Diversity of genetic studies by D^2 statistics in pearl millet *Pennisetum glaucum and* Genotypes under Aridity

ABSTARCT

The present study was carried out to estimate the genetic diversity for yield and its contributing traits in pearl millet (*Pennisetum glaucum (L.) R. Br.) genotypes*. The experimental material was consisting of 32 pearl millet released genotypes. The experiment was laid out in Randomized Block Design with three replications during *Kharif* 2021 under rain fed conditions. The observations were recorded on ten randomly selected plants from each genotype in each replication for nine different quantitative traits. Based on D^2 values, 32 genotypes were grouped into 3 clusters. Among 3 clusters, cluster I had more number of genotypes (23) followed by cluster II (6), and cluster III (3). The maximum intra cluster distance was observed in cluster III (12.2). The highest inter cluster distance was observed between cluster III and cluster I (18.29) followed by cluster III and cluster II (16.72), and cluster II and cluster I (14.24).The cluster III (49.96) had significant and higher cluster mean for seed yield per plant.

Key Words: Pearl millet, genetic diversity, intra cluster distance, inter cluster distance

Introduction

Pearl millet commonly known as bulrush millet (Pennisetum glaucum L.). R. Br. also classified as *P. typhoides, P. americanum, or P. spicatum*, is a cultivated small-grain tropical cereal grass. Vernacular names include: "bajra" (India), "gero" (Nigeria, Hausa language), "hegni" (Niger, Djerma language), "sanyo" (Mali), "dukhon" (Sudan, Arabic), and "mahangu" (Namibia). Pearl millet is quantitatively the most important millet, with world annual production ~14 million tons (Mt). It is cultivated mainly in the semi-arid tropics, almost exclusively by subsistence and small-scale commercial farmers.

Grain yield is an unpredictable character and relies upon number of component characters which are quantitatively inherited. Thus, before starting any breeding programmes, intensive information on the nature and greatness of genetic variability is extremely essential. The presence of genetic variability is of utmost importance for any breeding programme and due to this reason the plant breeders have emphasized the evaluation of germplasm for the improvement of crop yield as well as for utilization in further breeding programmes. Evaluation of plant genetic resources is a pre-requisite for which the future breeding work is based. Crop improvement depends on the magnitude of genetic variability present in the base population.

Genetic diversity is one of the criteria for parent's determination in the hybridization programmes. The accessibility of transgressive segregant in any breeding project depends upon the diversity between the parents associated. The evaluation of genetic diversity through biometrical methodology by Mahalanobis D^2-statistic has made conceivable to pick genetically diversed parents. The divergence analysis has a definite job to play in an effective decision of dissimilar parents for hybridization to exploit greatest heterosis or transgressive segregants for improving the grain yield. Identification of high grain yield traits of pearl millet genotypes is important to further breeding programmes to develop a hybrids or cultivar. This is done through variability and genetic divergence analysis.

Material and Methods

The present experiment was carried out at Agricultural Research Station, Bikaner during *Kharif,* 2021. The research farm is situated between 27°1' N latitude and 71°54' E longitude at an altitude of 228.50 meters above mean sea level. This region falls under agro-climatic zone 1C of Rajasthan. The experimental material for present investigation comprised of thirty two released genotypes of pearl millet. The experimental field was divided into 3 blocks of equal size and each plot consisted of six rows each of 4 meter length with row spacing of 60 cm and plant to plant spacing of 15 cm. All recommended agronomical cultural practices were carried out to raise a good crop. Observation were recorded based on ten randomly selected plants in each genotype in each replication for all important characters viz., plant height (cm), no. of productive tillers/plant, panicle length (cm), panicle diameter (cm), test weight (g), dry fodder yield/plant (g), and grain yield/plant (g) while for days to 50% flowering and days to maturity, observations were recorded on plot basis.

Data analysis:

The analysis of replicated data was worked out to test the signification test. It was done according to the procedure of RBD for each character as per methodology suggested by Fisher (1936). The total variance and degree of freedom were partition into three components viz. replication, treatment and error. The data were subjected to analysis of variance adopting standard statistical methods. Estimation of genetic divergence is used in many plant breeding programs for parental selection. Mahalanobis's D^2 statistics and multivariate (cluster) analysis is a unique statistical tool for analysing genetic diversity. D^2 statistic was developed by Mahalanobis in 1936. Assessment of genetic diversity by using this technique in plant breeding was suggested by Rao (1952).

