

Original Research Article

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Genetic Divergence analysis in Germplasm Lines of Pearl Millet

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ABSTRACT

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Pearl millet is a cross pollinated crop and 5th most important crop after rice, wheat, maize and sorghum. It is dual purpose crop which is mainly grown for food and fodder. It is well adopted to adverse environmental conditions. The experiment was conducted at Bajra Research Area, Department of Genetics and Plant Breeding during *Kharif*, 2017 and at Bajra Research Area, Department of Genetics and Plant Breeding and Dryland section of Department of Agronomy, Chaudhary Charan Singh Haryana Agricultural University, Hisar during *Kharif*, 2018. Data were recorded for yield and yield related traits and then pooled analysis was done. Genetic divergence analysis was done using the method given by Mahalanobis, 1936 with sixty germplasm lines. Seven major clusters were formed in which cluster 1 and cluster 2 were largest with 20 and 19 germplasm lines. A maximum difference among the germplasm lines within the same cluster was shown by cluster 7 (5.98). Cluster 1 and cluster 7 showed maximum inter-cluster distance of 8.21, followed by that between cluster 1 and cluster 4 (7.94). The crosses between the genotypes belonging to distantly located clusters are likely to produce good transgressive segregants.

Introduction

Pearl millet [*Pennisetum glaucum* (L.) R. Br.] is one of the most important cultivated cereals in the world which ranked after rice, wheat, maize and sorghum in terms of area planted to these crops (Khairwal *et al.*, 2007). It is grown on about 30 m ha in the world with the majority of this area in Asia (>10 m ha) and Africa (about 18 m ha) (Gupta *et al.*, 2015). It exhibits tremendous amount of genetic diversity because of its well adaptation under harsh environmental conditions and cross pollinated mechanism with protogynous

flowering (Satyavathi *et al.*, 2013 and Singh *et al.*, 2013). As we know that genetic diversity is the basic requirement for any crop improvement programme. There are several methods of divergence analysis based on quantitative traits *viz.*, Mahalanobis D² analysis, Principal component analysis and hierarchical cluster analysis based on Ward's minimum variance method. The evaluation and characterization of genotypes based on estimates of genetic diversity will help to identify diverse parental lines and these lines can be used in hybrid breeding to develop potential hybrids or varieties. Therefore, the

present investigation was undertaken to study the nature and magnitude of genetic divergence for grain yield and its component characters among the germplasm lines to provide a basis for selection of parents for hybridization in pearl millet hybridization programme.

Materials and Methods

An experiment was conducted using sixty germplasm lines of pearl millet including maintainer lines, hybrids, composites and restorer lines. The experiment was laid out in one environment at Bajra Research Area, Department of Genetics and Plant Breeding during *Kharif*, 2017 and in two environments at Bajra Research Area, Department of Genetics and Plant Breeding and Dryland section of Department of Agronomy, Chaudhary Charan Singh Haryana Agricultural University, Hisar during *Kharif*, 2018. Data were taken on the characters, days to 50% flowering, panicle length, panicle diameter, number of productive tillers/plant, dry fodder yield/plant, 1000 seed weight and grain yield/plant and then pooled analysis was done. D^2 values were worked out as suggested by Mahalanobis, 1936. All the germplasm lines used in the study were clustered into different groups using D^2 values.

Results and Discussion

Mean sum of squares was significant for all the characters studied for pooled analysis (E4). It means that further statistical analysis can be done with yield and yield related traits (Table 1).

Group constellation

Seven major clusters were formed by grouping all the sixty germplasm lines in such a way that germplasm lines within each cluster had smaller D^2 value than those between clusters (Table 2). Cluster pattern revealed that, cluster 1 and cluster 2 were the largest group consisting of 20 and 19 germplasm lines which was followed by cluster 3 (11 germplasm lines), cluster 4 (5 germplasm lines), cluster 5 and 6 (2 germplasm lines) and cluster 7 (1 germplasm lines). The results revealed that sufficient genetic diversity existed among the germplasm lines of pearl millet. Reddy *et al.*, (1996) and Shah *et al.*, (2012) had also reported genetic diversity in the pearl millet germplasm on the basis of cluster analysis. In a study by Lakshmana *et al.*, (2009) 105 accessions of pearl millet (26 from India and 79 from African countries) were characterized. These accessions were grouped in 22 clusters, indicating the presence of large amount of diversity among the genotypes.

