VARIABILITY AND GENETIC DIVERGENCE AMONG INTERSPECIFIC DERIVATIVES OF PIGEONPEA [(CAJANUS CAJAN (L.) MILLSP.]

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Abstract: Genetic diversity and information on gene action are of vital importance for crop improvement because they generate baseline data to guide selection of parental lines and design of breeding scheme. In the present study variability parameters and D2 cluster analysis were used to assess the genetic divergence among 44 interspecific derivatives and 12 advanced breeding lines of pigeonpea. The Analysis of variance revealed significant differences among the genotypes for all the 8 traits studied. High values of Phenotypic coefficient of variability (PCV) and genotypic coefficient of variability (GCV) were observed for Seed yield, Number of Secondary branches/plant (NSB/P) and Number of Pods/Plant. Low PCV and GCV were recorded for Days to 50 per cent flowering, Days to maturity and Test weight. Moderate heritability coupled with high genetic advance over mean was obtained for the number of pods/plant and seed yield. Maximum inter cluster distance was observed between cluster V and cluster VI while minimum genetic distance was observed between cluster I and cluster V. Based on the data on inter cluster distances, cluster means and per se performance, the study identified eight breeding lines namely ICPL15057, ICPL 15065, ICPL 99102, WRGE 107, WRGE 101, WRGE 92, WRGE 102 and WRGE 109 as potential parents for crossing with PRG 176 in developing high yielding mid early duration pigeonpea varieties. Days to fifty percent flowering contributed maximum to the total genetic divergence (65.8%) followed by seed yield (9.8 %) and plant height (6.04 %).

Keywords: Heritability, Genetic Advance, Multivariate Analysis, Principal Components.

Introduction: Pigeonpea is the second most important pulse crop of India after chickpea. 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. The crop has diversified uses such as food, feed, fodder and fuel. It is a rich source of protein, carbohydrate, vitamins, lipids and certain minerals. Annually pigeonpea is grown in an area of 5.83 M ha in the world producing 4.40 M t with a productivity of 754.9 kg/ ha. India has 5.06 million hectares area under pigeonpea cultivation and contributes about 3.29 million tonnes i.e. 67.7 % of the world production, with an average productivity of 650 Kg/ha (FAOSTAT, 2016). Several reasons were attributed for its low productivity among which narrow genetic base has been the major issue. Wild relatives of pigeonpea have been recently used to transfer several biotic and abiotic stress resistance genes and to improve the genetic base of cultivated pigeonpea. The putative progenitor species of cultivated pigeonpea *i.e. C. cajanifolius* and the species *C. acutifolius* which belong to the secondary gene pool contributed for

resistance to pests such as podborer,podfly, bruchids, disease resistance such as *Fusarium* wilt, *Phytophthora* blight, improved nutritional quality and drought tolerance (Mallikarjuna *et al* 2005, 2011).

Success in crop improvement programmes depends upon the extent of genetic variability/diversity in the germplasm, selection of appropriate parents for crossing and selection procedure adopted. Compared to other food legumes breeding in pigeonpea has been more challenging due to various crop specific traits and high sensitivity to biotic and abiotic stresses. The target of any plant breeding programme is to develop improved genotypes which are better than the existing ones in producing the economic yield.

The information about the nature and magnitude of genetic diversity existing in the available germplasm of a particular crop is crucial for selection of diverse parents, which upon hybridization may provide a wide spectrum of gene recombination for quantitatively inherited traits such as seed yield. The present experiment has been undertaken to study the variability and genetic diversity among the 56 pigeonpea genotypes and thereby identify divergent parents from among them suitable for development of high yielding mid early duration pigeonpea varieties suitable for different soil types in the state of Telangana