Custer analysis: The genotypes were grouped based on traits used in the primary analysis of cluster. The individuals with same descriptions are automatically grouped into same clusters. Eculidian or straight line measure is most commonly used statistic in diversity analysis based on biometrical traits was used. Euclidian distance among two individuals i and j having observations on traits denoted by x1k, x2k, x3k….xkk computed by using formula given below,

$$dij = \sqrt{\sum_1^k (Xik - Xjk)^2}$$

Where, k = number of genotypes

Group constellation: The genotypes are grouped into different clusters by using Tocher's method. The two genotypes having small inter-cluster distance from each other were considered as first, to which third genotype having small average D^2 value from the first two genotypes were added. Then the nearest fourth genotype added and it was done for remaining ones. At certain stage when it was felt that after adding particular genotype, the average D^2 value increase and this stage genotypes was not included in that cluster and another cluster was formed. Clusters were formed till all genotypes were added into one or other cluster.

Intra cluster distance: The intra-cluster D^2 was estimated by using the formulae $\sum D^2\, i/n$,where $\sum D^2\, i$ is the distance between all possible combinations [n=I (i-1)/2] of the genotype (i) includes in a cluster.

Inter cluster distance: All possible D^2 values between the genotypes of two clusters were added with aid of n1x n2 for calculating inter-cluster distance. Where, n1 and n2 is number of genotypes in two clusters.

Cluster means: Summing of mean values of all genotypes belonging to a particular cluster for each characters. It was divided by number of genotypes to obtain for cluster mean for a particular trait.

Character contribution towards divergence: All the possible combination of genotypes [n (n-1)/2], each trait was ranked based on d_i values (y_i^1-y_i^2). The highest mean difference was rank first and lowest mean difference was rank "p", where "p" is total number of traits were studied.

$$\text{Per cent contribution of traits} = \frac{\text{Number of times appearing first in ranking by Xi}}{100\ [\ \frac{n\,(n-1)}{2}}$$

Where, X_i = i^{th} character and n = number of genotypes.

Results and Discussion

The mean sum of squares values for 9 biometrical traits was presented in table-1. The mean sum of squares due to the genotypes were significant for all the characters studied at both level of significance 1% and 5%, suggesting the existence of high genetic variability among the genotypes for all the traits. This indicates that there is ample scope for selection of genotypes from the present gene pool for yield and its component traits. The presence of large amount of variability might be due to diverse source of material as well as environmental influence affecting the phenotypes.

Table 1: Mean sum of squares for different characters in pearl millet (*Pennisetum glaucum* (L.) R. Br.)

S. No.	Characters	Mean sum of squares		
		Replication (df=2)	Treatments (df=38)	Error (df=76)
1	Days to 50% flowering	8.573	76.366**	3.433
2	Days to 50% pod setting	10.51	82.688**	3.435
3	Plant height (cm)	67.885	1356.511**	22.423

4	Productive tillers/plant	0.03	0.446**	0.015
5	PL	2.698	11.923**	1.451
6	PD	0.066	0.163**	0.024
7	Test Weight	1.403	2.325**	0.527
8	Dry fodder yield/plant	71.651	1136.791**	56.209
9	Grain yield/plant	10.632	225.398**	4.64

**** significant at 1% level**

Genetic diversity: The mean value of grain yield and other components were converted into uncorrelated mean values. The D^2 values were calculated for all possible combinations through Tocher's (Rao (1952) clustering method. Based on D^2 values, 32 genotypes were grouped into 3 clusters and are presented in Figure-1 (Based on Dendrogram). Among 3 clusters, cluster I had more number of genotypes (23) followed by cluster II (6), and III (3).

Table-2 Inter and intra cluster group distance of 32 genotypes of Pearl millet

Clusters	**Cluster 1**	**Cluster 2**	**Cluster 3**
Cluster 1	8.92	14.24	18.29
Cluster 2	14.24	7.25	16.72
Cluster 3	18.29	16.72	12.2

Inter and intra cluster distance: Inter and intra cluster distances are furnished in Table-2. The intra cluster values ranged from 7.25 to 12.2. The maximum intra cluster distance was observed in cluster III (12.2). The minimum intra cluster distance for cluster II (7.25). The inter cluster distance ranges from 14.24(between I and II) to 18.29(between I and III). Other inter cluster distance were between these values. The highest inter cluster distance was observed between cluster I and cluster III (18.29). Similar results were reported by Thakur *et al*. (2020) and Nimbalkar *et al*. (2017).

