (kg), stover yield/plot (kg), number of productive tillers (No.'s) and 1000 seed weight (g) were recorded on five randomly selected plants for all the lines in each replication. The genetic divergence of those genotypes was studied by employing Mahalanobis' (1936) D^2 technique. The varieties were grouped into a number of clusters with D^2 being treated as the square of generalized distance, according to the method described by Tocher (Rao, 1952).

RESULTS & DISCUSSION

The analysis of variance (Table 2) is not a reliable basis for measuring the extent of genetic diversity. In order to overcome this problem and to quantify genetic divergence between any two genotypes or group of genotypes, the numerical measure of diversity was obtained with the help of D^2 – statistics and constellations of genotypes into clusters was done. To start a sound crossing programme, it is necessary that the genotypes should be genetically diverse.

On the basis of D^2 values, all the 48 genotypes were grouped into 5 clusters (Table 3). Cluster I was the largest and consists of 62 genotypes followed by cluster II with 10 genotypes, and cluster III, IV and V had only 1 genotype in each. Clusters III, IV and V were unique, since each had only one genotype. The pattern of group constellation proved the existence of significant amount of variability. Lakshmana (2008) reported 22 clusters for productivity traits in pearl millet restorer and maintainer lines and Meena *et al*., 2015 reported 9 clusters in cowpea for yield and related traits. The intra cluster D^2 value ranged from zero to 5.56 while inter cluster D^2 value ranged from 6.57 to 15.60 indicated that the selected genotypes were highly divergent (Table 4). Inter cluster distances are higher than the intra cluster distances indicating the presence of wider genetic diversity between the clusters rather than within the clusters. The maximum intra cluster distance was recorded for cluster I (5.56) followed by cluster II (5.15) while cluster III, IV and V (0.00) showed no intra-cluster distance values as they were solitary cluster indicating comparatively homogenous nature of the genotype within the cluster. The maximum inter cluster distance (D^2) was found between cluster II and V (15.69) followed by cluster II and IV (11.56), cluster I and V (10.93). Suggesting that the genotypes belonging to these clusters may be used as parents for hybridization programme to develop desirable type because crosses between genetically divergent genotypes will generate heterotic segregants. The cluster mean values for each character are presented in (Table 5). It is evident that different cluster exhibit distinct mean values for almost all the nine characters. A wide range of variation was observed among different clusters for all the cluster means. The cluster II showed the lowest mean for stover weight per plot (1.75). While cluster IV had maximum plant height (157.32). With respect to panicle girth (13.39) cluster III recorded highest mean. Regarding grain yield per plot, the genotypes having highest values were grouped into cluster V. Lowest cluster mean for days to 50 per cent recorded in the cluster V (43.00). In case of 1000 seed weight cluster II exhibited higher mean value (12.55). The maximum contribution to genetic divergence was made by Panicle weight (43.78%) followed by Panicle girth (20.36%), Stover weight per plot (11.50%), and 1000 grain weight (9.37%) had the greater contribution to genetic diversity therefore necessary attention is required to be focused on these characters (Table- 6). Lakshmana (2008) observed maximum contribution of days to maturity to genetic diversity in pearl millet restorers and maintainers. Vijayakumar *et al*. (2016) reported maximum contribution of number of pods per plant in mothbean, Sachin *et al*. (2014) in chickpea and Brijendra *et al*. (2014) in Wheat. The clustering pattern could be utilized in crossing the parents and deciding the cross combinations which may generate maximum possible variability for various traits. The genotypes with high values of any cluster can be used either for direct adoption or for hybridization for further selection and improvement. The top ten pair wise combination of genotypes B *vs* B, with maximum D^2 values among 48 maintainer lines given in (Table 7). In the R *vs* R combinations, the line LPRT-103 belongs to cluster I showed maximum D^2 values with EMRT-103 and EMRT-142 of cluster II. These lines in top ten R *vs* R pairwise combinations may be useful in development of trait specific heterotic pool of B lines.

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TABLE 4. Average intra and inter cluster D^2 values of pearl millet genotypes

Clusters	I	II	III	IV	V
I	5.56	7.86	7.04	7.10	10.93
II	7.86	5.15	9.11	11.66	15.60
III	7.04	9.11	0.00	6.57	10.00
IV	7.10	11.66	6.57	0.00	8.90
V	10.93	15.60	10.0	8.90	0.00

Note: 1. Above diagonal values are inter-cluster D^2 Values,
2. Diagonal values are intra cluster D^2 Values

TABLE 5 . The cluster means in respect of a total of nine characters involving productivity traits

		Characters								
		DFL	PH	PL	PG	PW	SW	GY	TSW	PD
Clusters	I	47.12	134.24	25.31	8.96	39.01	2.30	1.39	11.62	1.60
	II	44.35	124.16	22.17	9.80	22.17	1.75	1.45	12.55	1.65
	III	44.50	137.63	23.05	13.39	42.75	3.10	2.00	12.50	1.63
	IV	47.50	157.32	26.15	9.62	49.50	4.35	1.38	12.00	1.38
	V	43.00	123.38	24.20	10.65	66.75	1.50	2.25	12.00	2.25

Note DFL: Days to 50% flowering (days), PH: Plant height (cm), PL: Panicle length (cm), PG: Panicle girth (cm), PW: Panicle weight (g), SW: Stover weight (g), GY: Grain yield (g), 1000Gwt: 1000 grain weight (g), PD: Number of productive tillers.

TABLE 6. Per cent contribution of characters towards divergence in Pearl millet genotypes

Sl.no	Character	Times ranked 1st	Contribution %
1	Days to 50 per cent flowering	33	1.19
2	Plant height (cm)	39	1.41
3	Panicle length (cm)	64	2.31
4	Panicle girth (cm)	565	20.36
5	Panicle weight (g/panicle)	1215	43.78
6	Stover weight per plot (kg)	319	11.50
7	Grain yield per plot (kg)	206	7.42
8	1000-grain weight (g)	260	9.37
9	Number of productive tillers	74	2.67
	Total		100

TABLE 7. Pairwise combination (R X R) of genotypes with maximum diversity among 75 restorer lines used in pearl millet

Rankings	Distance between B lines		
	D^2 Values	R line 1	R line 2
1	5438.32	LPRT-103	EMRT-103
2	5130.00	LPRT-103	TPRT-110
3	4682.94	LPRT-103	EMRT-142
4	4626.18	LPRT-103	EMRT-102
5	4570.45	LPRT-103	LPRT-110
6	4545.74	LPRT-103	EMRT-104
7	4471.06	LPRT-103	CPRT-103
8	4402.03	LPRT-103	CPRT-113
9	4367.87	LPRT-103	CPRT-101
10	4364.15	LPRT-103	TPRT-117