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Genetic diversity assessment of pearl millet maintainer lines

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Abstract

Pearl millet [*Pennisetum glaucum* (L.) R. Br.] Is a multipurpose cereal belonging to the family Poaceae and primarily grown for grain on more than 26 million ha in the arid and semi-arid tropical regions of Asia and Africa. The present investigation was carried out by taking 48 maintainer genotypes of pearl millet developed at CCSHAU, Hisar and of these, 29 belonged to A_1, 11 to A_4, six to A_3, two each to A_2 and DSA and one to A_{egp} sterile cytoplasm. The material was evaluated in a Randomized Block Design (RBD) with three replications in *Kharif* season of 2014 and D^2 values were calculated as suggested by Mahalanobis, 1936. On the basis of nine quantitative characters, the 48 maintainer lines were grouped into 7 clusters in such a way that lines within each cluster had smaller D^2 value than those between clusters. Cluster pattern revealed that cluster 2 and cluster 4 had highest number of genotypes (10 each) followed by cluster 1 and cluster 3 (9 each). Maximum intra-cluster difference among the maintainer lines within the same cluster was shown by cluster 7 (4.498). Clusters 1 and 7 showed maximum inter-cluster distance of (7.421) whereas the lowest inter-cluster distance was recorded between clusters 2 and 3 (3.742). The cluster means for the thirteen quantitative characters in pearl millet maintainer lines revealed considerable differences among all the clusters. For days to 50% flowering, highest mean value possessed by cluster 4 (49) and lowest mean value by cluster 1 (42). Spike length was the highest in cluster 7 (27.5) and lowest in cluster 1 (15.0). For spike girth, cluster 4 (2.39) divulged the highest mean value and cluster 6 (1.52) divulged the lowest mean value. Cluster 5 (3.52) also revealed the highest mean value for number of productive tillers/plant, whereas, cluster 1 had the lowest mean value (1.38). The crosses between the genotypes belonging to distantly located clusters are likely to produce good transgressive segregants and genotypes with higher mean values in a trait(s) can be used in crossing program to develop promising maintainer lines.

Keywords: Clustering, pearl millet, intra-cluster, inter-cluster, diversity

Introduction

Pearl millet (*Pennisetum glaucum* (L.) R. Br.) Is one of the most cultivated cereals ranking after rice, wheat, maize, barley and sorghum in terms of area planted to these crops in the world [1]. The majority of production of this crop is in Africa (about 18 m ha) followed by Asia (>10 m ha) and Americas (>2 m ha) [2]. In arid and semi-arid regions of Asia and Africa, it plays vital role in food security and serves as staple food [3]. In comparison to another dry land crop i.e. sorghum, it provides much higher yield under abiotic stress conditions [1]. In addition to this, pearl mill *et al* lows double cropping after harvesting of leguminous crops as it is short duration crop (60-90 days). Pearl millet is consider as an excellent forage crop having considerable amount of protein which is higher than wheat or rice [4], calcium, phosphorous, amino acids which is higher than corn [5, 6] and other minerals. Another reason for considering it as good forage crop is that it has low hydrocyanic acid content. So, this crop can be considered as a 'new feed grain crop'. So, it can be said that it is economically important crop but in spite of all these characteristics, it has received relatively little research attention. Cultivated pearl millet gene pool contains an enormous amount of genetic diversity with few linkage problems [7]. The understanding of genetics and diversity of pearl millet could open a door of greater potentials for utilization of pearl millet as fodder and grain crop in present erratic climate changes [8]. Thus, the basic requirement of any crop improvement programme is analysis of genetic diversity as it gives information about various characters which are helpful in various breeding programmes. Keeping this in mind, present investigation was carried out to estimate nature and magnitude of genetic diversity of maintainer lines which provide a base for selection of parents in pearl millet hybridization programme.

Material and method
Experimental material
The present investigation was carried out using 48 pearl millet maintainer lines which were developed as CCSHAU, Hisar. Out of these 48 genotypes, 29 genotypes belonged to A_1,

11 genotypes to A_4, six genotypes to A_3, two genotypes each to A_2 and DSA and one genotype belong to A_{egp} sterile cytoplasm. The material was evaluated in a Randomized Block Design (RBD) with three replications in *Kharif* season of 2014. Data was recorded on nine quantitative characters based on five randomly selected plants.