Materials and Methods: The material comprised of 56 pigeonpea genotypes of which 44 were interspecific hybridization derived lines developed by crossing the wild species *Cajanus cajanifolius and Cajanus. acutifolius* with the cultivated species *Cajanus cajan* at International crop Research institute for semiarid tropics (ICRISAT). 4 were check varieties namely Maruti (ICP 8863), Asha (ICPL 87119), PRG 176 (elite mid early duration variety), CoRG 9701 and 8 were advanced breeding lines obtained from Regional Agricultural Research Station, Warangal. The present study was carried out in *Kharif* 2016-17 at Agricultural research Station, Tandur. The experimental site is located at 770 35' East longitude and 17° 15' North latitude and at 553.18m above Mean Sea Level. Each Genotype was sown in 4 rows of 4m length with a spacing of 120 cm between the rows and 15 cm within the row. The experiment was laid out in a randomized block design with 3 replications. Recommended package of practices were followed to raise a normal crop. In each genotype, five randomly selected plants were used to collect data on eight characters namely Days to 50% flowering (DFF), Days to maturity (DM), Plant height (PH, cm), Number of primary branches/plant (NPB/P), Number of Secondary branches/plant (NSB/P), Number of Pods/Plant (NP/P), Test weight (TW, g) and Seed yield (SY, Kg/ha)). The data was subjected to analysis of variance and covariance (Panes and Sukhatme, 1954), genotypic (GCV) and phenotypic coefficient of variation (PCV), heritability and genetic advance as per the method suggested by Johnson *et al* (1955).

The multivariate analysis of genetic divergence using D2 statistic (Mahalanobis, 1936) was carried out as described by Rao (1952). The data was analysed by INDOSTAT services Ltd (version 8.5), Hyderabad, India. The percent contribution of each character to the total divergence was calculated by ranking each character on the basis of transformed uncorrelated values. Rank 1 was given to the highest mean difference and for the lowest mean difference where n is the total number of characters. Finally the percent contribution for each character was calculated by taking total number of ranks of all the characters to hundred. Principal component analysis was done by using INDOSTAT software. The Principal components (PC) were used to determine the extent of genetic variation. Eigen-values were obtained from PC, which were used to determine the relative discriminative power of the axes and their associated characters.

Results and Discussion:

ANOVA: The analysis of variance revealed significant differences among the genotypes studied as the mean sum of squares (MSS) of the eight traits were found to be highly significant (Table 1). This variation provides ample scope for the plant breeder in selection of superior genotypes for crop improvement

Variability: Effectiveness of selection depends on the magnitude of genetic variability for a particular trait. Hence, the coefficients of variation expressed in percentage at phenotypic (PCV) and genotypic (GCV) levels have been used to compare the variability observed among the different characters. The PCV was higher than the GCV (Table 2) for almost all the traits which indicates that the traits were highly influenced by environment. High values of PCV and GCV were observed for Seed yield, Number of Secondary branches/plant (NSB/P) and Number of Pods/Plant as reported by Birhan *et al* (2013). Low PCV and GCV were recorded for days to 50 per cent flowering, days to maturity and test weight in conformity with earlier reports (Basavarajaiah *et al.* 2000, Gohil 2006b, Singh *et al.* 2008).

The effectiveness of selection for any character depends not only on the extent of genetic variability but also to the extent to which it is transferred from one generation to the next.

High heritability estimates were observed for days to 50% flowering (98%) and days to maturity (98%) (Table 2). Moderate heritability was observed for plant height (75%), seed yield (74%) and number of pods/plant (66%). This indicates the major role of additive genes in governing these traits and lesser influence of environment. Lower heritability values were reported for test weight (57%) and number of primary branches/plant (29%) indicating the role of non additive gene action and greater influence of environment in governing these traits. Similar findings were reported by Niranjana Kumara *et al* (2013).

Days to 50% flowering showed high heritability coupled with low genetic advance indicating the presence of non-additive gene effects and high genotype and environment (G x E) interaction. This reiterates the fact that it is difficult to make the progress in developing early maturing but high yielding genotypes. Moderate heritability coupled with high genetic advance over mean was obtained for the number of pods/plant and seed yield. These results are in confirmation with the results of Patel and Acharya, 2011, Basavarajaiah *et al.* (2000), Gohil, (2006b) and Singh *et al.* (2008).

Cluster Analysis: Based on D^2 analysis, the 56 genotyps were grouped into 6 clusters with variable number of entries in each cluster (Table 3). Cluster I had maximum number of genotypes i.e. 51 while cluster II, III, IV, V and VI represented single genotype each which independently diverged from others (Fig 1). The formation of solitary clusters may be due to total isolation preventing the gene flow or intensive natural/human selection for diverse adaptive complexes. These genotypes may be very unique and useful in breeding point of view. The major cluster consisted of 44 interspecific derivatives from ICRISAT, one check variety Asha and 6 advanced breeding lines from Warangal indicating their proximity and narrow genetic base. The elite short duration variety PRG 176 released from Telangana suitable for shallow soils, CoRG 9701 the short duration variety from Tamil Nadu, Maruti, the premium quality redgram variety released in seventy,s and two Warangal advanced breeding lines WRGE 101 and WRGE 109 diverged in to separate clusters. Earlier workers have also reported substantial genetic divergence in pigeonpea using D2 analysis (Sawant *et al.,* 2009; Bhadru, 2011; Pratap *et al*., 2011).