Table.1 Analysis of Variance (ANOVA) for morphological and yield characters for pooled data

Mean sum of squares									
Source of variation (SV)	Degree of freedom (df)	Days to 50% flowering	Panicle length	Panicle diameter	Productive tillers/plant	Plant height	1000 grain weight	Dry fodder yield/plant	Grain yield/plant
Replication	1	143.1	62.6	1.9	15.9	1223.1	48.7	23.4	0.2
Treatment	59	21.5**	28.8**	32.7*	0.6**	3794.5**	3.5**	7209.6**	2405.2**
Error	59	5.3	10.0	10.1	3.5	94.9	4.8	138.3	51.3

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

Table.2 Distribution of sixty pearl millet germplasm lines in different clusters (Pooled)

Cluster	Germplasm lines	Number of germplasm lines
Cluster I	HMS 38B, HMS 50B, HMS 68B, HMS 55B, HMS 20B, HMS 66B, HMS 40B, HMS 44B, HMS 46B, HMS 42B, HMS 69B, HMS 43B, HMS 45B, HMS 48B, WG 33-4, WG 35-4Y, WG 35-4, WHC 802, HMS 41B, HMS 21B	20
Cluster II	HMS 13B, HMS 14B, HMS 16B, HMS 26B, HMS 32B, HHB 216, HMS 7B, ICMB 94555, ICMB 843-22, HMS 37B, HMS 6B, HHB 67, HHB 117, HHB 94, HC 20, HMS 47B, HHB 146, HC 10, HBL 11	19
Cluster III	HHB 197, HHB 272, HMS 70B, HMS 58B, HMS 33B, HMS 34B, HMS 39B, HHB 234, HHB 226, HHB 223, SGP 10-107	11
Cluster IV	ICMB 94222, ICMB 97111, ICMB 89111, 36B×9422B, 04999B	5
Cluster V	78/711, HBL 34	2
Cluster VI	EBL 12/237, ISK 51	2
Cluster VII	HB 15/085	1

Table.3 Analysis for Intra- and Inter-cluster distances for sixty germplasm lines of pearl millet (Pooled)

	Cluster1	Cluster2	Cluster3	Cluster4	Cluster5	Cluster6	Cluster7
Cluster1	3.02	6.81	4.42	7.94	7.68	7.78	8.21
Cluster2		4.98	4.42	5.32	5.98	6.78	6.66
Cluster3			4.23	6.52	5.55	6.05	6.61
Cluster4				5.60	6.95	6.48	6.82
Cluster5					4.61	6.03	6.71
Cluster6						4.92	6.03
Cluster7							5.98

Diagonal values are intra-cluster distances

Intra- and inter-cluster distance

The intra- and inter-cluster distances are given in Table 3. A maximum difference among the germplasm lines within the same cluster was shown by cluster 7 (5.98). This was followed by cluster 4 (5.60), cluster 6 (4.92), cluster 5 (4.61), cluster 2 (4.98), cluster 3 (4.23) and cluster 1 (3.02). When diversity within clusters was studied, it showed a range of 4.42 to 8.21. Cluster 1 and cluster 7 showed maximum inter-cluster

distance of 8.21, followed by that between cluster 1 and cluster 4 (7.94). The lowest inter-cluster distance was noticed between cluster 2 and cluster 3 (4.42) and between cluster 1 and cluster 3 (4.42). The crosses between the genotypes belonging to distantly located clusters are likely to produce good transgressive segregants.

In conclusion, genetic divergence analysis is helpful tool in assessing diversity. The genotypes which belong to clusters which are

distantly related can be further use to make distant crosses and to search the diverse parents.

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