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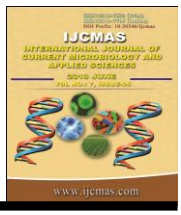

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Genetic Divergence Studies in Pearl Millet [*Pennisetum glaucum* (L.) R. Br.] Germplasm Using Mahalanobis D^2 Analysis Over Five Years in Hot Arid Climate of Rajasthan, India

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A B S T R A C T

The present investigation was conducted to evaluate the genetic divergence among forty pearl millet germplasm using Mahalanobis D^2 statistics for thirteen different traits under rainfed condition for five years pooled data. Analysis of variance indicated considerable diversity among genotypes showing significant variability for all the characters. D^2 clustering grouped the genotypes into eleven clusters. Based on cluster means, cluster II was suitable for early flowering and early maturity and cluster IV had highest grain yield per plant. The selection and choice of parents mainly depends upon contribution of characters towards divergence. The maximum contribution to genetic divergence was exhibited by number of productive tillers per followed by single plant yield, days to maturity, plant days to fifty per cent flowering, spike length, plant height, harvest index, test weight spike girth, reproductive period, ear exertion distance, stover yield and number of leaves per plant. Hence selection for these characters may be useful.

Introduction

Pearl millet is a cereal crop which is well adapted to drought, low soil fertility and high temperature and performs very well in soils with high salinity or low pH, hence it can be grown in areas where other cereal crops, such as maize or sorghum, would not survive (Harinarayana *et al.,* 1999). Grain yields of pearl millet are generally low, mainly because this crop is mostly cultivated under harsh conditions like eroded soils and uneven rainfall, low input conditions, marginal environments. Hence, it is imperative to develop high yielding varieties through heterosis breeding is a potential approach to increase the pearl millet production in India. Genetic diversity is one of the basic criteria for selection of parents in the hybridization program and the availability of transgressive segregants depends upon the diversity between the parents involved in the breeding program. As the crosses between divergent parents usually produce greater heterosis than those between closely related ones (Birchler *et al.,* 2010). Hence genetic reconstruction of a plant type is essential for developing high yielding varieties by incorporating and improving yield components and adaption traits from the available germplasm (Lakshmana *et al.,* 2010). The higher genetic distance between parents, the higher heterosis

in progeny can be observed (Anand and Murrty, 1968). Estimation of genetic distance is one of appropriate tools for parental selection in pearl millet breeding programs. Several measures, *viz.,* multivariate analysis, heterosis, combining ability, geographical distances *etc.* have been used to assess genetic diversity among the plant populations, parental selection, tracing the pathway to evolution of crops, centre of origin and diversity, and study interaction between the environment are currently available (Eivazi *et al.,* 2007). Among the multivariate analysis, Mahalanobis's generalized distance estimated by D^2 statistics (Rao, 1952) serves as potential tools and unique tools for phenotypic diversity evaluation, identifying genetically distant clusters of genotypes and selecting important traits contributing to the total variation in the germplasm and this method has been followed by several scientists in several crops. The information obtained from these analyses could help in selection of superior parental genotypes with specific target traits and in devising breeding strategies for trait specific improvement. However, very little information on these aspects is available in pearl millet. Hence, the present study was aimed to determine the genetic diversity among 40 genotypes of pearl millet (*Pennisetum glaucum* L.) of using Mahalanobis's D^2 analysis based on morphological traits for utilization in breeding programme.

