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Genetic diversity analysis in pigeonpea (*Cajanus cajan* (L.) Millsp.)

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Abstract
In plant breeding programme, knowledge on existing genetic diversity in the crop species is crucial. In this study, diversity of the fifty two genotypes of pigeonpea were accessed for 12 characters in randomized block design with two replications during semi *rabi*-2017 at Regional Research Station, AAU, Anand. Fifty two genotypes were grouped into 8 clusters. More number of genotypes were found in cluster I (16 genotypes), whereas less number of genotypes were in clusters VII and VIII (single genotype). The average intra-cluster distance was maximum in cluster VI (171.02). Clusters V and VII were the farthest (1640.73) from each other, followed by clusters V and VI (1248.98) as they have maximum inter-cluster distance. On the basis of cluster mean values, cluster VII was superior for seed yield per plant, number of pod clusters per plant and pods per plant and cluster VIII was good for 100-seed weight. On the basis of R^2 value, the characters, *viz.*, days to maturity, number of pods per plant and number of pod clusters per plant contributed much to the total genetic divergence.

Keywords: Clusters analysis, Diversity, Pigeonpea

Introduction
Pigeonpea is a major pulse crop of the tropical and subtropical regions. It is a diploid species (2n=2x= 22) consisting of a genome of 8331. Mbp into 11 linkage groups. Pigeonpea belongs to the family *Leguminosae* and sub-family *Papilionoideae*. *Cajanus cajan* is the only domesticated species among *Cajanea* family. India is considered as primary centre of origin of pigeonpea. Pigeonpea assures sustainable returns from marginal lands even in minimal inputs as it is a hardy and drought tolerant crop; hence it is more suitable for subsistence agriculture. Pigeonpea seeds contain about 20-24 per cent of protein and specifically enriched with some essential amino acids making it is an important source of dietary protein, mainly in vegetarian based diets.

Classification and identification of diverse heterotic group in germplasm with possible breeding values in manifestation of breeding potential of genotypes can be possible through the assessment of genetic diversity. Genetic diversity can provide an ample scope for identification of genetic parents for various heterosis breeding programme and progenies derived from diverse crosses are expected to show a broad spectrum of variability, helps for isolating transgressive segregates in advanced generations (Singh and Mishra, 1996) [6]. Mahalanobis (1936) [3]. D^2 analysis is useful to measure genetic diversity among different genotypes. It is the most popularly used method for assessing genetic diversity in various crops. Hence in present study, an effort has been made to assess the presence of genetic diversity in fifty two pigeonpea genotypes in order to identify diverse parents for future breeding programme.

Materials and Methods
Extent of genetic variability and diversity present in fifty two pigeonpea genotypes were studied. The experiment was carried out at Regional Research Station, AAU, Anand during semi *rabi* -2017 in randomized block design with two replications. The experimental material consisted of diverse pigeonpea genotypes representing different geographic origin and pure seeds of these genotypes were procured from different pulse pulse breeding institutes across the India. The data for different characters *viz.*, days to 50 per cent flowering, days to maturity, plant height, number of pods per plant, number of seeds per pod, pod length, number of primary and secondary branches per plant, number of pod clusters per plant, 100-seed weight, seed yield per plant and protein content were recorded for each replications selecting 5 random plants in each row and mean values were estimated. The replication wise mean values of each genotype for twelve different characters were used for statistical analysis. Analysis of variance for each character was calculated as per the standard procedure suggested by Panse and

Suktame (1978). Grouping of the genotypes into different clusters were done by using Torcher's method (Rao, 1952). The criterion used in clustering is the genotypes belonging to single cluster have smaller D^2 values and belong to different clusters have larger D^2 values. Average intra-cluster distance was calculated by using formula and inter-cluster distance was calculated by estimating distance between cluster I and II, I and III, I and IV likewise for all the clusters.

