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Genetic Divergence in Pigeon Pea [*Cajanus cajan* L.]

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ABSTRACT
The nature and magnitude of genetic diversity was assessed among 45 genotypes of pigeonpea in randomized completely block design. The Non-hierarchical Euclidean cluster analysis grouped all the genotypes into eight distinct non-overlapping clusters indicated existence of high degree of genetic diversity in the materials. The crossings between the members of diverse clusters separated by high inter-cluster distances are likely to throw desirable segregants. The genotypes were grouped into eight clusters namely cluster I (5 genotypes), cluster II (7 genotypes), cluster III (3 genotypes), cluster IV (13 genotype), cluster V (2 genotype) cluster VI (6 genotype) cluster VII (8 genotype) and cluster VIII (1 genotypes). The maximum intra cluster distance exhibited for cluster II (2.575) and lowest for cluster V (1.334). The maximum inter cluster distance was showed between cluster VIII and I (8.144) whereas, minimum between clusters VII and V (2.547). So, genotypes from these groups could be used as parents in hybridization program to generate the highest possible variability and wide spectrum of variability in subsequent generations. The grain yield per plant followed by days to maturity, plant height, number of pod per plant, number of primary branches per plant, days to 50% flowering, pod length, number of secondary branches per plant and number of seed per pod were major contributors towards the total genetic divergence.
Key Words: *Genetic diversity, Pigeon pea Cajanus cajan L., cluster and hybridization*

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INTRODUCTION

Pigeonpea [*Cajanus cajan* (L.) Millsp.] is the second most important pulse crop of India after chickpea. It is commonly known as Arhar, Red gram and Tur. It has been recognized as a good source of vegetarian protein particularly in the developing countries where majority of the population depends on the low priced vegetarian foods. In fact, this crop has diversified uses such as food, feed, fodder and fuel. It is a rich source of protein, carbohydrate, vitamins, lipids and certain minerals. Mahalanobis D^2statistics has extensively been used by several workers to study the genetic diversity in different agronomic crops and to identify the characters or characters responsible for such type of divergence. Using Mahalanobis D^2 statistics, the population can be classified in to different groups. Therefore, the present investigation was undertaken to estimate the nature and magnitude of genetic diversity in a collection of pigeon pea genotypes by multivariate analysis. Success of crop improvement programme in any crop depends upon the extent of genetic variability and genetic diversity, association of characters, choice of parents for hybridization and selection procedure adopted. Compared to other food legumes breeding in pigeonpea has been more challenging due to various crop specific traits. The final target of any plant breeding programme is to develop improved genotypes which are better than the existing ones in producing the economic yield. This requires genetic amelioration through maximum utilization of allelic resources to develop ideal genotype. Genetic diversity can be measured by different methods such as pedigree analysis, Mahalanobis-D^2 statistics and Nonhierarchical Euclidean cluster analysis. Keeping in view, present experiment has been undertaken to study genetic diversity for selecting suitable parents for pigeonpea breeding programme aimed at isolating desirable segregants for seed yield and other important characters [6].

MATERIAL AND METHODS

The experiment was laid out in a randomized completely block design (RCBD) with three replications at crop research center, (Chirodi) of Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut. This study was performed with forty five genotypes of pigeon pea to assess the genetic diversity among the genotypes. Rows were spaced 75 cm apart and plant to plant distance was maintained at 25 cm. Data were recorded on individual plant basis from 5 randomly selected plants of each genotype from the two rows per plot in each replication. Among the characters studied as reproductive traits, *i.e.* Days to 50% flowering, Days to maturity, Plant height (cm), No. of primary branches per plant, No. of secondary branches per plant, No. of pods per plant, Pod length, No. of chambers per pod, No. of seeds per pod, 100 grain weight (g) and grain yield per plant were recorded in the field or laboratory. Data were subjected to D^2 analysis following canonical root method of [8], which was originally developed by [1]. Genetic divergence among forty five genotypes planted in randomized completely block design was studied through Nonhierarchical Euclidean cluster analysis [1, 9].

RESULTS AND DISCUSSION

The Mahalonobis D^2 cluster analysis grouped all the forty five pigeonpea genotypes of the present investigation into eight distinct non-overlapping clusters (Table-1).

Table 1. Average intra and inter cluster D^2 values in forty-five genotypes of pigeonpea.