Materials and Methods

The present investigation was carried out with 40 pearl millet germplasm (EC 516577, IC 285152, IC 285200, IC 323995, IC 324035, IC 325176, IC 325739, IC 325804, IC 329029, IC 329070, IC 329909, IC 333121, IC 333179, IC 333240, IC 369836, IC 370487, IC 370507, IC 373424, IC 373504 IC 373558, IC 420330, IC 420367, IC 426704, IC 426811, IC 426892, IC 426907, IC 449439, IC 449474, IC 537957, IC 537996, IC 538001, IC 541018, IC 541900, NIC 17769, NIC 17795, NIC 17819, JBV-2, CZP-9802, Pusa-383, Raj-171) conserved in the regional seed gene bank, ICAR- National Bureau of Plant Genetic Resources (NBPGR), Regional station, Jodhpur. The experiment was conducted in randomized block design with three replications for five consecutive years (environments) *viz., Kharif* 2012, *Kharif* 2013, *Kahrif* 2014, *Kharif* 2015 and *Kharif* 2016 at Research field of NBPGR, Regional station, Jodhpur, India, which is situated at about 28^0 35' N, longitude of $70^0$18' E and an altitude of 226 m above mean sea level. The recommended agronomic packages of practices were followed during the experimental period. Data was recorded on five randomly selected plants from each replication of each accession for the 13 quantitative characters, namely days to fifty percent flowering, days to maturity, reproductive period, plant height (cm), number of productive tillers per plant, number of leaves per plant, ear exertion distance (cm), spike length (cm), spike girth (cm), test weight (g), stover yield per plant(g), single plant yield (g) and harvest index (%) as per the standard descriptors described for pearl millet. The data for 13 quantitative traits based on pooled data of overall environment (five seasons) was statistically analyzed to study diversity and relative importance of different traits in capturing the variation by Mahalanobis' D^2 statistic as per Rao (1952).

Results and Discussion

Mahalanobis (1936) D^2 statistic is based on multivariate analysis of quantitative traits is a powerful tool for measuring divergence among a set of population using the concept of statistical distance utilizing multivariate measurements. Mahalanobis originally developed the concept of D^2 statistic in 1936. Rao (1952) suggested the application of this technique for the assessment of genetic

diversity in plant breeding. In the present investigation, D^2 values were calculated for 1225 possible pairs of combinations (n(n-1)/2) from means of fifty genotypes for ten characters and 40 (including checks) genotypes were grouped in to eleven clusters (Table 1). Among the eleven clusters, Cluster IX had maximum number of genotypes (10) *viz.*, IC 329070, EC 516577, IC 426811, IC 370507, IC 426907, NIC 17795, IC 541900, IC 323995, IC 369836, IC 333240, followed by Cluster IV which had six genotypes *viz.*, IC 420330, NIC 17819, IC 373504, IC 538001, IC 333179, IC 285200. Cluster I (IC 329029, IC 329909, IC 449439, IC 325739), Cluster III (IC 285152, IC 373424, IC 537957, NIC 17769) and Cluster XI (IC 325804, IC 325176, IC 449474, IC 333121) had four genotypes each. While Cluster V had three genotypes *viz.*, (IC 420367, IC 537996, JBV-2) and Cluster II, Cluster VI, Cluster VIII and Cluster X had two genotypes and Cluster VII comprises single genotype each. This irregular distribution of genotypes into various clusters indicating the high divergence among the genotypes of the cluster and genotypes originated from different geographical areas were fallen in to one cluster and also the genotypes of same geographical area were grouped into same cluster as well as in different cluster indicating that there was no formal relationship between geographical diversity and genetic diversity. Hence no association was observed between clustering pattern and eco-geographical distribution of the genotypes, which could be due to the factors like heterogeneity, genetic architecture of the populations, past history of selection, developmental traits and degree of general combining ability (Amasiddha *et al.,* 2013). Similar observations were made by various other researchers in pearl millet that geographical diversity and genetic divergence have no relation Dave and Joshi (1995), Shanmuganathan *et al.*, (2006), Dhanpal *et al.*, (2008), Aruselvi and Selvi (2009), Dinesh *et al.*, (2010), Lakshmana *et al.*, (2010), Veena Priya *et al.*, (2010) and Govindaraj *et al.*, (2011) and Wolie *et al.*, (2013). Among the eleven clusters, each cluster expressed in different manner for different characters. In the present study, the irregular distribution of genotypes into different clusters may be due to the high out crossing and populations maintained as open varieties which leads to heterozygosity. The unpredictable environments in the arid areas may also be a cause for the genetic diversity.