In order to increase the possibility of isolating good segregants in the segregating generations it is logical to attempt crosses between the diverse genotypes belonging to clusters with large inter-cluster distance. In the present study Average inter cluster D^2 values among 56 genotypes (Table 4) revealed maximum inter cluster distance values between cluster V and cluster VI (D=21.76) followed by cluster IV and cluster VI (D=16.98) and cluster I and Cluster V (D=16.89) while minimum genetic distance was observed between cluster II and cluster III (D=1.65). The data on cluster means (Table 5) revealed considerable differences among the clusters for the 8 traits studied. The cluster V recorded the least value for days to 50% flowering and days to maturity. So the genotypes of I cluster need to be crossed with genotypes of cluster V to develop short duration cultivars suitable for light textured soils. Genotypes of I cluster need to be crossed with Cluster II and Cluster III for improvement of seed yield. Genotypes of cluster I are to be crossed with PRG 176 (cluster IV) to develop high yielding mid early duration varieties with high pod number.

The genotypes of cluster I exhibited best agronomic performance with reference to higher cluster means for seed yield. Based on the data on cluster means and per se performance three interspecific derivatives namely ICPL15057, ICPL 15065, ICPL 99102 and five advanced breeding lines from Warangal namely WRGE 107, WRGE 101, WRGE 92, WRGE 102 and WRGE 109 can be deployed in crossing with PRG 176 to develop high yielding mid early duration types suitable for light textured soils of Telangana. Intercrossing of divergent groups leads to wide genetic base in the base population and greater opportunities for crossing over to occur, which releases hidden variability by breaking the close linkages (Thoday, 1960).

Principal Component Analysis: Information on the relative contribution of various plant characters towards the total divergence aids the breeder in the choice of parents for hybridization and effective selection. Among the 8 traits studied (Table 6), days to 50% flowering contributed the most (65.8 %) to the total genetic divergence followed by seed yield (9.8 %) while number of primary branches/plant recorded the least contribution (1.1 %). Similar results were reported by Firoz *et al*. (2006), Samal *et al*. (2001), Viramgama and Goyal, (1994), Sarma & Roy, (1994) and Singh *et al*. (2010). Principal component analysis divided the variance exhibited by these eight traits in to three components which cumulatively explained 92 % of the total variance

(Table 7). The PC 1 is the most important component accounting to 81.2 per cent while PC 2 and PC3 explained 7.7 % and 3.5 % respectively. The traits days to 50% flowering, days to maturity and plant height significantly loaded in PC1 contributed to maximum variability.

Conclusion: 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 is recommended for isolating desirable recombinants in the segregating generations. Based on the data on inter cluster distances, cluster means and per se performance, the study identified eight advanced breeding lines namely ICPL15057, ICPL 15065, ICPL 99102, WRGE 107, WRGE 101, WRGE 92, WRGE 102 and WRGE 109 as potential parents for crossing with PRG 176 in developing mid early duration pigeonpea varieties. Selection based on the number of pods/plant and seed yield/plant would be effective for deriving more genetic gain as they reported moderate heritability and high genetic advance.

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Table 1: Analysis of Variance (ANOVA) for the Yield Attributing Traits

S. No.	Trait	Genotype mean sum of squares	Replication mean sum of squares	Error mean sum of squares	CD at 5%	CD at 1%
1	Days to 50% flowering	360.2**	5.1	1.8	2.2	2.9
2	Days to maturity	373.8**	5.5	1.7	2.1	2.7
3	Plant height (cm)	1432.5**	1081.4	141.1	19.2	25.4
4	No of primary branches/plant	10.8**	9.8	1.7	2.1	2.8
5	No of secondary branches/plant	91.5**	69.9	22.0	7.6	10.0
6	No of Pods/plant	67993.6**	46834.7	9782.7	160.0	211.6
7	Test wt (g)	2.9**	2.5	0.6	1.2	1.6
8	Seed yield (kg/ha)	463944.5**	18414.8	47950.6	354.3	468.6