Statistical analysis
Data were subjected to statistical analysis using software NPSS. The squared Euclidean distance (D^2) values were worked out as suggested by [9] and all the maintainer lines used in the study were clustered into different groups using D^2 values.

Results
The analysis of variance for 48 pearl millet maintainer lines, as given in table 2, was found to be significant for nine quantitative characters at p=0.05. The results indicate that considerable amount of genetic diversity was present in the material and hence, divergence analysis was carried out.

1. Group constellation
The experimental material was classified into seven major clusters based on Mahalanobis squared Euclidean distance matrix in such a way that maintainer lines within each cluster had smaller D^2 value than those between clusters as shown in Figure 1 (Table 3).

Table 2: Analysis of Variance (ANOVA) for yield and its component characters in pearl millet maintainer lines

S. No.	Characters	Mean sum of squares		
		Replications df (2)	Treatments df (47)	Error df (94)
1.	Days to 50% flowering	44.33	32.03*	12.41
2.	Spike length (cm)	0.68	41.15*	2.32
3.	Spike girth (cm)	0.23	0.59*	0.08
4.	Number of productive tillers/ plant	0.05	1.91*	0.14
5.	Plant height (cm)	36.91	980.63*	23.66
6.	1000 grain weight (g)	9.97	21.35*	0.82
7.	Green fodder yield/plant(g)	1,531.42	1,777.29*	67.42
8.	Dry fodder yield/ plant (g)	11.18	320.10*	15.81
9.	Grain yield/ plant(g)	5,688.72	7,244.59*	297.94

df: degree of freedom; * Significant at p= 0.05

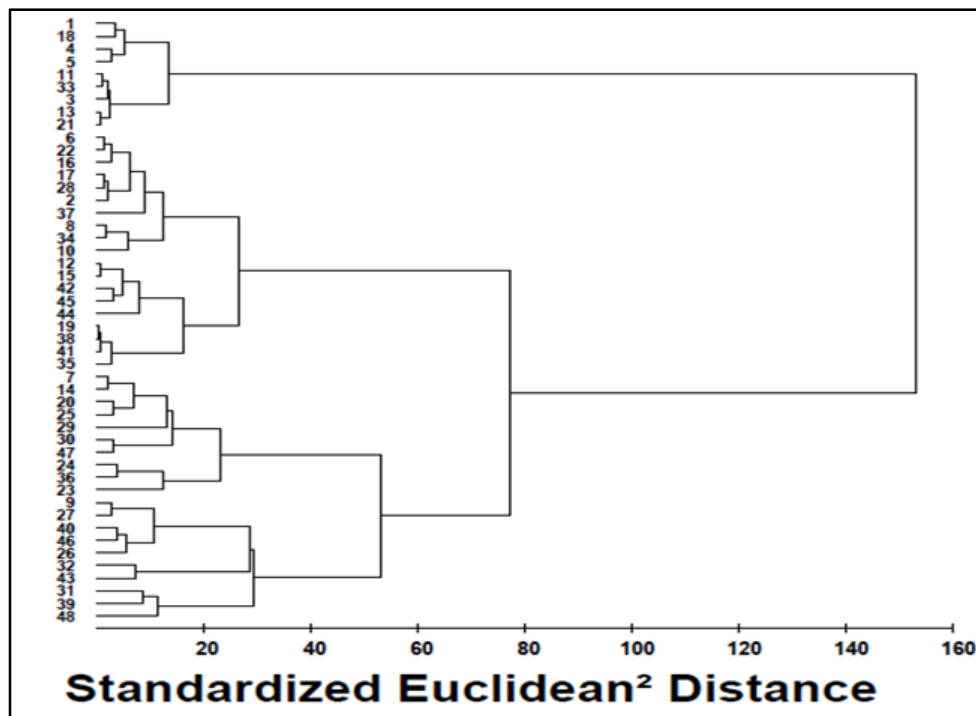**Fig 1:** Dendrogram showing the clustering pattern of forty eight maintainer lines of pearl millet

Table 3: Distribution of forty eight pearl millet maintainer lines in different clusters