Fig.1 Relative contribution of different traits for genetic divergence in 40 pearl millet genotypes

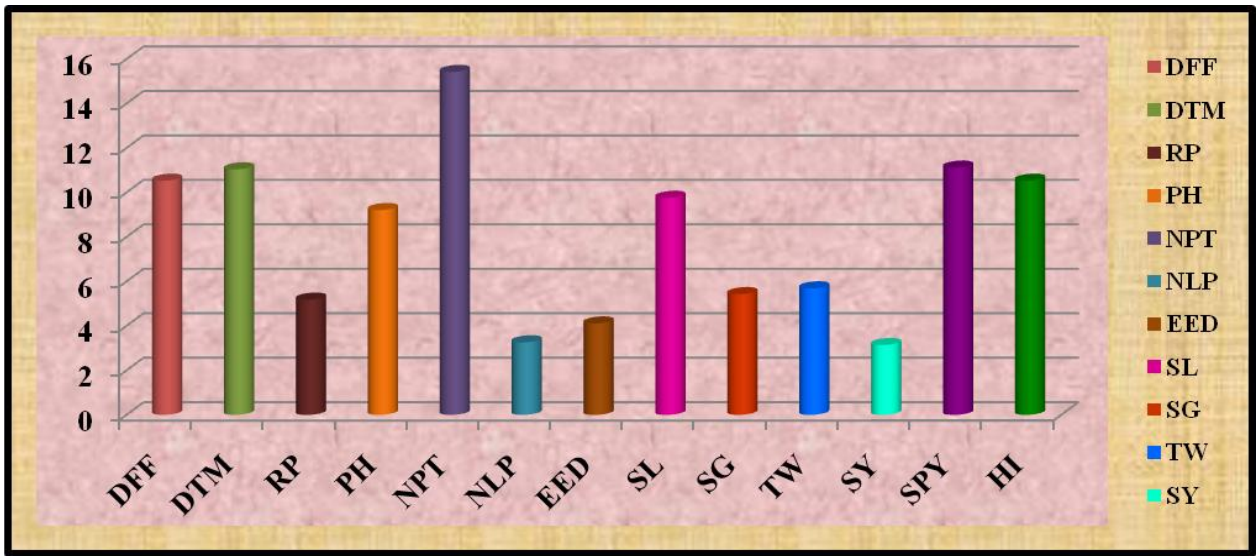

Table.1 Distribution of 40 pearl millet genotypes into different clusters based on thirteen quantitative characters

Cluster number	Number of genotypes	Name of the genotypes
I	4	IC 329029, IC 329909, IC 449439, IC 325739
II	2	IC 373558, IC 426892
III	4	IC 285152, IC 373424, IC 537957, NIC 17769
IV	6	IC 420330, NIC 17819, IC 373504, IC 538001, IC 333179, IC 285200,
V	3	IC 420367, IC 537996, JBV-2
VI	2	IC 370487, CZP-980
VII	1	Pusa-383
VIII	2	IC 426704, Raj-171
IX	10	IC 329070, EC 516577, IC 426811, IC 370507, IC 426907, NIC 17795, IC 541900, IC 323995, IC 369836, IC 333240
X	2	IC 541018, IC 324035
XI	4	IC 325804, IC 325176, IC 449474, IC 333121

Table.2 Inter and intra (diagonal) cluster average distance

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	**19.80**	16.15	18.63	16.58	18.80	20.87	19.68	20.13	17.25	30.52	21.46
II		**4.24**	15.36	7.53	14.52	14.94	16.15	11.69	9.72	31.27	19.24
III			**18.24**	16.47	17.02	18.59	19.47	19.24	16.63	35.36	21.58
IV				**4.45**	18.41	16.63	17.24	16.02	7.91	29.02	20.32
V					**4.80**	14.58	18.02	11.63	19.80	34.91	19.15
VI						**4.80**	21.79	12.91	18.36	29.36	23.47
VII							**20.24**	19.80	17.55	26.80	22.02
VIII								**6.69**	17.24	23.24	22.18
IX									**9.58**	32.36	21.60
X										**21.32**	34.72
XI											**27.47**

Table.3 Cluster means of 13 quantitative characters along with its relative contribution evaluated for genetic divergence in 40 pearl millet genotypes