Table -3 Cluster means of 12 biometrical traits of 32pearl millet genotypes

Genotypes	Days to 50% flowering	Days to maturity	Plant Height	Prod. tillers/plant	Panicle Length	Panicle Diameter	Test Weight	Dry fodder yield/plant	Grain yield/plant
Cluster 1	57.07	87.75	194.41	1.54	24.52	2.77	11.09	76.85	26.54
Cluster II	47.28	78.11	157.94	2.23	23.28	2.62	10.71	80.92	29
Cluster III	53.67	83.89	193.22	2	25.67	2.59	10.67	124.5	49.96

Cluster means: The results of cluster mean were furnished in Table-3, Cluster mean of days to 50% flowering ranged from 47.28 (cluster II) to 57.07 (cluster I). Similar results were reported by Thakur *et al*. (2020).Cluster mean of days to maturity were ranged from 78.11 (cluster II) to

87.75 (cluster I), similar results were reported by Jakhar *et al*. (2016).Cluster mean of plant height varied from 157.94 (cluster II) to 193.22 (cluster III). Cluster mean of productive tillers per plant varied from 1.54 (cluster I) to 2 (cluster III). Cluster mean of Panicle Length were ranged from 23.28 (cluster II) to 25.67 (cluster III). Cluster mean of PD were reported from 2.59 (cluster III) to 2.77 (cluster I). Cluster mean of test weight ranged from 10.67 (cluster III) to 11.09 (cluster I). Cluster mean of dry fodder yield per plant were reported from 76.85 (cluster I) to 124.5 (cluster III). Cluster mean of grain yield per plant were reported from 26.54 (cluster I) to 49.96 (cluster III).Similar results were reported by Kuldeep *et al*. (2015), Gaikwad *et al*. (2014), Jakhar *et al.* (2016), Nimbaldar *et al*. (2017), Thakur *et al*. (2020), Jakhar *et al*. (2016), Parashi *et al*. (2013), Pandey *et al*. (2013), Jivani *et al*. (2013) and Thakur *et al*. (2020).

Contribution towards divergence: The per cent contribution of 9 biometrical traits of 32 pearl millet genotypes towards genetic divergence was estimated and given in Table-4 and Figure-2. The trait plant height (32.52%) had maximum contribution towards to genetic divergence followed by grain yield per plant (29.24%), productive tillers per plant (10.08%), days to 50% flowering (6.85%), dry fodder yield per plant (6.05%), Panicle Diameter(4.84%). Similar results were reported by Kudeep *et al*. (2015), Jakhar *et al*. (2016), Nimbalkar *et al*. (2017), and Thakur *et al*. (2020).

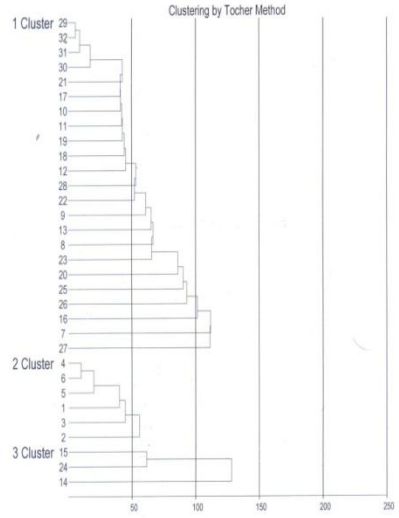

Fig-1: Dendrogram for 9 biometrical traits towards genetic divergence

Table-4: % contribution of 9 biometrical traits of 32 pearl millet genotypes towards genetic divergence

	Traits	Times ranked first	Contribution %
1.	Days to 50% flowering	34	6.85%
2.	Days to maturity	1	0.20%
3.	Plant height	196	32.52%

4.	Productive tillers /plant	50	10.08%
5.	Panicle length	9	1.81%
6.	Panicle diameter	24	4.84%
7.	Test weight	6	1.21%
8.	Dry fodder yield/plant	30	6.05%
9.	Grain yield per plant	146	29.44%