Clusters	I	II	III	IV	V	VI	VII	VIII
I	**1.915**							
II	3.607	**2.575**						
III	5.371	4.727	**2.498**					
IV	2.799	2.589	4.299	**1.927**				
V	4.720	5.111	4.979	3.583	**1.334**			
VI	4.312	4.643	6.521	3.306	3.116	**2.272**		
VII	4.074	3.677	4.840	2.583	2.547	2.621	**2.169**	
VIII	8.144	7.102	6.148	6.308	6.576	7.430	6.067	**2.064**

Diagonal and bold values are intra cluster distances

The discrimination of genotypes into discrete clusters suggested presence of high degree of genetic diversity in the material evaluated. Earlier workers have also reported substantial genetic divergence in the pigeonpea materials [5, 6]. Presence of substantial genetic diversity among the parental material screened in the present study indicated that this material may serve as good source for selecting the diverse parents for hybridization programme aimed at isolating desirable segregants for grain yield and other important characters. An examination of the clustering pattern of the forty five pigeonpea genotypes into eight clusters revealed that the genotypes of heterogeneous origin were frequently present in same cluster. Although the genotypes originated in same place or geographic region were also found to be grouped together in same cluster, the instances of grouping of genotypes of different origin or geographical regions in same cluster were observed in case of all the clusters. This indicated lack of any definite relationship or correlation between genetic diversity and geographic origin of the pigeonpea genotypes evaluated in the present study. Therefore, the selection of parental material for hybridization programme simply based on geographic diversity may not be rewarding exercise. The choice of suitable diverse parents based on genetic divergence analysis would be more fruitful than the choice made on the basis of geographical distances. This finding is in conformity with the previous reports advocating lack of parallelism between genetic and geographic diversity in pigeonpea [4]. In the present study forty five genotypes of pigeonpea was subjected to D^2 analysis using eleven component characters. Out of the eight clusters, cluster I, II, III, IV, V, VI, VII and VIII had 5, 7, 3, 13, 2, 6, 8 and 1 genotypes respectively, (Table-2). The maximum intra among various cluster distance exhibited for cluster II (2.575) and lowest for cluster V (1.134). The maximum inter cluster distance was showed between cluster VIII and I (8.144) whereas, minimum between clusters VII and V (2.547). The maximum intra cluster distance was because of wide genetic diversity among its genotypes. The chances of developing good segregate by crossing to genotype for the same cluster showing low value of intra cluster distance. Therefore, it would be logical to attempt crosses between the genotypes of clusters separated by larger inter cluster distances. The little diversity and selection of parents within the cluster having higher mean for a particular character may also be useful for further developing high yielding pigeon pea varieties. The estimates of average intra and inter-cluster distances for eight clusters (Table-1) revealed that the genotypes present in a cluster have little genetic divergence from each other with respect to aggregate effect of eleven characters under study,

while much more genetic diversity was observed between the genotypes belonging to different clusters. The maximum inter cluster distance was found between cluster VIII and I (8.144) followed by cluster VIII and VI (7.430), cluster VIII and II (7.102), cluster VIII and V (6.576), cluster VII and III (6.521), cluster VIII and IV (6.308), cluster VIII and III (6.148) and cluster VIII and cluster VII (6.067) (Table-1). The least inter cluster distance was between clusters IV and I (2.799) followed by cluster VII and VI (2.621), cluster IV and II (2.589), cluster VII and IV (2.583) and cluster VII and V (2.547). Thus, crossing between the genotypes of the above three cluster pairs having very low inter-cluster distances may not be rewarding owing to little genetic diversity among their genotypes. The intra-cluster group means for eleven characters (Table-3) revealed marked differences between the clusters in respects of cluster means for different characters. The intra-cluster group means for eleven characters revealed marked differences between the clusters in respects of cluster means for different characters. Cluster I, IV, V and VII having 5, 13, 2 and 8 genotypes respectively, showed highest cluster means for number of pods per plant, plant height, days to maturity and days to 50% flowering. Cluster II with 7 genotypes recorded highest cluster means for number of pods per plant, days to maturity, plant height and days to 50% flowering. Cluster III and cluster VIII comprising 3 and 1 genotypes respectively, exhibited highest cluster mean for plant height, days to maturity, number of pods per plant and days to 50% flowering. The lowest cluster means for pod length, number of chamber per pod, 100- grain weight, seed per pod and number of primary branches per plant to the entire cluster. Similar findings were also reported by [7]. These genotypes may be recommended for crossing with the genotypes of the clusters showing high inter cluster distances mentioned above for isolating transgressive segregants. However, caution should be exercised in selecting very diverse genotypes, because the frequency of heterotic crosses and magnitude of heterosis for yield and its components were found to be higher in crosses between parents with intermediate divergence than the extreme ones. Further, the efficacy of D^2-statistics is improved by its applicability to estimate the relative contribution of the various characters towards genetic divergence [2].