	Maintainer lines	Number of maintainer lines
Cluster1	HMS 6B, HMS 37B, HMS 16B, HMS 18B, HMS 28B, HMS 53B, HMS 13B, HMS 30B, HMS 40B	9
Cluster2	HMS 20B, HMS 41B, HMS 34B, HMS 36B, HMS 47B, HMS 7B, HMS 58B, HMS 22B, HMS 54B,HMS 26B	10
Cluster3	HMS 29B, HMS 33B, HMS 63B, ICMB 843-22, 81B, HMS 38B, HMS 59B, HMS 62B, HMS 55B	9
Cluster4	HMS 21B, HMS 32B, HMS 39B, HMS 44B, HMS 48B, HMS 49B, ICMB 97111, HMS 43B, HMS 56B, HMS 42B	10
Cluster5	HMS 23B, HMS 46B, HMS 61B, ICMB 94555, HMS 45B	5
Cluster6	HMS 52B, HMS 64B	2
Cluster7	HMS 51B, HMS 60B, Tift 23 D$_2$B	3

Clustering pattern revealed that cluster 2 and cluster 4 contained maximum number of maintainer lines and cluster 6 had smallest one. Cluster 2 and cluster 4 were the largest group consisting of ten maintainer lines each which was followed by cluster 1 and cluster 3 having nine maintainer lines, cluster 5 having five maintainer lines, cluster 7 having three maintainer lines and cluster 6 containing only 2 maintainer lines, respectively. These results revealed the clear differentiation of maintainer lines. For hybridization programme, it is very important to identify potent parent and based on phenotypic data, it is fast, simple and it can be considered as a general approach for assessing genetic diversity among genetically diverse lines.

2. Intra- and inter-cluster distance
The intra- and inter-cluster distances are given in Table 4 (Figure 2). The average intra cluster distance varied from 2.802 (cluster 1) to 4.498 (cluster 7). A maximum difference among the maintainer lines within the same cluster was shown by cluster 7 (4.498). This was followed by cluster 4 (4.260), cluster 6 (3.792), cluster 5 (3.361), cluster 2 (3.098), cluster 3 (3.023) and cluster 1 (2.802). The genetic diversity within clusters may be due to degree of general combining ability, heterogeneity and pedigree. Therefore, selection will be based on highest mean for desirable traits. When diversity within clusters was studied (inter-cluster), it showed a range of 3.742 to 7.421. Cluster 1 and cluster 7 showed maximum inter-cluster distance of 7.421, followed by that between cluster 1 and cluster 4 (6.994). Hence, diverse parents can be selected that may have high heterotic response. The lowest inter-cluster distance was noticed between cluster 2 and cluster 3 (3.742), followed by that between cluster 1 and cluster 3 (3.942) which indicated the narrow genetic diversity among maintainer lines.

Table 4: Analysis for Intra- and Inter-cluster distances for forty eight maintainer lines of pearl millet

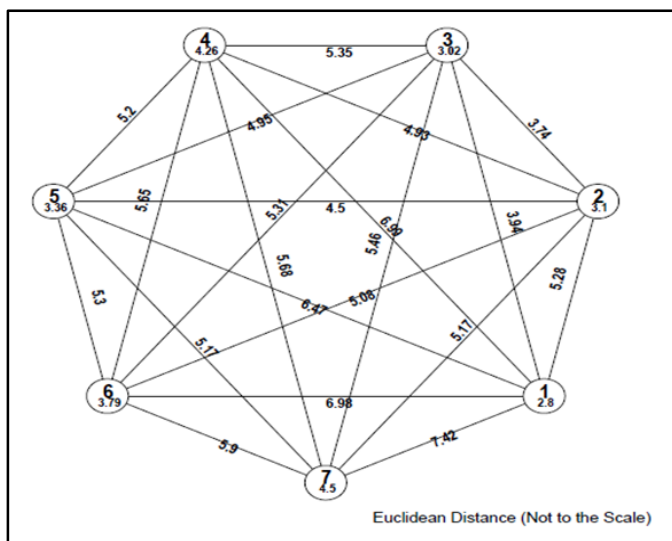|	Cluster1	Cluster2	Cluster3	Cluster4	Cluster5	Cluster6	Cluster7
Cluster1	2.802	5.281	3.942	6.994	6.468	6.978	7.421
Cluster2		3.098	3.742	4.932	4.498	5.078	5.166
Cluster3			3.023	5.352	4.955	5.305	5.461
Cluster4				4.260	5.195	5.648	5.682
Cluster5					3.361	5.303	5.171
Cluster6						3.792	5.903
Cluster7							4.498