Cluster	DFF	DTM	RP	PH	NPT	NLP	EED	SL	SG	TW	SY	SPY	HI
I	50.53	81.10	29.59	172.61	2.00	6.92	4.63	23.02	1.61	7.61	402.50	61.57	13.76
II	48.68	78.26	29.15	177.64	2.37	7.66	6.26	20.99	1.71	8.27	393.27	115.84	23.53
III	51.53	82.51	29.85	198.35	2.55	7.61	7.43	23.97	2.65	7.71	432.89	114.35	21.52
IV	49.74	84.32	29.51	156.28	2.50	7.14	4.68	24.61	1.57	7.24	440.21	119.06	18.70
V	50.06	82.84	29.82	189.86	2.67	8.97	5.56	24.40	1.82	7.43	503.83	116.18	16.45
VI	50.21	81.28	28.69	191.23	2.92	8.59	7.91	25.08	2.07	7.61	466.12	107.42	20.62
VII	51.88	83.14	30.44	166.99	3.12	9.28	3.47	31.43	2.48	7.60	473.30	119.38	19.18
VIII	52.35	82.28	28.53	197.30	2.01	8.14	7.23	30.27	2.11	7.49	494.67	110.92	19.96
IX	51.63	82.43	30.51	189.82	2.00	8.25	6.03	26.76	1.64	7.33	442.54	86.20	15.83
X	50.48	81.35	29.02	195.93	1.76	8.94	4.07	31.08	1.74	7.44	504.89	108.17	16.35
XI	52.51	82.22	30.27	178.89	2.11	8.13	5.99	26.92	1.67	7.61	510.36	119.29	17.52
Relative contribution	10.53	11.04	5.18	9.21	15.42	3.26	4.11	9.76	5.43	5.69	3.14	11.12	10.53
No. of times ranked first	110	150	24	95	315	10	20	127	36	63	14	185	110
Rank	**IV**	**III**	**X**	**VI**	**I**	**XIII**	**XI**	**V**	**IX**	**VIII**	**XII**	**II**	**VII**

The highest intra cluster distance (Table 2) was observed in cluster XI followed by cluster X, cluster VII and cluster I indicating differences in genotypes within cluster, while least intra cluster distance was observed in cluster I indicating that close resemblance between the genotypes presented in this cluster. The lowest inter cluster distance was observed between cluster II and IV followed by cluster IV and IX and cluster II and III showing these clusters were relatively less divergent and crossing between them cannot produce vigorous offspring (F_1 progenies). The maximum inter cluster distance was observed between cluster III and cluster X followed by cluster V and X, cluster X and XI and cluster IX and X and cluster II and X. The genotypes fallen into these clusters exhibited highest degree of genetic diversity may be utilized as parents for hybridization programme for developing high yielding recombinants. These results of genetic diversity study were in accordance with the finding of Wolie *et al.,* (2013) and Dinesh *et al.*, (2010)**.** Early flowering and early maturity was the most preferable type in crop plants for escape from severe drought condition. Based on cluster means, cluster II was suitable for early flowering and early maturity, while cluster VIII had minimum reproductive period. Hence, genotypes from the cluster II *viz*., IC 373558 and IC 426892 may be used to develop superior variety / hybrid with early flowering and early maturity, which in turn helps cultivars to escape from terminal drought. Cluster VII had the genotype with the highest mean value for number of productive tillers per plant and number of leaves per plant. Cluster VII recorded maximum mean value for spike length and cluster III had highest mean value for spike girth, while ear exertion distance was maximum in cluster VII. Cluster II had maximum test weight, cluster XI had maximum stover yield, cluster IV had highest grain yield per plant and cluster II had maximum harvest index. clusters with targeted traits can be selected for transferring specific traits through hybridization programme based on cluster mean for the better exploitation of genetic potential **(**Wolie *et al.*, 2012**).** The selection and choice of parents mainly depends upon contribution of characters towards divergence. The maximum contribution to genetic divergence (Fig. 1) was exhibited by number of productive tillers per followed by single plant yield, days to maturity, plant days to fifty per cent flowering, spike length, plant height, harvest index, test weight spike girth, reproductive period, ear exertion distance, stover yield and number of leaves per plant. Hence selection for these characters may be useful. Similar observation was recorded Quendeba *et al.,* (1995), Narkhede *et al.,* (2000), Anantharaju and Meenakshiganeshan (2008), Wolie *et al.,* (2013). There was considerable variation among the cluster means for the characters studied (Table 3), indicating the divergent nature of the clusters formed.

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