Results and Discussions

The analysis of variance for all twelve characters revealed that differences among the mean squares due to genotypic significant different for all these characters, which indicate all characters are significantly different among studied genotypes. Therefore sufficient amount of genetic variability is present for all the characters included in the study. Based on this knowledge one can go for further diversity study. Mahalonobis's $D^2$was calculated for all possible pairs of fifty two pigonpea genotype and genetic diversity was assessed. Fifty two genotypes were placed into 8 different clusters (Table 1). Cluster I was largest cluster comprised of 16 genotypes followed by cluster III (11 genotypes) and V (9 genotypes), whereas clusters VII and VIII were considered as solitary clusters with single genotype. Mono-genotypic clusters revealed that BDN-2 and GJP-1 were more diverse genotypes from rest of the genotypes, thus these two genotypes have entirely different genetic make-up.

Average intra-cluster distance ranged from 0.00 to 171.02 (Table 2). Maximum intra-cluster distance was observed in cluster VI (171.02) followed by clusters I (147.59) and III (138.35). Minimum intra-cluster distance was found in mono-genotypic clusters VII and VII (0.00).Inter-cluster distance was maximum between clusters V and VII (1640.73) followed by V and VI (1248.98), while minimum distance was exhibited by clusters III and VII (248.69).Selection of genotypes based on large intra-cluster and inter-cluster distance for hybridization can offer to get useful combination for improvement of pigeonpea varieties.

Table 1: Grouping of pigeonpea genotypes in various clusters on the basis of D^2 values

Sr. No.	Clusters	Genotypes	Names of genotypes
1	I	16	GT-103, AAUVT-F_6-43, AAUVT-16-2, SARDAR, GT-102, AAUVT-16-3, GT-101, BRG-4, BRG-5, AAUVT-16-5, TJT-501, AAUVT-2003-01, AVPP-1, PKV-TARA, Rajeshdari-PT-12, AAUVT-16-4
2	II	7	BRG-2, BRG-1, BRG-3, AAUVT-16-1, AAUVT-F_6-46, AAUVT-F6-44, GT-1
3	III	11	ICP-2376, VIPULA, SADABAHAR, ICPL-87119, GT-100, AGT-2, BANASH, AAUVT-13-35, VAISHALI (BSMR-853), AAUVT-14-02
4	IV	3	AAUVT-15-5, AAUVT-13-20, AAUVT-15-06
5	V	9	ICPL-20325, ICPL-11303, ICPL-11242, ICPL-11244, ICPL-20341, ICPL-20340, ICPL-11255, PAU-881, ICPL-87
6	VI	4	AAUVT-2007-10, AAUVT-97-45,IPA-203, BDN-711
7	VII	1	BDN-2
8	VIII	1	GJP-1

Table 2: Average intra-cluster and inter-cluster distance for 52 genotypes of pigeonpea

Clusters	I	II	III	IV	V	VI	VII	VIII
I	147.59	352.56	277.29	305.69	799.22	625.93	953.98	571.88
II		108.63	558.30	468.78	1218.73	314.32	763.21	764.04
III			138.35	286.49	763.33	403.28	248.69	470.35
IV				127.94	1094.95	424.20	339.52	278.14
V					110.91	1248.98	1640.73	936.81
VI						171.02	554.27	685.92
VII							0.00	737.76
VIII								0.00