** **1% Level of Significance**

Table 2: Variability Parameters

Trait	Mean	GCV %	PCV %	% Heritability	GA		GA as % of mean	
					5%	1%	5%	1%
Days to 50% flowering	121.2	9.0	9.0	0.98	22.3	28.6	18.4	23.6
Days to maturity	171.6	6.4	6.5	0.98	22.7	29.2	13.2	17.0
Plant height (cm)	164.6	12.6	14.5	0.75	37.0	47.5	22.5	28.8
No of primary branches/plant	6.4	13.0	24.2	0.29	0.93	1.19	14.4	18.5
No of secondary branches/plant	27.1	17.7	24.7	0.51	7.09	9.08	26.0	33.4
No of Pods/plant	550	25.3	31.0	0.66	233.9	299.8	42.5	54.5
Test wt (g)	9.5	9.2	12.2	0.57	1.38	1.77	14.4	18.4
Seed yield (kg/ha)	2071	17.9	20.8	0.74	661.2	847.4	31.9	40.9

Table 3: Clustering Pattern of the Pigeonpea Genotypes Based on D^2 Statistics

Cluster No.	No. of Genotypes	Genotypes
1	51	ICPL15003, ICPL 15004, ICPL 15006, ICPL 15007, ICPL 15010, ICPL 15014, ICPL 15017, ICPL 15019, ICPL 15023, ICPL 15021, ICPL 15024, ICPL 15030, ICPL 15034, ICPL 15040, ICPL 15041, ICPL 15042, ICPL 15046, ICPL 15054, ICPL 15057, ICPL 15058, ICPL 15060, ICPL 15062, ICPL 15065, ICPL 15067, ICPL 15071, ICPL 15072, ICPL 15075, ICPL 15077, ICPL 15079, ICPL 15085, ICPL 14001, ICPL 14002, ICPL 96053, ICPL 96058, ICPL 99046, ICPL 99050, ICPL 99092, ICPL 99102, TDRG 5, TDRG 107, ICPL 20108, ICPL 20116, ICPL 20123, ICPL 20125, Asha (ICPL 87119), WRGE 90, WRGE 92, WRGE 93, WRGE 102, WRGE 107, WRGE 108,
2	1	WRGE 109
3	1	WRGE 101
4	1	PRG 176
5	1	CoRG 9701
6	1	Maruti (ICP8863)

Table 4: Average Intra and Inter Cluster Distances among 6 Clusters of the Germplasm

	cluster1	cluster2	cluster3	cluster4	cluster5	cluster6
cluster1	6.84	9.05	9.24	12.14	16.89	12.45
cluster 2	9.05	0.00	1.65	5.69	10.16	14.68
cluster 3	9.24	1.65	0.00	6.09	9.75	15.02
cluster 4	12.14	5.69	6.09	0.00	7.95	16.98
cluster 5	16.89	10.16	9.75	7.95	0.00	21.76
cluster 6	12.45	14.68	15.02	16.98	21.76	0.00

Table 5: Cluster Means for Eight Yield and Yield Attributing Traits among Pigeonpea Genotypes

Cluster	DFF	DM	PH	NPb/P	NSb/p	NP/P	TW	SY
Cluster1	122.9	173.0	164.1	6.4	27.5	553.9	9.5	2060.5
Cluster2	108	158	175.4	5.5	18.8	396.7	10.5	2887.8
Cluster3	107.6	157.6	148.2	5.8	15.8	341.2	11.5	2615.2
Cluster4	99.3	149.3	176.2	4.1	32.6	875.6	8.5	2347.5
Cluster5	88.6	138.6	153.5	9.2	13.8	230.4	9.2	995.8
Cluster6	117.6	183	194.6	6.9	33.8	700.2	9.8	2041.6

Table 6: Percent Contribution of Different Traits to the Total Genetic Divergence

S.No.	Source of variation	Times ranked first	% Contribution
1	Days to 50% flowering	1013	65.78
2	Days to maturity	69	4.48
3	Plant height (cm)	93	6.04
4	No of primary branches/plant	17	1.10
5	No of secondary branches/plant	21	1.36
6	No of Pods/plant	76	4.94
7	Test wt (g)	100	6.49
8	Seed yield (kg/ha)	151	9.81

Table 7: Principal Component Analysis Depicting the Variance Explained by The First Three Principal Components