Table- 2 Grouping of 45 genotypes of pigeonpea in eight gene clusters

Cluster	No. of genotypes	Genotypes
I	5	ICPL 8863, ICPL 9120, ICPL 9268, ICPL 10978, ICPL 1258
II	7	ICPL 1088, ICPL 1090, ICPL 1123, ICPL 1150, ICPL 1151, ICPL 10912, ICPL 10222
III	3	ICPL 8861, ICPL 8862, ICPL 9145
IV	13	ICPL 1120, ICPL 1149, ICPL 9168, ICPL 7133, ICPL 7134, ICPL 7136, ICPL 7162, ICPL 11384, ICPL 8236, ICPL 8258, ICPL 10269, ICPL 10977, ICPL 11162
V	2	ICPL 10976, ICPL 11150
VI	6	ICPL 10979, ICPL 10981, ICPL 7161, ICPL 10235, ICPL 10505, ICPL 11966,
VII	8	ICPL 934, ICPL 1150, ICPL 10982, ICPL 7122, ICPL 7137, ICPL 8214, ICPL 10957, ICPL 10958
VIII	1	ICPL 11975

Table-3 Cluster mean values for eleven quantitative characters in forty-five germplasm lines of pigeonpea.

Characters	Clusters							
	I	II	III	IV	V	VI	VII	VIII
Days to 50 % flowering	**117.33***	131.76	127.00	133.05	135.00	139.11	138.38	**145.67****
Days to maturity	**167.27***	189.81	182.89	188.82	198.50	193.61	196.21	**219.33****
Plant height (cm)	184.42	**173.58***	188.39	194.48	221.83	**244.96****	199.40	238.00
No. of primary branches per plant	19.49	13.98	10.61	19.25	20.40	**22.11****	19.02	**8.00***
No. of secondary branches per plant	27.44	21.27	**17.18***	26.96	27.37	**34.63****	25.77	20.07
No. of pods per plant	248.60	200.88	153.44	196.52	294.27	**317.39****	291.88	181.67
Pod length (cm)	**3.53***	3.62	4.60	3.85	3.69	3.67	4.30	**5.40**
No. of chambers per pod	3.19	2.69	4.06	3.23	4.32	3.13	3.43	**4.90**
No. of seeds per pod	2.92	2.58	**3.60**	3.04	3.50	3.03	3.11	2.80
100-grain weight	6.13	8.80	**10.92**	7.12	7.75	6.76	6.88	4.83
Grain yield per plant (gm)	35.07	37.11	32.56	31.22	**51.62**	48.10	50.50	19.47

Bold values are highest value for that character

In this context, the highest contribution in manifestation of genetic divergence (Table-4) was exhibited by number of grain yield per plant (18.61) followed by days to maturity (11.86), plant height (9.88), number of pods per plant (9.55), number of primary branches per plant (8.53), days to 50% flowering (7.97), pod length (7.82) and number of secondary branches per plant (7.70). The above discussion clearly shows wide variation from one cluster to another in respect of cluster means for eleven characters, which indicated that genotypes having distinctly different mean performance for various characters were separated into different clusters. The crossing between the entries belonging to cluster pairs having large inter-cluster distance and possessing high cluster means for one or other characters to be improved may be recommended for isolating desirable recombinants in the segregating generations in pigeonpea.

Table -4 Contributions of different characters in creating diversity in pigeon pea based on Mahalanobis's D^2 analysis.

Character	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primary branches per plant	No. of secondary branches per plant	No. of pods per plant	Pod length	No. of chambers per pod	No. of seeds per pod	100 grain weight (g)	Grain yield per plant
Contribution	7.97 %	11.86 %	9.88 %	8.53 %	7.70 %	9.55 %	7.82 %	6.79 %	7.22 %	4.07 %	18.61 %

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