Table 3: Cluster means of different characters in pigeonpea genotypes

Clusters	Days to 50 per cent flowering	Days to maturity	Plant height (cm)	Pods per plant	Seeds per pod	Pod length (cm)	Primary branches	Secondary branches	Pod clusters	100-seed weight (g)	Yield per plant (g)	Protein content (%)
I	83.68	142.06	115.84	100.7	4.23	5.25	15.75	6.59	46.62	11.29	44.34	22.12
II	87.5	161.14	108.71	83.98	4.53	5.86	14.19	5.35	39.74	12.29	36.13	22.76
III	82.86	143.31	109.57	161.19	3.82	4.26	16.55	7.84	74.32	9.97	53.11	21.81
IV	84.50	145.16	121.93	148.77	4.52	5.61	23.45	13.80	68.07	11.15	73.75	22.10
V	75.61	127.27	89.48	68.99	3.73	4.27	12.07	2.78	29.93	7.83	15.41	21.29
VI	90.87	167.5	123.12	121.47	3.86	4.11	19.63	13.17	56.43	9.93	38.52	21.81
VII	85.00	149.00	104.06	231.51	3.93	4.27	14.11	10.16	89.5	10.11	94.00	21.20
VIII	82.50	137.50	121.00	121.64	3.80	5.79	16.48	25.20	58.27	13.12	60.05	21.39
S.Em.±	1.31	2.4	8.18	8.2	0.16	0.22	1.2	1.26	3.82	0.54	3.71	0.33
CD@ 5 %	3.68	6.76	23	23.06	0.46	0.63	3.39	3.55	10.74	1.52	10.45	0.93
CV%	3.64	3.85	17.23	16.78	9.41	10.71	17.66	39.61	17.1	11.98	20.18	3.51
R2*	0.83	0.92	0.39	0.91	0.59	0.80	0.71	0.83	0.90	0.77	0.90	0.41

*** R2:** Ratio of theinter cluster varianceto thetotal variance

NS: Non-significant

-: Not estimated due to –ve variance

The character wise analysis was conducted for eight clusters these are represented in Table 3. Mean of clusters for all the characters were found significant. Late flowering (90.87) and late *maturing* (167.50) genotypes fall in the cluster VI and early flowering (75.61) and early maturing (127.27) genotypes were found in cluster V. The maximum cluster mean value for plant height was observed in cluster VI (123.12), whereas dwarf genotypes were found in cluster V (89.48). If we consider number of pods per plant, more number of pods per plant were observed in cluster V (231.51), while less number of pods per plant were present in cluster V (68.99). More number of seeds per pod was found in cluster II (4.53) which is at par with cluster IV (4.52) and less number of seeds per pod was observed in cluster V (3.73).Similarly long pods were observed in cluster II (5.86), whereas short pods were recorded in cluster VI (4.11).

Highest numbers of primary branches per plant were found in cluster IV (23.45), while lowest numbers of primary branches were observed in cluster VII (14.11) which is at par with cluster II (14.19). More number of secondary branches per plant was recorded in cluster VIII (25.20), whereas less number of secondary branches per plant was observed in cluster V (2.78). Cluster VII (89.50) had more number of pod cluster per plant, while cluster V (29.93) had less number of pod clusters per plant. Bold seeded genotypes were found in cluster VIII (13.12) and small seeded genotypes were found in cluster V (7.93). Genotypes fall in cluster VII (94.00) were high yielder, while low yielding genotypes fall in cluster V (15.14). Genotypes were having highest protein content was present in cluster II (22.76), whereas lowest protein content observed in cluster VII (21.20). The data indicated GJP-1 used as a parent in breeding programme for development of genotype with bold seeded with more number of secondary branches per plant and use BDN-2 for development of variety with more number of pods per plant.

The inter cluster and intra cluster variances along with ratio R^2 (inter cluster variance to the total variance) were estimated for all the twelve characters and represented in Table 3. R^2 value gives an idea about contribution of individual characters to the total diversity (Dixit 1984). Maximum extent of R^2 value was found for a character days to maturity (0.92) followed by pods per plant (0.91), number of pod clusters per plant (0.90) and yield per plant (0.90). Therefore characters *viz.*, days to maturity, numbers of pods per plant), number of pod clusters per plant (0.90) and yield per plant (0.90) are considered as important characters in discrimination of different genotypes under study.

Above results concluded that maximum genetic divergence was observed between cluster V and VII and cluster V and VI indicate the large genetic deference among the genotypes, hence genotypes *viz.*, ICPL series including PAU-881 and BDN-2 can be used in hybridization programme. The characters, *viz.*, days to maturity, number of pods per plant, number of pod clusters per plant and 100 seed weight contributed much to the total genetic divergence. On the basis of cluster mean values, cluster VII was superior for seed yield per plant and number of pod clusters per plant, whereas cluster VII was good for pods per plant and cluster VIII was good for 100- seed weight.

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