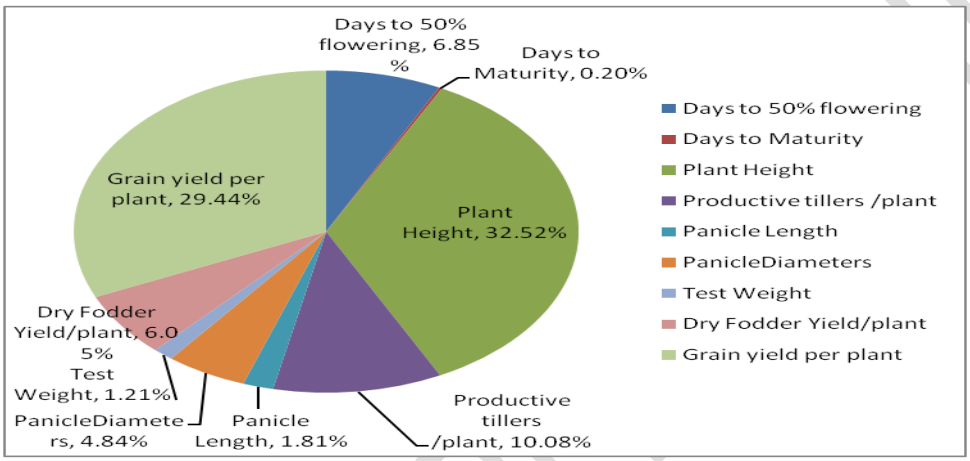

Fig-2 % contribution of 12 biometrical traits towards genetic divergence

Conclusion:

It is concluded that maximum number of genotypes were grouped into 1st cluster which included 23 genotypes. The maximum intra cluster distance was shown by cluster III (12.2). The highest inter cluster distance was found between cluster III and cluster I (18.29). Therefore, genotypes present in these clusters may be used as parents to produce transgressive segregants.

References

Ali, M. and S. Kumar.(2001). An overview of pearl millet research in India.**Indian J. Pulses Res. 14(2):81-89.**

Fisher, R.A. (1936). The correlation between relative on the supposition of genotypes grown in Kumaun Himalaya. ***Indian Journal Genetics.*****66(1): 37-38.**

Gaikwad, A. R., Desai, N. C., Pawar, G. H. and Langhi, A. M. (2014). Geneticdivergenceinpearl millet.***InternationalJournalof AgriculturalSci*****ences,10(2):812-815.**

Ibrikci, H., Knewtson, S.J.B. and Grusak, M.A. (2003). Pearl millet leaves as vegetable greens for humans: evaluation of mineral composition. ***Journal of the Science of Food and Agriculture,* 83:945-950.**

Jakhar,D.S.,Singh,R.andKamble,M.S.(2016). Geneticdiversitystudiesin pearl millet (*Cicer arietinum* L.) in Kolhapur region ofMaharashtra.***Bangladesh Journal of Botany,* 45(3):459-464.**

Jivani, J.V., Mehta, D. R., Vaddoria, M. A., Raval, L. (2013). Correlation andpathcoefficientanalysisinpearl millet (*Cicer arietinum*L.).***Research inEnvironmentand Life Sciences*4(2):1167-1170.**

Kuldeep, R., Pandey, S., Babbar, A. and Prakash, V. (2015). Genetic diversity analysis in Pearl millet grown under heat stress conditions of Madhya Pradesh.*Electronic Journal of Plant Breeding*, 6(4): 962-971.

Mahalanobis, P.C. (1936). On the Generalized Distance in Statistics.*Proceeding of the National Institute* of *Science of India*2: 49-55.

Nimbalkar, R. D., Katre, Y. Y. and Phad, D. S. (2017). Genetic diversity in Pearl millet (*Cicerarietinum* L.).

Pandey,A.,Gupta,S.,Kumar,A.,Thongbam,P.D.andPattanayak,A.(2013). Genetic divergence, path coefficient and cluster analysis of pearlmillet cultivars,in the mid altitudes of Meghalaya. ***Indian Journal of agricultural Sciences, 83 (12):1300-1304*.**

Panse V. G., and Sukhatme P. V. (1967).Statistical Methods for Agricultural Workers.***Indian Council of Agricultural Research:*103-108.**

Parashi, V. S., Lad, T. B., Mhase, L. B., Kute, N. S. and Sonawane, C. J. (2013). Genetic diversities studies in Pearl millet (*Cicerarietinum* L.). ***Bioinfolet,*10(1B): 337-341.**

Rao, C.R. (1952). Advanced Statistical Methods in Biometrical Research.*John Wiley and Sons Inc., New York*:383p.

Varshney, R.K, Mohan, S.M, Gaur, P.M, Gangarao, NVPR, Pandey, M.K, Bohra, A. (2013). Achievements and prospects of genomics-assisted breeding in three legume crops of the semi-arid tropics.***Biotech Advance 31(8):*1120–1134.**