Particulars	PC1	PC 2	PC3
Eigen value (Root)	144.4	137.2	62.7
% variance explained	81.20	7.71	3.52
Cum. variance explained	81.20	88.91	92.43
Days to 50% flowering	0.89068	0.38839	0.16794
Days to maturity	0.40970	-0.78562	-0.22575
Plant height (cm)	0.09575	-0.32495	0.31478
No of primary branches/plant	-0.07124	0.19069	-0.18359
No of secondary branches/plant	-0.02203	-0.11169	-0.15264
No of Pods/plant	0.07873	-0.14935	-0.06238
Test wt (g)	-0.11173	-0.22640	0.36065
Seed yield (kg/ha)	-0.07362	-0.06294	0.79422

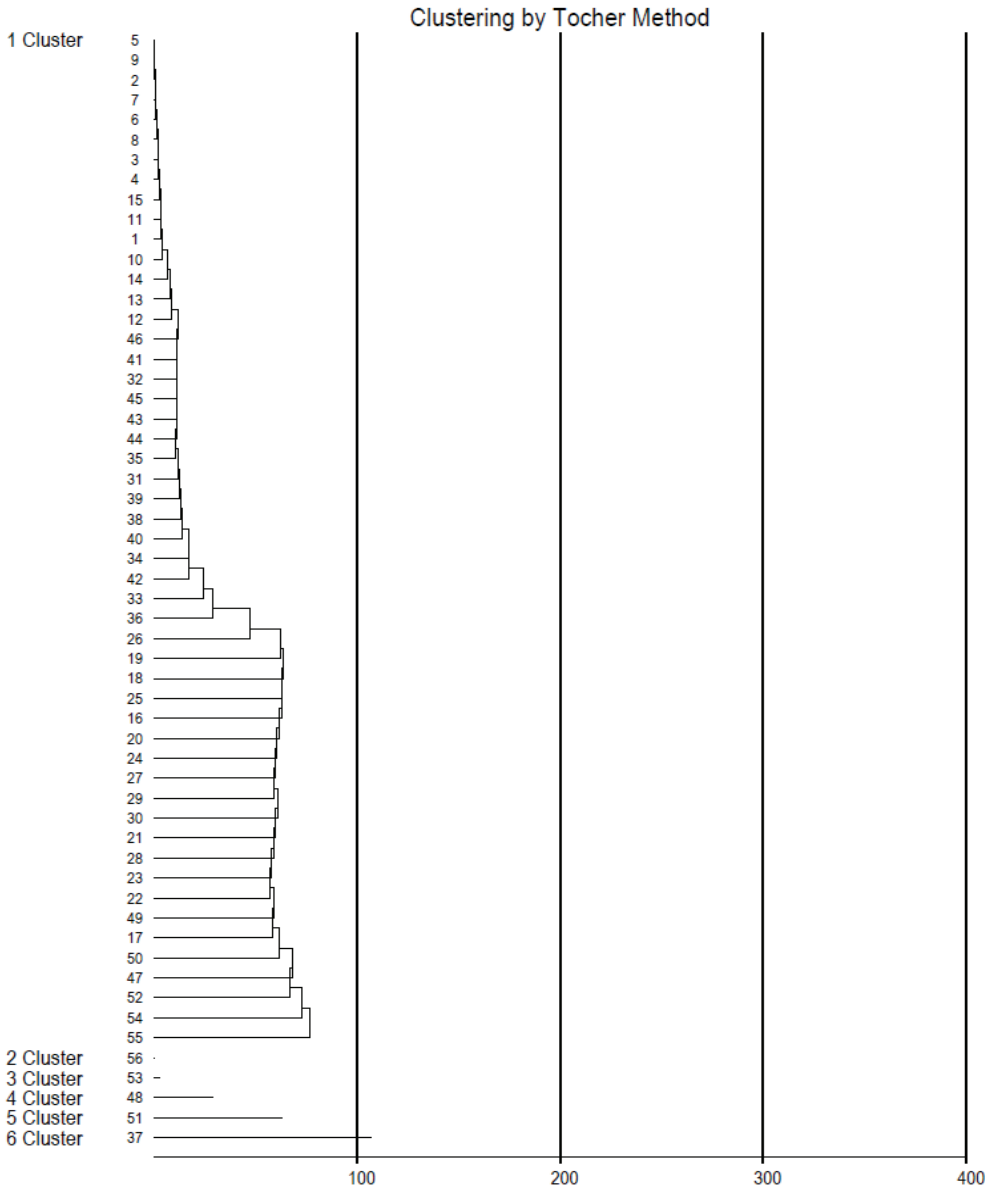

Fig1: Clustering of Pigeonpea Genotypes Based on D2 Analysis

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