Diagonal values are intra-cluster distances

Fig 2. Intra- and inter-cluster distance for the 7 groups of forty eight maintainer lines of pearl millet

3. Cluster means
The cluster means for the nine quantitative characters in pearl millet maintainer lines revealed considerable differences among all the clusters. Cluster wise mean and over all cluster mean for the characters are presented in Table 5. Cluster 6 had shown highest mean values for 1000 grain weight (12.30), green fodder yield/plant (275.8), dry fodder yield/plant (128.3) and grain yield/plant (52.6). Cluster 4 showed highest mean values for the days to 50% flowering (49), spike length (21.5) and spike girth (2.39). Highest mean value for number of productive tillers/plant was shown by the cluster 5 (3.52) and for plant height, by cluster 7 (109.3). Hence, cluster 4 and cluster 6 were considered most desirable for selecting maintainer lines.

Discussion
Plant breeders are always interested in assessing the genetic diversity among the varieties or advanced breeding material available with them so as to utilize them in directed breeding programme to produce wide spectrum of variability. This could be facilitated by genetic divergence analysis which clusters the genotypes in different groups based on genetic distance. D^2 statistic is a useful tool for estimating the genetic divergence in plant breeding experiments. Being a numerical estimate, it has the added advantages over other criteria permitting precise comparison among all possible pairs of population in any group.

On the basis of nine quantitative characters, 48 maintainer lines were divided into 7 clusters (Table 3 and Figure 1). Cluster pattern revealed that cluster 2 and cluster 4 had highest number of genotypes (10 each) followed by cluster 1 and cluster 3 (9 each). The results revealed that sufficient genetic diversity existed among the maintainer lines of pearl millet. Likewise, [10-23] had also reported genetic diversity in the pearl millet germplasm on the basis of cluster analysis.

A perusal of Table 4 revealed that maximum difference among the maintainer lines within the same cluster was shown by cluster 7 (4.498). This was followed by cluster 6 (3.792) and cluster 2 (3.361). Clusters 1 and 7 showed maximum inter-cluster distance of (7.421) followed by that between clusters 1 and 4 (6.994). The lowest inter-cluster distance was recorded between clusters 2 and 3 (3.742), followed by that between clusters 1 and 3 (3.942). The crosses between the genotypes belonging to distantly located clusters are likely to produce good transgressive segregants and genotypes with better mean values can be selected among all the genotypes to suit the breeding programme.
These findings were also supported by [12, 19, 20, 22, 23].

Conclusion
In conclusion, this study had differentiated the forty eight

maintainer lines into seven clusters. On the basis of divergence study, the genotypes from clusters 1, 4, 7 having most diverse parents could be used in hybridization programme to develop most promising hybrids. Parents and hybrids generated should be evaluated over diverse location to assess the general combining ability so that successful hybridization programme can be launched and also hybrid performance for grain and stover yield can be tested.

Table 5: Cluster means analysis of forty eight maintainer lines of pearl millet

	Days to 50% flowering	Spike length (cm)	Spike girth (cm)	Number of productive tillers/plant	Plant height (cm)	1000 grain weight (g)	Green fodder yield/ plant(g)	Dry fodder yield/ plant(g)	Grain yield/ plant (g)
Cluster 1	42	15.0	1.97	1.38	63.8	6.74	133.1	58.8	24.5
Cluster 2	44	18.3	2.27	2.46	80.0	11.07	199.6	88.5	38.6
Cluster 3	43	17.6	1.93	2.31	77.7	7.65	173.3	77.2	33.5
Cluster 4	49	21.5	2.39	2.93	95.6	11.54	231.1	99.0	47.4
Cluster 5	43	17.0	2.24	3.52	109.1	11.65	247.0	104.0	49.9
Cluster 6	45	16.9	1.52	2.46	60.2	12.30	275.8	128.3	52.6
Cluster 7	44	27.5	1.64	2.82	109.3	9.40	232.7	113.3	48.4
Mean	45	18.6	2.10	2.46	83.8	9.72	198.9	87.8	39.2

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